Production of α-Galactosylceramide by a Prominent Member of the Human Gut Microbiota

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Abstract

While the human gut microbiota are suspected to produce diffusible small molecules that modulate host signaling pathways, few of these molecules have been identified. Species of Bacteroides and their relatives, which often comprise >50% of the gut community, are unusual among bacteria in that their membrane is rich in sphingolipids, a class of signaling molecules that play a key role in inducing apoptosis and modulating the host immune response. Although known for more than three decades, the full repertoire of Bacteroides sphingolipids has not been defined. Here, we use a combination of genetics and chemistry to identify the sphingolipids produced by Bacteroides fragilis NCTC 9343. We constructed a deletion mutant of BF2461, a putative serine palmitoyltransferase whose yeast homolog catalyzes the committed step in sphingolipid biosynthesis. We show that the Δ2461 mutant is sphingolipid deficient, enabling us to purify and solve the structures of three alkaline-stable lipids present in the wild-type strain but absent from the mutant. The first compound was the known sphingolipid ceramide phosphorylethanolamine, and the second was its corresponding dihydroceramide base. Unexpectedly, the third compound was the glycosphingolipid α-galactosylceramide (α-GalCerbf), which is structurally related to a sponge-derived sphingolipid (α-GalCer, KRN7000) that is the prototypical agonist of CD1d-restricted natural killer T (iNKT) cells. We demonstrate that α-GalCerbf has similar immunological properties to KRN7000: it binds to CD1d and activates both mouse and human iNKT cells both in vitro and in vivo. Thus, our study reveals BF2461 as the first known member of the Bacteroides sphingolipid pathway, and it indicates that the committed steps of the Bacteroides and eukaryotic sphingolipid pathways are identical. Moreover, our data suggest that some Bacteroides sphingolipids might influence host immune homeostasis.

Introduction

Sphingolipids and their breakdown products modulate a variety of eukaryotic signaling pathways involved in proliferation, apoptosis, differentiation, and migration (Figure 1). Although sphingolipids are ubiquitous among eukaryotes, few bacteria produce them [1]. The genus Bacteroides and its relatives are an important exception; 40%-70% of the membrane phospholipids of these prominent symbionts are sphingolipids [2,3]. While the structures of several Bacteroides sphingolipids have been solved, the full repertoire of these molecules has not yet been defined [1–19]. Here, by systematically exploring the sphingolipid repertoire of Bacteroides fragilis, we show that this gut commensal unexpectedly produces an isofrom of α-galactosylceramide, a sponge-derived sphingolipid that is the prototypic ligand for the host immune receptor CD1d.

Results and Discussion

Bioinformatic Insights into Bacteroides fragilis Sphingolipid Biosynthesis

To gain insight into the potential role of Bacteroides sphingolipids in mediating microbiota-host interactions, we set out to define the
Author Summary

While human gut bacteria are thought to produce diffusible molecules that influence host biology, few of these molecules have been identified. Species of Bacteroides, a Gram-negative bacterial genus whose members often comprise >50% of the gut community, are unusual in that they produce sphingolipids, signaling molecules that play a key role in modulating the host immune response. Sphingolipid production is ubiquitous among eukaryotes but present in only a few bacterial genera. We set out to construct a Bacteroides strain that is incapable of producing sphingolipids, knocking out a gene predicted to encode the first enzymatic step in the Bacteroides sphingolipid biosynthetic pathway. The resulting mutant is indeed deficient in sphingolipid production, and we purified and solved the structures of three sphingolipids that are present in the wild-type strain but absent in the mutant. To our surprise, one of these molecules is a close chemical relative of a sponge sphingolipid that is the prototypical ligand for a host receptor that controls the activity of natural killer T cells. Like the sponge sphingolipid, the Bacteroides sphingolipid can modulate natural killer T cell activity, suggesting a novel mechanism by which Bacteroides in the gut might influence the host immune response.

complete set of sphingolipids produced by Bacteroides fragilis NCTC 9343 [20], a genome-sequenced, genetically manipulable human gut isolate. Reasoning that a chromatographic comparison of lipid extracts from wild-type B. fragilis and a sphingolipid-deficient mutant would reveal the complete set of B. fragilis sphingolipids, we began by attempting to identify genes involved in B. fragilis sphingolipid biosynthesis. We took a candidate gene approach, hypothesizing that the Bacteroides sphingolipid pathway would harbor homologs of the eukaryotic pathway [17]. BLAST searches of the B. fragilis genome using the Saccharomyces cerevisiae sphingo-

lipid biosynthetic enzymes as queries yielded two hits encoded by adjacent genes: BF2461, a putative serine palmitoyltransferase, and BF2462, a putative sphinganine kinase. Bioinformatic analysis suggested that BF2461, like its yeast homolog, is a pyridoxal-phosphate-dependent 2-oxoamine synthase that conjugates serine and a long-chain acyl-CoA to form 3-dehydrodrosphinganine. In eukaryotes, this serves as the first committed step in the sphingolipid biosynthetic pathway. Therefore predicted that a Δ2461 mutant would be completely deficient in the production of sphingolipids. The eukaryotic homolog of BF2462, sphingosine kinase, phosphorylates sphingosine to form sphingosine-1-phosphate (S1P). Given that this reaction diverts the flux of the sphingosine base away from ceramide and toward S1P, we hypothesized that a Δ2462 mutant would produce a higher titer of mature sphingolipids than the wild-type strain.

Using Genetics and Chemistry to Define the B. fragilis Sphingolipid Repertoire

We constructed a mutant harboring a deletion of BF2461 (Δ2461) (see S1.8 in Supporting Information S1). Although we obtained co-integrates for the BF2462 mutant, double crossover mutants were never obtained despite repeated attempts to screen through thousands of colonies, suggesting that BF2462 may be

Figure 1. Chemical structures of the B. fragilis sphingolipids and related molecules. (A) B. fragilis produces the phosphosphingolipid ceramide phosphorylethanolamine (CPE, top) and the corresponding free ceramide (ceramidexBf, middle), which are similar in structure to the most abundant (4,5-dehydro) and third-most abundant (4,5-dihydro) forms of sphingomyelin in human plasma (bottom). (B) B. fragilis produces the glycosphingolipid α-galactosylceramide (α-GalCerBf, top), which is similar in structure to the sponge-derived α-galactosylceramide agelasphin-9b (middle) and a widely used derivative of agelasphin-9b, KRN7000 (bottom). Chemical groups that vary among the molecules in each column are colored red and blue for B. fragilis and non–B. fragilis sphingolipids, respectively. CPE, ceramidexBf, and α-GalCerBf were each purified as inseparable mixtures of varying lipid chain length. The proposed structures of the most abundant species are shown here.

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Bacteroides fragilis Produces α-Galactosylceramide

Essential for Bacteroides viability. An interesting alternative comes from the observation that dihydrosphingosine, the putative substrate of BF2462, is toxic to Bacteroides melaninogenicus at 4 μM [11]; the absence of BF2462 could therefore lead to the buildup of a toxic intermediate.

Nevertheless, since the yeast homolog of BF2461 constitutes the entry point to the sphingolipid pathway, we hypothesized that the Δ2461 mutant would be sphingolipid-deficient, providing an ideal starting point for enumerating the B. fragilis sphingolipids. To test our hypothesis, we used comparative HPLC-ELSD to analyze alkaline-stable lipid extracts from the wild-type (WT) and Δ2461 strains. Our analysis revealed three primary peaks that were consistent with the hypothesis, we used comparative HPLC-ELSD to analyze alkaline-stable lipid extracts from the wild-type (WT) and Δ2461 strains. Our analysis revealed three primary peaks that were present in the WT but not the Δ2461 extract (Figure 2). Preparative thin layer chromatography was used to purify multimilligram quantities of these compounds, and HPLC-MS analysis of the purified material revealed that each peak consists of a mixture of co-migrating compounds that vary in mass by 14 Da. Measured in negative mode, the most abundant mass ions for peaks 1, 2, and 3 were 677.5 Da, 554.5 Da, and 716.6 Da, respectively.

Elucidating the Structures of the B. fragilis Sphingolipids

To solve the chemical structures of the sphingolipid species, we first subjected the purified compounds to high-resolution MS. The mass of peak 1 was consistent with a ceramide phosphorylethanolamine (CPE) (C₃₄H₆₈NO₄; [M-H]⁻ m/z calculated 677.5234, observed 677.5221), a sphingomyelin isomer previously found to be the principal B. fragilis sphingolipid, while the mass of peak 2 was consistent with the corresponding dihydroceramide base (C₃₄H₆₈NO₄; [M-H]⁻ m/z calculated 554.5148, observed 554.5156) (Figure 1A; Figure S1 in Supporting Information S1). A set of 1D and 2D NMR experiments on the purified compounds from peaks 1 and 2 yielded resonances and couplings consistent with these assignments (see S4.1 and S4.3 in Supporting Information S1). We term this novel glycosphingolipid GalCerBf.

α-GalCerBf and the sponge-derived agelasphins, no naturally occurring α-galactosylceramides have ever been discovered. Substantial data have accumulated suggesting that α-GalCer is a ligand for a subset of human and mouse T cells, termed invariant natural killer T cells (iNKT), which express a conserved T cell receptor (TCR) that recognizes glycolipids presented by the major histocompatibility complex class I-like molecule, CD1d [22]. A synthetic derivative of agelasphin-9b termed KR7N000 (Figure 1B) is the prototypical agonist of iNKT cells and has become a critically important reagent for studying NKT cell biology both in vitro and in vivo. Indeed, iNKT cells are often identified or isolated by flow cytometry on the basis of their ability to bind a synthetic tetramer of CD1d loaded with a derivative of KR7N000. A variety of NKT cell ligands have been described. One class consists of low-affinity host-derived self-ligands such as isoglobotrihexosylceramide and β-glucopyranosylceramide [23,24]. Another class includes glycolipids from bacterial species including GSL-1 from Sphingomonas, BlGL-II from Bordetella, and a family of diacetylgalactosaminocylated glycolipids from Streptococcus pneumoniae, all of which have been postulated to be naturally occurring ligands for CD1d [25–27]. It has also been proposed that liver infection by Novosphingobium aromaticivorans, a close relative of Sphingomonas that produces CD1d-binding sphingolipids, results in an NKT-cell-dependent autoimmune response against the liver and bile ducts [28].

Purified α-GalCerBf Binds to CD1d and Stimulates Mouse and Human iNKT Cells

Based on the striking chemical similarity of α-GalCerBf to KRN7000, we reasoned that α-GalCerBf might serve as an endogenous ligand for CD1d and stimulate iNKT cell activity. To test our hypothesis, we began by loading synthetic mouse CD1d tetramers with purified α-GalCerBf and determining the ability of the sphingolipid/CD1d-tetramer complex (hereafter “tetramer”) to stain two iNKT-cell-derived hybridomas [29,30]. As with KRN7000, the α-GalCerBf-loaded tetramer (but not an empty tetramer) bound both hybridomas but not a CD1d MHCIi restricted hybridoma reactive to GFP (GFP-36) (manuscript in preparation, Yadav and Bluestone), indicating that the tetramer staining was ligand- and TCR-specific (Figure 3A; Figure S2 in Supporting Information S1). The iNKT cell hybridomas tested produced IL-2 in response to both the marine-sponge-derived and B. fragilis-derived sphingolipids in a dose-dependent manner and in absence of antigen presenting cells (APCs). These results suggested that α-GalCerBf is a stimulatory ligand that directly activates iNKT cells in vitro (Figure 3B-C; Figure S3 in Supporting Information S1).

We next examined the ability of purified α-GalCerBf to stimulate freshly isolated mouse and human iNKT cells in vitro and in vivo. Liver mononuclear cells, 30%–50% of which are NKT cells, were incubated with splenocytes as APCs in the presence of increasing doses of α-GalCerBf and examined for IFN-γ production. α-GalCerBf induced IFN-γ in a dose-dependent and CD1d-dependent manner. The response was inhibited completely by anti-CD1d antibodies (Figure 3D), consistent with our previous result that NKT cell stimulation required ligand presentation by CD1d (Figure 3B).

To explore whether the response of NKT cells to α-GalCerBf is conserved in humans, we determined whether Vα24+ cells could be expanded in vitro with purified α-GalCerBf as previously described for KRN7000 [31]. We cultured peripheral blood mononuclear cells (PBMCs) from six independent donors with 0.1 μg/ml KRN7000, 1 μg/ml α-GalCerBf or 1 μg/ml ceramide-Bf for 13 d and assessed the presence of CD3Vα24+ cells by...
Ceramide phosphorylethanolamine

Formula           Calculated     Observed     ppm difference
C_{36}H_{74}N_{2}O_{7}P-  677.5239   677.5222      2.52
C_{37}H_{76}N_{2}O_{7}P-  691.5396   691.5387      1.24
C_{38}H_{78}N_{2}O_{7}P-  705.5552   705.5538      2.00

α-GalCerBf

Formula           Calculated     Observed     ppm difference
C_{40}H_{79}NO_{9}Cl-  752.5449   752.5442      0.88
C_{41}H_{81}NO_{9}Cl-  766.5605   766.5602      0.43
C_{42}H_{83}NO_{9}Cl-  780.5762   780.5739      2.95
flow cytometry (Figure 3E–F). PBMCs cultured with KRN7000 or α-GalCerBf showed that the activity of CD3+Vα24+ cells, while PBMCs left untreated or treated with ceramideBf did not show an expansion of this population. Importantly, this result shows that the activity of α-GalCerBf is specific and not due to a contaminant of the lipid purification process since ceramideBf, which was purified in a similar manner, did not exhibit this effect. These results demonstrate that α-GalCerBf has similar activities in murine and human NKT cells and binds human CD1d.

To test whether α-GalCerBf can activate iNKT cells in vivo, mice were immunized with BMDCs pulsed with LPS alone or LPS + purified α-GalCerBf [32]. Consistent with activation, iNKT cells isolated from the liver showed upregulation of the cell surface markers CD25 and CD69 (Figure 3G), 15% of these liver-resident iNKT cells expressed IFN-γ after treatment (Figure 3H), and elevated IFN-γ levels were observed in the serum of these mice (Figure 3I). Anti-CD1d blocking antibodies inhibited liver iNKT cell activation and IFN-γ production, demonstrating the specificity of iNKT cell activation (Figure 3G–I). We therefore conclude that α-GalCerBf is capable of stimulating iNKT cell activation and cytokine production in vivo.

A Physiological Context for the Activity of KRN7000

The marine sponge-derived agelasphins and the nonphysiological CD1d ligand KRN7000 have previously been isolated, Scholar, 5/29/12). Unlike the pathogens from which CD1d ligands have previously been isolated, Bacteroides is extraordinarily prevalent in the human population, comprising >50% of the trillions of cells in the gut community of a typical human [33]. By showing that B. fragilis produces the only known α-galactosylceramide other than the sponge-derived agelasphins, and demonstrating that α-GalCerBf binds to CD1d and activates iNKT cells in vitro and in vivo, our results suggest a physiological basis for the activity of KRN7000. It is tempting to speculate that CD1d and iNKT cells function in the context of a microbiota–host interaction, especially in light of a recent report showing that neonatal colonization of germ-free mice by a conventional microbiota downregulates the level of iNKT cells in the colonic lamina propria and lung [34]. Indeed, it has been hypothesized that the agelasphins are not produced by Agelas mauritianus, but instead by a bacterial symbiont that inhibits the sponge [22].

In an attempt to determine the in vivo effect α-GalCerBf on NKT cells, we colonized germ-free (GF) mice with WT or sphingolipid-deficient B. fragilis by gavage and measured the percent and activation status of NKT cells in the liver and spleen. Colonization was confirmed by fecal cultures and PCR. We varied the length of colonization (1, 3, 4, and 14 d), the mice’s age at the time of colonization (4 and 8 wk old), sex, and strain (Swiss Webster and C57BL/6). Several of these experiments indicated an expansion of NKT cells in GF mice colonized by WT but not mutant B. fragilis. However, the effect was inconsistent and the levels of NKT cells in our control mice—germ-free (GF) and specific-pathogen-free (SPF)—fluctuated widely. As a percentage of total liver lymphocytes in the GF mice, NKT cells (CD3+ tetramer) varied between 8% and 48%, making it difficult to draw any conclusions about differences in NKT cell number or activation markers between our experimental data points.

Blumberg and coworkers recently showed that GF mice have increased levels of NKT cells in the colon compared to SPF mice and that colonization of neonatal, but not adult, GF mice with microbiota from SPF mice can reverse this effect [34]. Interestingly, neither the increase nor the reversal after colonization is seen in the liver or the spleen and there were no changes in the activation status of NKT cells. Taken together, our results suggest that the microbiota may affect NKT cells in the colon but not the liver or spleen, and that interventions to change the numbers of NKT cells must occur very early in life and may take weeks to be evident. Although Blumberg and coworkers showed the effects of the microbiota on NKT cell numbers and morbidity in models of IBD and allergic asthma, they did not identify the strain or the molecular pathway responsible for these effects; our results raise the possibility that α-GalCerBf, produced by B. fragilis, may be at least partially responsible for the results seen in their models.

There are subtle but important differences between KRN7000 and α-GalCerBf, indicating that the natural ligands for CD1d may be less potent than KRN7000. The principal structural differences between α-GalCerBf and KRN7000 are (i) a shorter N-acyl chain bearing a hydroxyl group on the β- rather than the α-carbon, (ii) the absence of a hydroxyl group at C4 of the sphinganine base, and (iii) iso-branched lipid termini (Figure 1B). Synthetic derivatives of KRN7000 that either have shorter N-acyl chains or lack the C4 hydroxy group have been shown to have less potent activity and/or an altered cytokine response, an effect that might be due to a change in the conformation of the CD1d-lipid complex [35]. Notably, one of the iso-branched lipid termini of α-GalCerBf is shared with agelasphin 9b. Since iso-branched lipids are commonly associated with specific bacterial genera (for example, comprising 53%–96% of the total fatty acid pool in Bacteroides) [36], their presence in agelasphin 9b is consistent with a bacterial origin for these sponge-derived sphingolipids.

A Proposed Pathway for Bacteroides Sphingolipid Biosynthesis

The absence of CPE, dihydroceramide, and α-GalCerBf from the Δ2461 mutant confirms that BF2461 is involved in B. fragilis sphingolipid biosynthesis, marking the first known member of the Bacteroides sphingolipid pathway (Figure 4). BF2461 is widely conserved among human-associated genera of Bacteroidales including Bacteroides, Parabacteroides, Porphyromonas, and Prevotella (known sphingolipid producers) but absent from Akkotipes [a nonproducer], supporting its role in the bacterial sphingolipid pathway. Our inability to construct a deletion mutant of BF2462 prevents us from exploring its potential role in the pathway, though it is tempting to speculate that it generates dihydrospingosine-1-phosphate from dihydrospingosine. Although the later steps of the pathway remain unclear, the intermediary of dihydroceramide is supported by the fact that CPE and α-GalCerBf share a common C4 scaffold and by our direct
observation of dihydroceramide production by *B. fragilis*. On the basis of these observations, we propose a model of *Bacteroides* sphingolipid biosynthesis that closely mirrors the eukaryotic pathway (Figure 4). Given that sphingolipids comprise ~30% of total cellular lipids and *Bacteroides* lacks an endoplasmic reticulum (the site of eukaryotic sphingolipid synthesis), the regulation of this pathway in the context of lipid metabolism and the localization of its biosynthetic enzymes will be important areas to explore.

Figure 3. α-GalCerBf binds CD1d and activates NKT cells. (A) Hybridomas were stained with anti-CD3 antibodies and empty mCD1d tetramers or CD1d tetramers loaded with α-GalCerBf or KRN7000. Flow cytometry plots are pregated on DAPI− events in lymphocyte gate stained with CD3 antibodies and the specified tetramer. Plots representative of three independent experiments are shown. (B) Hybridomas were cultured with BMDCs pre-pulsed with LPS or LPS + α-GalCerBf in the presence of control Ig or anti-CD1d blocking antibodies. IL-2 secretion was measured in supernatants 16 h later. Data are representative of three independent experiments. (C) Plates were coated with CD1d monomers and loaded with the specified amounts of α-GalCerBf. Hybridomas were then incubated for 16–18 h and IL-2 was measured in the supernatants by ELISA. Data are representative of three independent experiments. (D) Liver mononuclear cells were cultured with splenocytes plus increasing amounts of α-GalCerBf in the presence or absence of anti-CD1d blocking antibodies. IFN-γ secretion was measured in supernatants on day 5. Data are representative of three independent experiments. (E and F) Representative flow cytometry plots and pooled data of PBMCs cultured for 13–14 d with 0.1 μg/ml KRN7000, 1 μg/ml α-GalCerBf or 1 μg/ml ceramideBf. Dot plots show all events in the lymphocyte gate stained with 6B11 (specific for Vα24) and CD3 antibodies. Gate shows percentage of Vα24+CD3+NKT cells pre- and postexpansion. Pooled data showing six individual donors tested in three independent experiments. *p = 0.0078, **p = 0.0020 compared to control day 13 culture. (G–I) Bone-marrow-derived dendritic cells were pulsed in vitro with LPS only or LPS + α-GalCerBf for 24 h. The 0.4 × 10^6 cells were transferred to WT mice, which were treated with control Ig or anti-CD1d blocking antibody prior to cell transfer. Liver mononuclear cells were analyzed 16–18 h later. Data shown were pooled from three independent experiments. (G) Expression of CD25 and CD69 on gated CD3+tetramer+ cells. Representative flow cytometry plots and pooled data showing fold change of CD25 and CD69 surface expression compared to NKT cells isolated from mice transferred with LPS-pulsed BMDCs. (H) Representative flow cytometry plots and pooled data of intracellular IFN-γ expression on gated CD3+tetramer+ cells. (I) Serum IFN-γ levels. 

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Materials and Methods

Detailed methods are provided in Supporting Information S1.

Construction of Mutant Strain ΔBF2461

Primer sequences are listed in Table S1 in Supporting Information S1. DNA fragments flanking BF2461 were PCR amplified from B. fragilis NCTC9343 using the following primers: LF_5; LF_3; RF_5; RF_3. These fragments were digested with SstI and MluI and cloned into the SstI site of pNJR6. The resulting plasmid was introduced into B. fragilis NCTC9343 by conjugation, and cointegrates were selected using erythromycin. Cointegrates were passaged, plated on nonselective medium, and replica plated to medium containing erythromycin. Erythromycin-sensitive colonies were screened by PCR to detect those acquiring the mutant genotype.

Purification of α-GalCerBF

B. fragilis NCTC9343 was cultured under standard conditions, and harvested cells were extracted with CHCl₃:MeOH (2:1). The organic extract was subjected to alkaline hydrolysis, neutralized, and extracted with CHCl₃:MeOH (2:1). The crude extract was purified by preparative TLC (CHCl₃:MeOH:H₂O, 65:25:4) to give α-GalCerBF (Rf = 0.6). For complete experimental details, including yields and full characterization (NMR, high-resolution mass spectrometry) of all compounds, see Supporting Information S1. α-GalCerBF was isolated in five independent batches, and the in vitro and in vivo experiments were repeated with different batches of purified compound.

α-GalCerBF Used for Immunological Experiments

α-GalCerBF, CPE, and the ceramide base were each purified as an inseparable mixture of varying lipid chain length. Mass spec analysis of the methanolyzed long chain base (LCB) (S4.6 in Supporting Information S1) suggests that this portion of the structure carries the variation (see next paragraph). The inseparable mixture of alpha-galactosylceramides (>95% pure), referred to as “purified α-GalCerBF,” was the material used for the immunological experiments.

Figure 4. Proposed pathway for Bacteroides sphingolipid biosynthesis. BF2461, a putative serine palmitoyltransferase, would catalyze the pyridoxal-phosphate-dependent conjugation of serine and a long-chain acyl-CoA to form 3-ketodihydrosphingosine, which would undergo a ketoreductase-catalyzed conversion to dihydrosphingosine. At this branchpoint, dihydrosphingosine could either be phosphorylated by the putative sphingosine kinase BF2462 to form S1P, or it could undergo N-acylation to yield the observed dihydroceramide intermediate (compound 2). This common C₃₄ scaffold would then be the substrate for two alternative head group modifications: glycosylation to form α-GalCerBF, or phosphorylethanolamine group transfer to form CPE.

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Analysis of Lipid Tail Length Variation

Methanalysis of ceramide produced a mixture of three LCB amines that could be separated and analyzed by HPLC-MS (Supporting Information S1). Analysis of each by HRMS indicated that they are structural variants that differ in tail length. These data suggest the major parent \( \alpha\)-GalCer variants (m/z 716.37, m/z 730.58, and m/z 744.60) also differ in chain length of the LCB.

Hybridoma Stimulation

For dose titration experiments, BMDCs and DN3A1-2 and N30-2C12 NKT hybridomas (M. Kronenberg) and GFP36 CD1d* hybridoma were cultured at a 3:1 hybridoma:BMDC ratio and the indicated doses of KRN7000 or \( \alpha\)-GalCerBf in the presence of 1 \( \mu \)g/mL LPS. Supernatants were harvested after 24 h and IL-2 production was measured by ELISA. For APC-free experiments, CD1d monomers were coated on a 96-well plate for 1 h, and wells were blocked with PBS/10% FBS. The indicated amount of \( \alpha\)-GalCerBf was added to each well and incubated at 37°C for 3 h. After washing unbound \( \alpha\)-GalCerBf, hybridomas were added. Supernatants were harvested after 16–18 h and IL-2 production was measured by ELISA. For in vitro CD1d blocking experiments, \( \alpha\)-GalCerBf pulsed BMDCs were cultured at a 3:1 hybridoma:BMDC ratio in the presence of 10 \( \mu \)g/mL anti-CD1d antibody (Clone 1B1, BD Pharmingen). Supernatants were harvested after 16–18 h and IL-2 production was measured by ELISA.

In Vitro Stimulation of Human NKT Cells

For blood draws from healthy donors, informed consent was obtained in accordance with approved University of California, San Francisco IRB policies and procedures (IRB 10-02596). PBMCs were cultured for 13–14 d in RPMI containing 10% autologous serum plus lipids as described in Figure 3. On day 1 of culture, 100 U/mL IL-2 was added. Cultures were harvested on day 13 and the percentage of CD3\(^{+}\)\(\text{V}24\)\(\text{V}24\) NKT cells was determined by flow cytometry after staining with CD3 and 6B11 antibodies.

In Vivo Activation of NKT Cells

Mice were sacrificed 16–18 h after transfer of 0.4 \( \times \)10⁶ mature CD90\(^{hi}\)MHCI\(^{hi}\) BMDCs. Livers were cut into small pieces and passed through a stainless mesh. Cells were resuspended in 40% Percoll solution, and centrifuged at 2,300 rpm for 20 min at room temperature. All isolations were performed in the presence of brefeldin A (Sigma). After cell surface staining, cells were fixed in PFC BBW. Analyzed the data: LCB CP PCK BBW JC MK JLS LEC JAB

References