Uncoupling of Chondroitin Sulfate Glycosaminoglycan Synthesis by Brefeldin A

Robert C. Spiro,* Hudson H. Freeze,‡ Deepak Sampath,‡ and Joseph A. Garcia*

*Department of Immunology, The Scripps Research Institute, La Jolla, California 92037; and ‡Glycobiology/Carbohydrate Chemistry Program, The La Jolla Cancer Research Foundation, La Jolla, California 92037

Abstract. Brefeldin A has dramatic, well-documented, effects on the structural and functional organization of the Golgi complex. We have examined the effects of brefeldin A (BFA) on the Golgi-localized synthesis and addition of chondroitin sulfate glycosaminoglycan carbohydrate side chains. BFA caused a dose-dependent inhibition of chondroitin sulfate glycosaminoglycan elongation and sulfation onto the core proteins of the melanoma-associated proteoglycan and the major histocompatibility complex class II-associated invariant chain. In the presence of BFA, the melanoma proteoglycan core protein was retained in the ER but still acquired complex, sialylated, N-linked oligosaccharides, as measured by digestion with endoglycosidase H and neuraminidase. The initiation of glycosaminoglycan synthesis was not affected by BFA, as shown by the incorporation of [6-3H]galactose into a protein–carbohydrate linkage region that was sensitive to β-elimination. The ability of cells to use an exogenous acceptor, p-nitrophenyl-β-D-xylloside, to elongate and sulfate core protein-free glycosaminoglycans, was completely inhibited by BFA. The effects of BFA were completely reversible in the absence of new protein synthesis. These experiments indicate that BFA effectively uncouples chondroitin sulfate glycosaminoglycan synthesis by segregating initiation reactions from elongation and sulfation events. Our findings support the proposal that glycosaminoglycan elongation and sulfation reactions are associated with the trans-Golgi network, a BFA-resistant, Golgi subcompartment.

The biosynthesis of glycosaminoglycan (GAG) carbohydrate side chains involves an extensive series of posttranslational enzymatic reactions that occur during the intracellular transport of core proteins from the ER through the Golgi complex. These reactions use specific initiation, elongation, and sulfation enzymes to modify appropriate core proteins and assemble them into mature proteoglycan molecules. For chondroitin sulfate (CS) GAGs, the carbohydrate–protein linkage region is initiated by a xylosyltransferase that transfers xylose from UDP-xylose to the hydroxyl groups of specific serine residues within a core protein. Initiation is completed by the addition of two galactosyl and one glucuronosyl residue through the action of galactosyltransferase I, II, and glucuronosyltransferase I, respectively. Once initiated, the repeating disaccharide backbone of glucuronosyl and N-acetylgalactosaminyl residues is elongated by specific glucuronosyl- and N-acetylgalactosaminyltransferases. Sulfation of the repeating disaccharides by the 4- and/or 6-sulfotransferases completes the synthesis of mono- or disulfated CS (27) (see Fig. 11 for summary).

It is generally accepted that GAG synthesis is a Golgi complex-related event. Early studies using electron microscopy and radioautography showed that the Golgi complex is the major site of GAG chain synthesis (21, 24, 25). Golgi-enriched preparations isolated from some cell types have also been shown to contain GAG synthesizing activity (32). More recent studies examining the kinetics of entry of radiolabeled sugars into GAG chains, as well as the localization of GAG sugar nucleotide and sulfate donor transport systems, have clearly localized GAG synthesis to the Golgi complex (14, 18, 23). The exact spatial organization of the cascade of enzymatic reactions involved in GAG synthesis is not known, due, in part, to the lack of understanding of the dynamics and spatial differentiation of the Golgi complex.

The Golgi complex can be divided into at least four distinct regions, the cis-, medial, and trans-Golgi and the trans-Golgi network (TGN) (2, 5, 12, 13, 15). The specific changes induced by the fungal metabolite, brefeldin A (BFA), have provided new information on how the structural organization of the Golgi complex relates to function. BFA dramatically, yet reversibly, alters Golgi morphology and function by disrupting the budding of nonclathrin-coated transport vesicles responsible for anterograde movement (3, 22). The result is a block in anterograde protein transport out of the ER (20) and a redistribution of cis-, medial, and trans-Golgi–resident enzymes back to the ER through a retrograde, microtubule-dependent pathway (16, 17). In contrast, the compartmen-
tialization processes involved in the formation of the TGN, lysosomes, and endocytic vesicles are resistant to the redistribution induced by BFA (2, 20).

The aim of this study was to further define the dynamic topology of GAG synthesis using BFA and the human melanoma-associated proteoglycan (MPG) model system. We demonstrate that BFA reversibly uncouples GAG chain initiation from elongation and sulfation events. In the presence of BFA, the MPG core protein is retained in the ER and acquires complex N-linked oligosaccharides but is not converted to a CS proteoglycan form. In addition, BFA-treated cells fail to elongate and sulfate GAG chains onto the exogenous, artificial GAG acceptor, p-nitrophenyl-β-D-xyloside (βDX). Initiation of GAG synthesis in the presence of BFA proceeds through to the addition of the xylosyl residue and the galactosyl residues of the carbohydrate-protein linkage region. These results indicate that GAG chain elongation and sulfation are BFA-resistant events which are associated with the TGN.

Materials and Methods

Materials

BFA was obtained from Sandoz Pharmaceuticals (Basel, Switzerland). Deoxynojirimycin (DMJ) and endoglycosidase H (endo-β-N-acetyl-
glucosaminidase) were purchased from Boehringer Mannheim Diagnostics, Inc. (Indianapolis, IN) and Genzyme Corp. (Boston, MA). Sephadex G-25 PD-10 columns and protein A-Sepharose CL-4B were purchased from Pharmacia Fine Chemicals (Piscataway, NJ). [35S]Methionine (1,295 Ci/mmol), [35S]sulfate (25-40 Ci/mmol), [6-3H]galactose (25.5 Ci/mmol) and NaF (15.8 mCi/μg) were obtained from Amersham Corp. (Arlington Heights, IL). All reagents used for cell surface iodination procedures (Enzymobeads) and SDS-PAGE were purchased from Bio-Rad Laboratories (Richmond, CA). Neuraminidase (Clostridium perfringens or Vibrio cholera), chondroitinase ABC, chondroitin sulfate A and C carriers, βDX, FITC- and TRITC-conjugated wheat germ agglutinin (WGA) and anti-mouse immunoglobulin antibodies were from Sigma Chemical Co. (St. Louis, MO). Cytokinetin was purchased from Calbiochem-Behring Corp., San Diego, CA. The A5HPLC column was purchased from Varian Instruments (Palo Alto, CA). β-Galactosidase (chicken liver) was purchased from Oxford Glycosystems (Rosedale, New York). [14C]AcAsnMan3GlcNAc2 glycopeptide was prepared as previously described (6). All other materials were reagent grade.

Cell Lines and Treatment with Inhibitors

The M21 human melanoma cell line is a subclone, propagated in our laboratory, of the UCLA-SO-M21 cell line provided by Dr. D. L. Morton (UCLA, Los Angeles, CA). The UACC-903 human melanoma cell line was provided by Dr. J. M. Trent (University of Michigan, Ann Arbor, MI). The human B-lymphoblastoid cell line, Raji, was obtained from Dr. A. N. Theofilopoulos (The Scripps Research Institute, La Jolla, CA) and was produced as described previously (10). Sera from preimmunized rabbits or fusion partner culture supernatants served as negative controls in all immunoprecipitation experiments.

Radiolabeling and Immunoprecipitation Analysis

Metabolic radiolabeling, cell surface iodination, and immunoprecipitation of specific antigens were performed as described previously (33, 34). 5–8 × 106 cells per sample were used in all experiments. Labeling with [6-3H]galactose was carried out in glucose culture media (DME, 1,000 mg glucose/liter or RPMI 1640, 0.1 mg glucose/ml) with 100 μCi/ml of [3H]galactose for 4-6 h at 37°C. The choice of [6-3H]galactose is important because it cannot be converted into [3H]glucuronic acid. Quantitation of SDS-PAGE profiles was performed by densitometric scanning of autoradiographs.

Quantitation of Proteoglycans and β-D-Xyloside-initiated GAGs

The quantitation of [35S]sulfate-labeled macromolecules was carried out as previously described (33, 34).

Isolation of [3H]Galactose-labeled Molecules

Immunoprecipitates isolated with mAb 9.2.27 from [6-3H]galactose-labeled cells were washed extensively in PBS containing 0.5% Tween-20 and 1 mg/ml ovalbumin. [3H]Galactose-labeled O-linked oligosaccharides were then released from the MPG core protein by treatment with 20 μl of 0.05 N NaOH and 0.3 M NaBH4, overnight at room temperature. The released chains were neutralized with acetic acid and evaporated three times in MeOH/CH2OAc to remove borate salts. The sample was diluted to 1.5 ml in 2-mM Tris base and passed over a 2-cm column of QAE-Sephadex equilibrated in 2 mM Tris. Neutral species that ran through the column (56% of the starting material) were desalted on a mixed bed ion exchange resin (MB3). Recovery was >90%.

HPLC Analysis of Neutral Oligosaccharides

Neutral oligosaccharides were analyzed on an AXS anion-exchange column using a 40–80% gradient of acetonitrile in 25 mM NaPO4, pH 6.5, at 30 min at a flow rate of 1 ml/min. Fractions of 0.5 ml were counted. Each run included an internal standard of 14C-chetrol and an ovalbumin glycopeptide, [14C]AcAsnMan3GlcNAc2; β-galactosidase digests were carried out in 50 μl of 100-mM citrate-P04 buffer at pH 4.5 for 16 h at 37°C using 0.05 U of enzyme.

Immunofluorescence Microscopy

M21 cells were grown on 12-mm round glass coverslips placed in 24-well culture dishes and pretreated with BFA for 1 h at 37°C. The coverslips were then washed in ice-cold PBS/0.1% BSA and fixed immediately in a 3% paraformaldehyde solution in 0.1 M sodium phosphate, pH 7.4, for 15 min on ice. The coverslips were then washed in PBS followed by 0.1 M glycine. Cell surface immunofluorescence was blocked before permeabilization with a human/mouse chimeric form of mAb 9.2.27, containing human heavy and light chain constant regions (11), and with WGA for 30 min at room temperature. The fixed and blocked cells were then permeabilized in 0.15% saponin in PBS/0.1% BSA for 15 min and incubated with primary antibody for 1 h at room temperature. After washing, the coverslips were incubated with fluorescently labeled anti-mouse secondary antibody or WGA for 1 h at room temperature, washed and mounted on glass slides in Fluoromount G (Southern Biotechnology Assoc., Birmingham, AL). Mounted slides were viewed with a 100 X oil Neofluor lens on a microscope (both from Carl Zeiss, Inc., Thornwood, NY) equipped with barrier filters to prevent crossover of fluorescein and rhodamine fluorescence.

Results

BFA Inhibits CS GAG Chain Elongation and Sulfation on the MPG Core Protein

The human melanoma MPG antigen recognized by mAb 9.2.27 is synthesized initially as a 240-kD precursor that con-
Figure 1. Effect of BFA on the synthesis and assembly of the MPG.
M21 cells were pretreated with the indicated concentrations of BFA for 1 h before a 4-h label with [35S]methionine at 37°C in the presence of drug. The MPG complex was then isolated from detergent lysates of cells by immunoprecipitation with mAb 9.2.27 and was subjected to SDS-PAGE (5% gel) and autoradiography. A dose-dependent inhibition of the conversion of the 240-kD form to the 250-kD and proteoglycan form (PG) is observed in the presence of BFA. Molecular mass standards are in kilodaltons.

Figure 2. BFA inhibits sulfation, cell surface expression and release of the MPG. M21 cells were pretreated in the presence or absence of BFA (1 μg/ml) for 1 h before a 3-h label with either [35S]sulfate (left panel) or [35S]methionine (right panel) at 37°C in the presence and absence of the drug. The MPG complex was then isolated from either detergent cell lysates or dialyzed spent media by immunoprecipitation with mAb 9.2.27. Cell surface analysis (middle panel) was performed on M21 cells harvested by trypsin treatment to remove the cell surface MPG component. Harvested cells were incubated in suspension for 4 h at 37°C in the presence or absence of BFA (1 μg/ml) to allow recovery of the cell surface MPG. Cell surface iodination was then performed as previously described (33) and MPG complexes were isolated from detergent lysates (5% gel). No forms of the MPG complex are observed in [35S]sulfate-, cell-surface-, or spent media–labeled samples prepared in the presence of BFA. Molecular mass standards are in kilodaltons. PG designates the proteoglycan form of the MPG.

BFA Blocks MPG Core Protein Transport out of the ER

The complete transport and assembly of the MPG complex results in the expression of both the 250-kD and proteoglycan components on the cell surface (33, 34). Truncated forms of both these species are also released into the culture media (Spiro, R., unpublished observation). MPG forms could not be isolated from either 125I cell surface–labeled M21 cells that were trypsinized and pretreated with BFA or from the [35S]methionine-labeled culture media of such cells (Fig. 2, middle and right panels). The absence of MPG cell surface expression and release is consistent with an arrest in intracellular transport of the core protein. To determine the subcellular site of the arrest, the distribution of the MPG core protein in the presence of BFA was examined by immunofluorescence microscopy with mAb 9.2.27. The MPG complex shows a localized perinuclear staining pattern in fixed and permeabilized M21 cells when stained with mAb 9.2.27 and a FITC-conjugated secondary antibody (Fig. 3A). This staining pattern is typical of the Golgi complex as confirmed by the co-localization of the TRITC-
Figure 3. BFA blocks MPG transport at the ER level. M21 cells were treated without (A and B) or with (C and D) 1 μg/ml BFA for 1 h before fixation, blocking, and permeabilization as described in Materials and Methods. Cells were then incubated with mAb 9.2.27 and fluorescently labeled secondary antibody (A and C) or with fluorescently labeled wheat germ agglutinin (B and D). A and C were photographed with fluorescein optics and B and D with rhodamine optics. BFA causes a morphologic redistribution of the Golgi complex. The MPG core protein shows an ER-like distribution in the presence of BFA. Bar, 10 μm.

The MPG N-linked Oligosaccharides Are Processed in BFA-treated Cells

The BFA-induced effects on the Golgi complex have been previously shown to cause a redistribution of cis-, medial, and trans-Golgi-resident enzymes back to the ER (2, 16, 17). To examine if Golgi enzymes are redistributed in BFA-treated melanoma cells, the processing of the MPG core protein N-linked oligosaccharides was monitored by endo H digestion of MPG immunoprecipitates isolated from M21 cells pretreated, pulse labeled, and chased in the presence of BFA. Immediately after the pulse label, the 240-kD form of the MPG is susceptible to endo H digestion in both control and BFA-treated cells. After 15–30 min, and throughout the remainder of the chase period in control cells, the 240-kD precursor is converted to the 250-kD, endo H-resistant form and the high molecular mass CS proteoglycan (Fig. 4 A) (33, 34). In BFA-treated cells, the 240-kD form gradually acquires endo H resistance during the chase period and becomes completely resistant by 9 h. This acquisition of endo H resistance is accompanied by a slight increase in molecular mass, but complete conversion to the 250-kD or the proteoglycan form is inhibited by BFA (Fig. 4 A). Neuraminidase digestion of the MPG isolated from cells labeled with [35S]methionine for 1 h and chased for 3 h in the presence of BFA results in a shift in mobility of the core protein, indicating the acquisition of sialic acid residues (Fig. 4 B). These results are consistent with the recycling, back to the ER, of the Golgi resident enzymes that trim and terminally process the N-linked oligosaccharides of the ER-retained MPG core protein. The absence of the proteoglycan form of the MPG suggests that the redistribution of CS GAG enzymes to the ER does not occur or that their redistribution results in a loss of functional activity.

BFA Does Not Block Initiation of CS GAG Synthesis on the MPG Core Protein

The extent of CS GAG chain initiation occurring in the presence of BFA was evaluated by metabolically labeling the carbohydrate–protein initiation linkage region (Ser-Xyl-Gal-Gal-GlcUA) with [6-3H]galactose. Pretreatment of cells with DMJ was used to inhibit the labeling of complex N-linked oligosaccharides, thereby limiting the incorporation of [3H]galactose exclusively to O-linked oligosaccharides. DMJ has previously been shown to block the processing of the MPG core protein N-linked oligosaccharides at the high mannose stage without affecting conversion to the pro-
teoglycan form (34) (Fig. 5, left side). In control M21 cells labeled with \[^3\text{H}\]galactose, label is incorporated into both the 250-kD and proteoglycan forms of the MPG complex (Fig. 5, right side). In cells pretreated with DMJ, incorporation into the core protein form is blocked by 97%, but is only partially reduced in the proteoglycan form. Cells pretreated with BFA also incorporate \[^\text{3H}\]galactose into the MPG core protein, even in the presence of DMJ (Fig. 5, right side). This result is consistent with the addition of the xylosyl residue and at least one of the galactosyl residues of the GAG carbohydrate–protein linkage region in the presence of BFA.

To precisely determine the effects of BFA on the synthesis of the carbohydrate–protein linkage region, the \[^\text{3H}\]galactose-labeled sugar chains were released from the MPG core protein by \(\beta\)-elimination and their size and charge were analyzed by HPLC and QAE-Sephadex ion exchange chromatography, respectively. About 56% of the released chains are neutral, and two peaks are seen in HPLC analysis (Fig. 6). \(\beta\)-galactosidase digestion eliminates both peaks and generates a monosaccharide peak, presumably free \[^\text{3H}\]galactose, which elutes slightly later than the \(^{14}\text{C}\)-fucitol standard, as expected (7). The major peak is probably the linkage region, XylH \(\beta\)\(1\rightarrow4\)-Gal \(\beta\)\(1\rightarrow3\)-Gal, and the minor peak is probably XylH \(\beta\)\(1\rightarrow4\)-Gal. Chromatography on QAE-Sephadex showed that 43% of the labeled material carries one to three negative charges, based on comparison with appropriate standards (data not shown). The characterization and identity of this material will be reported elsewhere. These results suggest that the BFA-induced block in the MPG GAG chain elongation and sulfation is not due to a complete block in the initiation events.

**BFA-treated Cells Fail to Synthesize GAG Chains onto Xyloside Acceptors**

To evaluate the activity of the GAG chain enzyme machinery
in the presence of BFA, independent of the MPG core protein, treated cells were tested for their ability to elongate and sulfate GAG chains onto the exogenous acceptor, βDX. As an artificial GAG acceptor, βDX diffuses freely into cells to the sites of GAG synthesis where it substitutes for the xylose residue of the initiation linkage region and allows polymerization and sulfation of GAGs onto itself. The smaller βDX-bound GAGs are then efficiently exocytosed into the culture media (30). Since initiation and elongation are prerequisites for sulfation, the integrity of the GAG enzyme machinery can be evaluated, independent of core protein structures, by monitoring the increase in incorporation of [35S]sulfate into macromolecules in the presence of βDX.

In a representative experiment, incubation of M21 cells with 1 mM βDX results in a 10-fold increase in the mean incorporation of [35S]sulfate into [35S]-macromolecules (33, 34) (Fig. 7). The proportion of [35S]-macromolecules released into the culture media increases from 40 to 79% in the presence of βDX, representative of the exocytosis of the free, βDX-initiated, GAG chains. In contrast, pretreatment of the cells with BFA results in a dose-dependent inhibition of incorporation of sulfate into βDX-initiated macromolecules. The observed inhibition is not due to a block in the uptake of βDX since identical results are obtained in cells that are preloaded before BFA treatment (data not shown). At 20 ng/ml of BFA, incorporation of [35S]sulfate is only 59% of control cells, and at higher concentrations (0.2 and 2 μg/ml) the inhibition is virtually complete with incorporation diminishing to 1% of control cells (Fig. 7). Similar experiments performed with [6-3H]galactose demonstrated the accumulation of [3H]galactose intermediates linked to βDX (data not shown). The dose response range demonstrated here correlates well with that observed in Fig. 1 for inhibition of conversion of the MPG core protein to the proteoglycan form. These results indicate that BFA completely disrupts the ability of cells to use an exogenous, artificial acceptor for the elongation and sulfation of GAG chains. To determine if BFA permanently damages the GAG enzyme machinery, the reversibility of its effects was tested in the absence and presence of new protein synthesis.

Reversibility of BFA Effects

The effects of BFA on the synthesis of the MPG proteoglycan form are completely reversible. In M21 cells pretreated with BFA for 30 min, pulse-labeled for 10 min, and then washed and chased in the absence of BFA, conversion of the MPG core protein to the proteoglycan form begins between 1 and 2 h of release from BFA (Fig. 8). After an overnight release, both the 250-kD and CS proteoglycan forms can be isolated from the BFA-treated cells, as demonstrated by chondroitinase ABC digestion of the immunoprecipitates before SDS-PAGE analysis (in Fig. 8, 24 hour time point). Interestingly, after recovery from BFA treatment, a higher proportion of the MPG is expressed as the 250-kD rather than the proteoglycan form. This indicates that not all of the core protein that accumulates in the presence of BFA can serve as substrate for chondroitin sulfate synthesis after removal of the drug. The reversibility of the BFA-induced effects does not require new protein synthesis. Identical results are obtained in cells treated with BFA and released under conditions where protein synthesis is inhibited >90% by cycloheximide (data not shown).

The effects of BFA on the ability of M21 cells to use the exogenous βDX acceptor are also completely reversible. Cells pretreated with BFA and then released in drug-free media for 2 h incorporate [35S]sulfate into βDX-initiated GAG chains at levels equal to control cells. Identical results are obtained in cells released in the presence of cycloheximide (Fig. 9). The reversibility in the absence of new protein synthesis indicates that the GAG elongation and sulfation enzymes are present, but inactive, in BFA-treated cells.

BFA Inhibits the Conversion of the Class II–associated Invariant Chain to a Proteoglycan Form

To address the generality of the BFA-induced inhibition of GAG chain synthesis, the effects on the conversion of the ma-
Figure 7. BFA inhibits β-D-xyloside-initiated GAG synthesis. M21 cells were pretreated for 1 h with or without BFA (1 μg/ml) and p-nitrophenyl-β-D-xyloside (1 mM) for 15 min before a 1 h label with [35S]sulfate in the presence or absence of BFA. Cell-associated (hatched region) or exocytosed (nonhatched region) [35S]-labeled macromolecules were quantitated after their exclusion from Sephadex G-25 under dissociative conditions as described (33, 34). The height of the bar indicates total [35S]sulfate incorporation. The percent of total [35S]sulfate incorporation into control cells is indicated at the top of each bar. A dose-dependent inhibition of the ability of cells to elongate and sulfate GAGs onto an exogenous acceptor is observed in the presence of BFA. Data are expressed as the mean of duplicate cultures with the range of values indicated.

Figure 8. The effects of BFA on assembly of the MPG are reversible. M21 cells were pretreated for 1 h with or without BFA (1 μg/ml) before a 10-min pulse with [35S]methionine at 37°C. The cells were then washed and chased in unlabeled media in the absence of BFA. At the indicated time points, an aliquot of cells was harvested and MPG immunoprecipitates were isolated from detergent cell lysates with mAb 9.2.27. Digestion or mock digestion of immunoprecipitates with either endo H (Endo H) or chondroitinase ABC (Case ABC) was performed for 1 h at 37°C before being subjected to SDS-PAGE (5% gel) and autoradiography. Conversion of the MPG core protein to the proteoglycan form (PG) begins to appear after 1–2 h of release from BFA treatment. Molecular mass standards are in kilodaltons.
jor histocompatibility complex class II-associated invariant chain were examined in the Raji B-lymphoblastoid cell line. The invariant chain consists of a family of 31-41-kD glycoproteins that are associated with the class II α and β subunits. The invariant chain is also converted to a CS proteoglycan form that can only be identified in [35S]sulfate-labeled cells (10, 29). Treatment of Raji cells with BFA completely blocks the conversion of the invariant chain to a proteoglycan, as judged by the inhibition of [35S]sulfate incorporation into this form (Fig. 10, right panel). The increase in resistance to endo H digestion of the [35S]methionine-labeled invariant chain forms demonstrates the acquisition of complex N-linked oligosaccharides in the presence of BFA (Fig. 10, left panel). Therefore, the effects of BFA on GAG chain synthesis are not restricted to melanoma cells and are not a peculiarity of the MPG system.

Discussion

The current model for the posttranslational addition of GAG chains proposes that synthesis and maturation occur during the intracellular vesicular transport of core proteins from the ER through the Golgi complex (18, 27). This assembly process requires the precise coordination of temporal and spatial parameters that can influence core protein access to initiation, elongation, and sulfation enzymes. Previous studies have shown that agents which disrupt vesicular transport, or inhibit core protein release from the ER, also inhibit GAG chain addition to the MPG core protein with little or no effect on βDX-dependent GAG synthesis (33, 34). However, the interpretation of these previous results is restricted by the limited data on the effects of these agents on the structural and functional integrity of the vesicular pathway and associated organelles. The well-defined effects of BFA now make it possible to further delineate the topology of the CS GAG enzymatic machinery.

The results presented in this study demonstrate that the Golgi-specific changes induced by BFA have a profound effect on CS GAG synthesis. BFA caused a dose-dependent, yet completely reversible inhibition of CS GAG elongation and sulfation onto the MPG and invariant chain core proteins, as well as onto the exogenous, artificial GAG acceptor, βDX. BFA did not affect the initiation of CS GAG synthesis, including addition of the xylosyl residue and the galactosyl residues of the initiation linkage region. The simplest explanation for these findings is that CS GAG chain elongation and sulfation enzymes are resistant or insensitive to the redistribution induced by BFA, while the initiation enzymes are not (Fig. 11). This results in the complete uncoupling of CS GAG chain initiation from the elongation and sulfation events in a manner completely analogous to the BFA-induced uncoupling of glycosphingolipid synthesis (39, 40).

The strongest line of evidence supporting the idea that BFA uncouples CS GAG synthesis comes from the experiment that demonstrates GAG initiation, in the absence of elongation and sulfation, by analyzing the incorporation of [3H]galactose into the carbohydrate–protein linkage region. Under conditions where incorporation was restricted to O-linked oligosaccharides, by treatment with DMJ, label was incorporated into the MPG core protein that accumulated in the presence of BFA (Fig. 5). Since GAG chains represent the majority of, if not the only, O-linked oligosaccharides of the MPG complex (9, 28), the incorporation of [3H]galactose into the BFA-treated core protein is consistent with the addition of the xylosyl residue and the galactosyl residues of the initiation linkage region. Results from the fine structure analysis indicated that the [3H]galactose is predominately (56%) incorporated into neutral species that are sensitive to β-galactosidase digestion and probably represent the linkage region (Fig. 6). A portion (43%) of the material is anionic and its identity will be reported elsewhere.

The complete inhibition of βDX-dependent CS GAG chain synthesis...
polymerization and sulfation induced by BFA is also consistent with an uncoupling of GAG synthesis. As a xylose analogue, βDX diffuses freely into the cell to substitute for the normal carbohydrate–protein linkage residue (30). The anterograde intracellular transport of βDX molecules through the Golgi complex results in the formation of core protein free GAG chains that are efficiently exocytosed from the cell. In the presence of BFA, the βDX molecules that diffuse into the ER become properly initiated due to the redistribution of enzymes from BFA-sensitive compartments. The initiated molecules do not, however, gain access to the elongation and sulfation enzymes in BFA-resistant compartments because of the BFA-induced block in anterograde vesicular transport. Similarly, the βDX molecules that initially diffuse to the BFA-resistant compartments do not become properly initiated to serve as substrates for elongation and sulfation. This results in the complete inhibition of βDX-dependent CS GAG synthesis. Upon removal of BFA, transport between BFA-sensitive and resistant compartments is reestablished and βDX-initiated CS GAG synthesis quickly recovers within 1 h. The complete recovery in the absence of new protein synthesis is further proof that the elongation and sulfation enzymes are present but segregated from the initiation enzymes in BFA-treated cells.

There are other possible explanations for the inhibition of CS GAG synthesis induced by BFA, including the direct inhibition of the elongation and sulfation enzymes or the absence of redistribution of the proper nucleotide sugar and sulfate donor transport systems. Either mechanism would result in the observed inhibition of CS GAG synthesis, regardless of the location of the elongation and sulfation enzymes after the BFA-induced redistribution. However, results from previous studies argue against these possibilities. BFA does not inhibit the in vitro activity of several glycosyltransferases and does not affect the uptake of UDP-sugars (20, 36). In addition, the sialylation of the MPG core protein in the presence of BFA demonstrates that the Golgi-resident CMP–sialic acid transport system (14, 23) and some sialytransferase can be redistributed to the ER. The recent data demonstrating that BFA causes the disruption of a Golgi-specific structural protein suggests that its mode of action is directed towards the structural integrity of the Golgi rather than the resident enzymes (3, 22). For these reasons it is more likely that the BFA-induced inhibition of CS GAG synthesis is due to the segregation of initiation and elongation–sulfation enzymes into BFA-sensitive and -resistant compartments, respectively (Fig. 11).

The results presented here strongly support the proposal that CS GAG chain elongation and sulfation are TGN-associated events. This follows directly from the results of Chege and Pfeffer (2) who showed that the TGN is a BFA-resistant, Golgi sub-compartment. The localization of CS elongation and sulfation events to the TGN extends the list of TGN-resident enzymes to include the specific glycosyl- and sulfotransferases involved in these reactions. It has been previously shown that some classes of sialyltransferases and the GA2/GM2/GD2 synthase are localized in a BFA-resistant compartment (2, 31, 38–40). Further structural studies on the specific enzymes involved in these reactions will help to determine the mechanism responsible for their specific targeting to the TGN.

The mapping of CS GAG elongation and sulfation to the TGN is completely consistent with previous kinetic studies of GAG synthesis (18, 19, 35). While the exact site of the initial xylosylation reaction has been debated, it is generally agreed that elongation and sulfation are later Golgi events. The results presented here do not distinguish between an ER or early Golgi site for GAG initiation, but clearly segregate it from GAG elongation and sulfation. It will be important to determine whether a similar topology exists for the synthesis of other classes of GAGs.

The TGN differs from the cis–medial, and trans–Golgi in that it functions to sort proteins into transport vesicles that are bound for distinct organelles or domains of the cell surface (2, 4, 8, 26, 37). It is interesting to speculate that the addition of a GAG side chain might influence the packaging of core proteins into distinct transport vesicles bound for different regions of the cell. The expression of core proteins,
such as the MPG and invariant chain, in both glycoprotein and proteoglycan forms, may ultimately reflect distinct subcellular localization and/or function.

We are grateful to Sandoz Pharmaceuticals (Basel, Switzerland) for the gift of brefeldin A.

This work was supported by National Institutes of Health grants CA49243 (to R. C. Spiro) and CA38701 (to H. H. Freeze). H. H. Freeze is an Established Investigator of the American Heart Association. This work was supported by National Institutes of Health grants CA49243 (to R. C. Spiro) and CA38701 (to H. H. Freeze).

Received for publication 11 March 1991 and in revised form 12 August 1991.

References


Figure II. Schematic summary of the effects of BFA on CS GAG synthesis. The initiation, elongation and sulfation of a CS GAG chain onto a specific core protein serine residue (Ser), along with the enzymes xylosyltransferase (Xyl-T), galactosyltransferase I and II (Gal-TI and Gal-TII), glucuronyltransferase 1 and II (GlcUA-TI and GlcUA-TII), ß-N-acetylgalactosaminyl transferase (GalNAc-Ac-T), 4- and 6-sulfotransferase (4-6-sulfo-T), and linkages ß(1,3), ß(1,4) involved are depicted schematically. Monosaccharide symbols are as follows: O, xylose; Δ, galactose; O, glucuronic acid; O, N-acetylgalactosamine. Dashed vertical line segre-gates proposed BFA-sensitive and resistant compartments. Enzymes located in sensitive compartment redistribute to the ER in the presence of BFA while those in resistant compartment remain unaffected by BFA.


