Human CD1a Deficiency Is Common and Genetically Regulated


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Human CD1a Deficiency Is Common and Genetically Regulated

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CD1 proteins evolved to present diverse lipid Ags to T cells. In comparison with MHC proteins, CD1 proteins exhibit minimal allelic diversity as a result of nonsynonymous single nucleotide polymorphisms (SNPs). However, it is unknown if common SNPs in gene regulatory regions affect CD1 expression and function. We report surprising diversity in patterns of inducible CD1a expression on human dendritic cells (DCs), spanning the full range from undetectable to high density, a finding not seen with other CD1 isoforms. CD1a-deficient DCs failed to present mycobacterial lipopeptide to T cells but had no defects in endocytosis, cytokine secretion, or expression of costimulatory molecules after LPS treatment. We identified an SNP in the 5′ untranslated region (rs366316) that was common and strongly associated with low CD1a surface expression and mRNA levels (p = 0.03 and p = 0.001, respectively). Using a CD1a promoter-luciferase system in combination with mutagenesis studies, we found that the polymorphic allele reduced luciferase expression by 44% compared with the wild-type variant (p < 0.001). Genetic regulation of lipid Ag presentation by varying expression on human DCs provides a mechanism for achieving population level differences in immune responses despite limited structural variation in CD1a proteins. The Journal of Immunology, 2013, 191: 1586–1593.

Major histocompatibility complex genes are among the most polymorphic in the human genome. For example, the human MHC class I locus consists of three genes, HLA-A, HLA-B, and HLA-C, each of which is represented by >1000 variant alleles (1). This variation is important to achieve population level diversity in the adaptive immune response to pathogens, which coevolve with their human hosts. Within an individual, the breadth of the adaptive immune response is further enhanced by the ability of T cells to rearrange and combine genes encoding Ag receptors. Therefore, MHC allelic diversity and TCR sequence diversity ensure the ability of T cells to recognize a wide array of peptide Ags. T cells have also evolved the capacity to recognize diverse lipids in the context of CD1 proteins (2, 3). CD1 H chains are homologous to MHC class I and bind noncovalently to β2-microglobulin (4). The human CD1 locus contains five genes (CD1A, CD1B, CD1C, CD1D, and CD1E) clustered on chromosome 1 (5). CD1a, CD1b, CD1c, CD1d, and CD1e proteins differ in which lipid Ags they bind, their patterns of expression on cells, and trafficking within cells (6). Notably, the mouse and rat genomes contain only orthologs of human CD1D (7–9), so mice provide a convenient experimental model for CD1D only. The other CD1 proteins are largely unexplored in the context of human immunology.

Despite their structural homology to MHC class I H chain genes, CD1 genes exhibit limited allelic diversity as a result of nonsynonymous polymorphisms. In early studies, Southern blots revealed largely conserved CD1 sequences among human and inbred mouse strains (5, 7, 10). Human sequence diversity in exon 2 and exon 3, which code for the α-1 and α-2 lipid–Ag-binding domains, respectively, is limited with only two variant alleles in CD1a, CD1d, and CD1e and zero variants in CD1b and CD1c (11, 12). Four other rare variants of CD1e have also been reported in single individuals (13, 14). More recent data derived from The International Haplotype Mapping Project (http://www.hapmap.org) and 1000 Genomes Project (http://www.1000genomes.org) reveal that common genetic variation exists in the CD1 locus, but this variation is enriched outside of protein coding exons and thus does not alter protein structure and lipid binding. Taken together, these studies suggest that modulation in the T cell response to lipids is not achieved by the diversity of CD1 coding region alleles but might be influenced by genetic variation in noncoding regions of the gene.

The CD1a protein presents lipopeptide Ags to T cells and is expressed on Langerhans cells, thymocytes, and certain subsets of dendritic cells (DCs) (6, 15). Data regarding the importance of CD1a function for human health are limited. Individual T cell clones that recognize host or pathogen derived lipids have been described and provide isolated examples of CD1a-presented lipids (16–18). Mammalian sulfatide is recognized by a CD4+ T cell clone, which produces TNF-α and shows a Th1 phenotype upon TCR engagement (18, 19). Mycobacterial diodeoxymycobactin is...
recognized by a CD14+ T cell clone, which produces IFN-γ and IL-2 upon stimulation and is capable of lysing cells infected with Mycobacterium tuberculosis (4, 17, 20). More recently, CD1a-autoreactive T cells have been identified in the blood of human donors, in some cases with precursor frequencies as high as 0.1–10% of all peripheral blood T cells (21, 22). These studies have begun to reveal population-level differences in CD1a-restricted T cell responses, but the immunologic mechanisms underlying this variation remain unexplored.

In this study, we report that CD1a deficiency on in vitro–derived DCs is a common phenotype, detected in 15% of study subjects. A common polymorphism in the 5′ untranslated region (UTR) of CD1a is strongly associated with both low surface expression and mRNA levels, and this polymorphism directly regulates gene expression in a promoter-luciferase assay. These studies provide a transcriptional regulatory mechanism for population level differences in T cell responses to lipids Ags that does not depend on non synonymous allelic diversity in the CD1 locus.

Materials and Methods

Human subjects

The Seattle study group consisted of 122 healthy individuals who provided blood for genotyping, and 33 also provided blood for functional studies. In this cohort, 68 (55%) were female, and self-described ethnic composition was 90 (73%) white, 27 (22%) Asian, and 5 (5%) other.

Ethics

All protocols were approved by human subject review committees at the University of Washington.

Single nucleotide polymorphism selection for genotyping

We used data from the International Haploview Mapping Project (http://www.hapmap.org; version 3, release 2) to select single nucleotide polymorphisms (SNPs) within 10 kb of CD1a. We used the CEU population, which consists of Utah residents of Northern and Western European ancestry. Haploview-tagging SNPs with a minimum allele frequency of 4% and R2 cutoff of 0.80 for linkage disequilibrium were identified using Haplovie v4.2 (http://www.broad.mit.edu/haplovie).

Genomic techniques

Genomic DNA was prepared from saliva (Genotek) or peripheral blood (Qiagen). Multiplex genotyping was performed using allele-specific primer extension on the MassARRAY (Sequenom) platform (23, 24). Single SNP genotyping was performed using the TaqMan SNP Genotyping Assay (Applied Biosystems). Genotypes were confirmed in a subset of individuals by DNA sequencing or genotyping on an alternate platform.

Quantitative RT-PCR

RNA was extracted from DCs by TRizol (Invitrogen) and ethanol precipitation. Single-stranded cDNA was generated using Multiscribe reverse transcriptase (Invitrogen). Real-time PCR was performed on StepOnePlus Real Time PCR System (Applied Biosystems) using ABI primer probe sets CD1A-FAM (Hs00233332_m1), CD1C-FAM (Hs00233332_m1), and GAPDH-JOE (402869).

In vitro generation of DCs and phenotyping

Monocytes were isolated from PBMCs by positive selection using CD14 microbeads (Miltenyi Biotec) and magnetic cell separation. Monocytes were incubated in RPMI + 10% FCS (Life Technologies) supplemented with 1-glutamine and GM-CSF (100 ng/ml) plus IL-4 (20 ng/ml) (PeproTech) for 3 to generate DCs. For experiments in Fig. 2, monocytes were also cultured with IL-4 from R&D Systems at a concentration of 100 ng/ml or cultured for 6 d. Differentiation of monocytes into DCs was confirmed also cultured with IL-4 from R&D Systems at a concentration of 10 ng/ml or FITC-conjugated dextran (Sigma-Aldrich) at a concentration of 100 mg/ml for 1 h at either 37˚C or 4˚C as a control. MFI was obtained and fold induction was calculated as MFI37C/MFI4C. To test the capacity of DCs to mature after stimulation, DCs were incubated in the presence of Ultra Pure LPS (List Biological Labs) 10 ng/ml or media overnight. Expression of costimulatory markers was assessed by flow cytometry and fold induction for each marker was calculated as MFI probes/MFI media. Abs were CD40-allophyocyanin (Bion Legend), CD80-PE/Cy7 (BioLegend), CD83-FITC (BioLegend), CD68-PerCPCy5.5 (BioLegend), and HLA-DR–APC/Cy7 (BioLegend).

Statistics

Statistical analyses were performed using Stata Statistical Software: Release 11 (StataCorp LP, College Station, TX). Simple linear correlation between continuous variables was described using the Pearson r correlation coefficient. The nonparametric Kruskal-Wallis or Mann–Whitney U test was used to compare continuous variables stratified by genotypes. The p values for two-tailed hypothesis testing are reported except where specifically noted. Function ‘pwld’ was used to calculate R2 measurements of linkage disequilibrium between polymorphisms.

Cloning and mutagenesis

Genomic DNA was isolated from whole blood using QIA-Amp (Qiagen). We separately amplified 998 bases and 555 bases proximal to the CD1a transcription start site using an Eppendorf Mastercycler Gradient 5331 (Eppendorf). We performed mutagenesis using the QuikChange II Site-Directed Mutagenesis Kit (Stratagene). Two sets of primers were used: the first for mutating rs366316 from C to T (C→T) and the second for mutating rs366316 from T to C (T→C). Primers and PCR parameters are detailed in Table II.

Cloning was performed using the pcR2.1 TOPO TA Cloning Kit according to manufacturer’s instructions (Invitrogen). DNA was extracted from bacterial pellets using the QIAprep Spin Miniprep Kit (Qiagen). Sequencing was performed on an Applied Biosystems 3730XL DNA Analyzer (Applied Biosystems).

Constructing pGL4 expression vectors

Wild-type and mutated 5′ UTR sequences as well as the minimal promoter from pGL4.14[luv/2/minimal/Hygro] (Promega) were isolated by digestion with XbaI and HindIII restriction endonucleases (New England Biolabs) and gel purification (QIAquick Gel Extraction Kit). Ligation was performed with T4 Ligase (New England Biolabs) using equal amounts of insert and vector. Endotoxin-free plasmid DNA of these constructs and of the control vectors pGL4.51 [luc2/CMV/Neo], pGL4.14 [luc2/minimal/Hygro], and pGL4.73 [hRluc/SV40] (Promega) were generated using the NucleoBond Xtra Midi EF plasmid preparation kits (Macherey-Nagel).

Transfection and luminometry

HEK293T cells were plated in 96-well flat-bottom plates (BD Falcon) at a density of 10,000 cells/well in DMEM (Life Technologies) supplemented with 10% FBS (Life Technologies). The next day, cells were transfected with pGL4 expression vectors using X-tremeGENE HP DNA Transfection Reagent (reagent to plasmid DNA ratio 3:1 and 2:1) (Roche Applied Science). After 24 h, cells were cultured using 5% CO2. The medium was changed with Opti-MEM (Promega), and luminescence from firefly (luc2) and Renilla (hRluc) luciferase was assessed using the Dual Luciferase Reporter Assay System (Promega). Luminometry was performed on a Veritas Microplate Lumin-
ompetency of peripheral blood DCs

Whole blood collected in ACD tubes from healthy donors was stained to determine the level of CD1a and CD1c expression on peripheral blood DCs using a previously described method for staining (26). The cells were gated to distinguish DC populations by first gating lymphocytes and monocytes using CD45 and side scatter. Then, monocytes were excluded by gating CD14-negative cells. DCs were distinguished by gating HLA-DR-positive and CD3/CD19/CD20/CD56-negative cells and subsequently excluding any possible contaminating inflammatory monocytes or NK cells by excluding any CD16-positive cells. Plasmacytoid and myeloid DCs were then distinguished by their CD11c and CD123 expression, and CD1a and CD1c expression was examined for each subset as shown.

Results

We measured inducible CD1 surface expression using flow cytometry on monocyte-derived DCs generated after activation with GM-CSF and IL-4. Initial screening of blood bank donors for induction of CD1a, CD1b, and CD1c revealed two donors that induced CD1b and CD1c but not CD1a, a reproducible finding that was not attributable to media or culture conditions such as the lot of FCS or density of cells in culture (data not shown). Therefore, we undertook a more formal analysis of CD1a induction on monocytes in 19 healthy adults. We found >100-fold variability in the absolute expression intensity of CD1a among donors, a pattern that was not linked to variable expression of the other two inducible CD1 isoforms, CD1b and CD1c (Fig. 1A, 1B, Supplemental Fig. 1).

Several lines of evidence indicated that donor-specific factors contributed to varied CD1a surface density rather than the conditions of culture or measurement (27, 28). First, CD1b and CD1c, two other inducible forms of CD1, showed high density among all donors (Fig. 1B, Supplemental Fig. 1). Second, the high or low levels of CD1a were reproduced upon repeated blood collection (r = 0.97; Fig. 1C). Third, low expression of CD1a was consistent over at least three experiments and seen with two mAbs, OKT6 and HI149 (r = 0.97; Fig. 1D), suggesting that low staining was not a result of differences in epitope binding. These data identify a CD1a-specific effect in which we observed high variance of CD1a surface density on DCs among all donors and identified three donors (15%) without detectable CD1a surface protein. We refer to the phenotype of extremely low or absent CD1a surface staining as CD1a deficiency in this study.

Previous studies suggest that the induction of CD1a is particularly sensitive to the presence of IL-4 and time in culture (29, 30). Therefore, we examined the effect of two sources and two concentrations of IL-4 as well as 3 and 6 d of culture. Based on suppression of CD14 expression, we confirmed that monocytes differentiated into DCs in all conditions tested (Fig. 2A–C). Similarly, we observed induction of CD1c in all donors and in all conditions tested (Fig. 2D–F). Among CD1a-sufficient donors, we confirmed increased CD1a expression after 6 d in culture compared with 3 d, but there was no effect of the source or concentration of IL-4. However, among CD1a-deficient donors, neither the source of IL-4, concentration of IL-4, nor extended time in culture could reverse the low expression of CD1a (Fig. 2G–I).

Together, these data further confirm that CD1a deficiency is a donor-specific phenomenon that is independent of culture conditions. The host-specific nature of the effect led us to hypothesize that this phenotype was genetic. Because the expression of CD1b and CD1c did not vary substantially among donors, we considered defects in β2-microglobulin unlikely and instead focused on potential defects near or within the CD1a H chain. There are seven common SNPs located near the CD1a H chain. Only one polymorphism codes for an amino acid substitution, and the rest are located in regulatory or noncoding regions (Table I). Because of the high density of linkage disequilibrium among these SNPs, all of the major haplotypes of an individual are defined by only three SNPs (Fig. 3A). When we stratified expression levels by genotype, rs411089 and rs366316 but not rs2269714 were associated with CD1a deficiency (Fig. 3B). Of note, rs2269714 codes for one of the two most common allelic variants of CD1A. Our data confirmed published studies showing rs2269714 is not associated with defects in surface expression on transfected cells and extends this finding to include DCs (31). The association appeared strongest with the minor homozygous genotypes, so we performed a recessive model analysis and found that the minor homozygous genotypes of rs411089 and rs366316 were associated with low CD1a expression (p = 0.03 and p = 0.01, respectively) (Fig. 3C). By contrast, there was no association between rs2269714 and CD1a expression (p = 0.65; Fig. 3C), and there was no difference in CD1b or CD1c expression when stratified by any SNP (Supplemental Fig. 2A, 2B). Thus, rs411089 and rs366316 are genetic markers for CD1a deficiency.

Having identified donors with CD1a deficiency on in vitro-derived DCs, we next examined the expression of CD1a on peripheral blood DCs ex vivo. It had been previously reported that CD1a is normally expressed on a subset of CD11c+ peripheral blood myeloid DCs (32), though later work revealed that the Ab clone actually

**FIGURE 1.** Deficiency of CD1a on human DCs. (A) Viable monocyte-derived DCs, identified by high forward and side scatter profiles, were stained with fluorescently conjugated Abs against CD1a, CD1b, and CD1c (dark lines) as well as isotype control Ab (shaded histogram). Shown are representative plots from two donors. (B) MFI of CD1a and CD1c are shown for 19 healthy blood donors. In four donors, CD1a MFI is <10. p value reflects Bartlett’s test for nonhomogeneity of variances. (C) Simple linear correlation between CD1a staining results of sequential blood draws for eight subjects. Data are represented as percent positive cells rather than MFI to adjust for temporal variation in flow cytometry calibration. (D) Simple linear correlation of staining between two Abs (OKT6 and HI149) that bind CD1a.
bound to CD1b/c (33). Therefore, we first used K562 cells that had been stably transfected to express CD1a to validate the specificity of the CD1a staining Ab (Supplemental Fig. 3A). We stained fresh whole blood and examined expression of CD1a and CD1c on plasmacytoid and myeloid DCs (Supplementary Fig. 3B). As expected, we were able to detect CD1c on the surface of myeloid DCs but not on plasmacytoid DCs. However, we were unable to detect CD1a on either DC subset, indicating CD1a is not endogenously expressed on unstimulated circulating DCs. Further experiments were therefore conducted on monocyte-derived DCs.

The identification of three donors with CD1a deficiency allowed mechanistic investigation of the extreme phenotype. First, we evaluated CD1a-sufficient and CD1a-deficient DC presentation of lipid Ag to T cells by coincubating DCs with dideoxymycobactin and Ag-specific T cells. Only CD1a-expressing DCs stimulated the release of IFN-γ from T cells (Fig. 4A). Next, we stimulated DCs with LPS and examined expression of costimulatory molecules as well as secretion of cytokines. Compared to media, LPS stimulation resulted in the expected increase in expression of CD40, CD80, CD83, CD86, and HLA-DR; however, we did not find any difference based on CD1a expression (Fig. 4B, 4C). Similarly, LPS induced the production of IL-12p70, IL-6, and CCL1, though again there was no difference in the analysis stratified by CD1a expression (Fig. 5A, 5B). Finally, we exposed cells to fluorescently conjugated particles to assess endocytic and phagocytic capacity. We observed no difference in the uptake of dextran, BSA, or E. coli based on CD1a expression (Fig. 5C, 5D). Our data show that CD1a-deficient DCs are selectively impaired in their ability to present lipid Ag to T cells, but appear to maintain other important aspects of DC function.

We then sought to determine the mechanism by which an SNP might affect CD1a expression at the cell surface. Previous studies have revealed that most CD1a is localized to the cell surface, and the primary mechanism of CD1a expression at the cell surface is via transcription of new protein rather than altered trafficking (34–36). However, the lack of cell-surface CD1a staining led us to consider the possibility that a trafficking defect could result in the intracellular accumulation of mature CD1a. We stained permeabilized

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</table>

SNPs were tabulated from dbSNP (http://www.ncbi.nlm.nih.gov/SNP) based on human genome assembly GRCh37.p5, build 37.3. SNPs with a minor allele frequency >4% were included.
DCs from CD1a-sufficient and CD1a-deficient donors and noted that intracellular actin was detected in all donors only after permeabilization (Fig. 6A, 6B). Among CD1a-sufficient donors, CD1a staining in permeabilized cells was qualitatively similar to that of unpermeabilized cells. However, among CD1a-deficient donors, there was no additional CD1a detected upon permeabilization (Fig. 6C). These data reveal that the CD1a deficiency phenotype is not the result of a defect in protein trafficking to the cell surface.

In myeloid cells, CD1a expression is an inducible phenomenon that is controlled by transcription, but the regulatory factors involved are poorly understood (36, 37). We found a strong positive linear correlation between CD1a mRNA and surface staining ($r = 0.79$; Fig. 7A). When we stratified CD1a mRNA by genotype, we found that the minor homozygous genotypes of rs411089 and rs366316 were associated with lower transcript level (Fig. 7B), a pattern similar to what we had observed for surface staining (Fig. 3C). Again, there was no association with rs2269714 (Fig. 7B), and the level of CD1c mRNA was not associated with any SNP (Supplemental Fig. 2C). Because rs366316 is located in the 5’ UTR of CD1a, we hypothesized that one or more promoter variants might directly regulate CD1a transcription. To study the function of CD1a promoter variants, we developed a promoter-luciferase assay to compare the activity of promoters cloned from a one CD1a-sufficient and one CD1a-deficient subject (Table II). The cloned DNA contains 998 bases composed of 555 bases of the 5’ UTR as well as an additional 443 bases upstream of the transcription start site. We found that the CD1a-sufficient promoter construct showed a 30-fold higher luciferase expression than the CD1a-deficient promoter construct ($p = 0.003$) (Fig. 7C). This result was consistent with reduced transcription of CD1a (Fig. 7B) but did not show a causal relationship between rs366316 and gene expression. We analyzed the 998 bp promoter sequence from a total of 3 CD1a-deficient and 6 CD1a-sufficient individuals and found 11 variants, including 8 SNPs, 2 deletions, and 1 insertion (data not shown). However, none of these variants correlated as strongly with CD1a deficiency as rs366316, suggesting this SNP...

**FIGURE 3.** Association between CD1A SNPs and expression. (A) Linkage disequilibrium plot of SNPs in CD1A coding region ± 10 kB flanking regions among the Europeans of Caucasian descent population from HapMap. CD1A spans 4132 bases on chromosome 1 and consists of six exons (black squares) and two UTRs (gray squares). Minor allele frequencies (dotted boxes) and linkage disequilibrium as measured by $R^2$ values (shaded box) are indicated. Three haplotype-tagging SNPs selected for genotyping are emphasized in bold, italic, underlined text. (B) CD1a MFI stratified by SNP genotypes. The bars indicate the median value. The nonparametric Kruskal-Wallis test was used to determine statistical significance for a genotypic model. (C) Recessive model analysis combines SNP genotypes AA and Aa.

**FIGURE 4.** CD1a-deficient DCs fail to present Ag to T cells but are able to induce expression of costimulatory molecules. (A) CD1a-sufficient (CD1a+) or CD1a-deficient (CD1a−) DCs were coincubated with T cell clone CD8-2 in the presence or absence of mycobacterial lipopeptide Ag dideoxymycobactin (DDM). IFN-γ levels were measured in overnight supernatants by ELISA for one donor per group. Shown are mean and SD for triplicate measurements. (B) Shown are expression profiles for cells derived from two healthy blood donors and treated with media (shaded) or LPS (dark line) overnight and then stained with Abs against costimulatory molecules and HLA-DR. (C) Results from nine subjects are combined and shown as fold change (LPS/media) in MFI for CD40, CD80, CD83, CD86, and HLA-DR. All data are representative of two or three independent experiments.
might account for the difference in luciferase expression. We repeated the cloning with a focus on the 5′ UTR and performed site-directed mutagenesis of rs366316 (Table II). These constructs allowed us to compare normalized luciferase expression among naturally occurring and mutated 5′ UTR sequences. We found that the T allele showed on average 56% higher expression than the C allele, whether it was naturally occurring (p < 0.001) or the result of mutagenesis (p < 0.001). Further, luciferase expression by the C→T mutant approximated that of the natural T allele, and expression by the T→C mutant substantially reduced promoter activity (Fig. 7D). Our data reveal that the C variant of rs366316 is causally related to reduced luciferase expression in our assay. Because rs366316 is strongly associated with CD1a deficiency, these data suggest rs366316 directly regulates CD1a gene expression.

Discussion
In this study, we report the discovery of three aspects of CD1a function in humans. First, we demonstrate the surprisingly diverse and donor-specific capacity for CD1a induction on DCs. Second, we identify individuals whose DCs lack detectable CD1a expression and are unable to present mycobacterial lipid Ag to T cells. Third, we associate two common SNPs with functional CD1a deficiency and demonstrate that rs366316, which is located in the 5′ UTR of CD1a, is causally associated with gene expression. In the

MHC Ag-presenting system, high rates of amino acid sequence variation among individuals control patterns of peptide Ag presentation and T cell activation. In contrast, our data reveal that activation of CD1a-restricted T cells is influenced by genetically determined differences in surface expression despite amino acid sequence conservation.

We found that CD1a-deficient DCs were selectively impaired in their ability to present lipid Ag to T cells, but showed no defects in endocytosis, cytokine secretion, or expression of costimulatory molecules after LPS treatment. In contrast, studies of DCs sorted by CD1a expression from a single individual revealed higher phagocytic capacity and decreased production of IL-12p70 and CCL1 from DCs with low CD1a expression (27, 38, 39). The authors associate the relative lack of CD1a expression with developmental arrest in the transition from monocyte to immature DC. In these studies, culture conditions, such as the presence of serum lipoproteins, were shown to influence the induction of CD1a as well as DC function more generally. Our data are compatible with this observation because we would not expect SNPs in cis with CD1a to affect aspects of DC development and function that might be more susceptible to modulation by external factors.

We determined that rs366316 and rs411089 were associated with CD1a deficiency in monocyte-derived DCs within a primarily Caucasian population. We attempted to extend these studies to peripheral blood myeloid DCs but were unable to detect CD1a on the surface of these cells. Whether CD1a deficiency exists within dermal DCs, Langerhans cells, or thymocytes is the focus of future studies. The frequency of these SNPs varies by ethnicity (data not shown), so the prevalence of CD1a deficiency in other populations may differ. Also, multiple transcription factors have been shown to modulate gene expression within the CD1a promoter (37), so it is possible that CD1a deficiency may correlate with a different SNP in a different population.

Because rs366316 is located in the 5′ UTR of CD1a, it may influence CD1a surface expression by reducing translation. Our data do not exclude this possibility, though we chose to focus on the effect of rs366316 on transcription. We found rs366316 was strongly associated with reduced CD1a mRNA levels as well as reduced luciferase expression in transfection studies. Polymorphisms in the 5′ UTR of a gene can affect gene expression by altering transcription factor binding sites or DNA methylation
sites or by reducing the stability of the transcript and increasing mRNA degradation (40, 41). Notably, GATA transcription factor binding sites located within the 5' UTR of CD1a but downstream of rs366316 have been shown to affect luciferase expression in a system similar to ours (37). Finally, our data leave open the possibility that multiple SNPs may be involved in regulating CD1a transcription. We show rs366316 is in high linkage disequilibrium with rs411089, which is located in the first intron and also associated with decreased mRNA levels. It is therefore possible that a deficiency haplotype of multiple SNPs within CD1a is collectively responsible for the molecular mechanism of CD1a deficiency.

Our data suggest that donor-specific variation in CD1a expression can modulate CD1a-restricted T cell activation. Recently, high frequencies of CD1a-autoreactive T cells were reported from most but not all healthy blood donors (21, 22). Thus, it is possible that genetically determined variation in CD1a expression could account for differences in frequencies of CD1a-autoreactive T cells. We also found that CD1a-deficient cells had a selective functional deficiency in lipid Ag presentation to T cells. By linking a genetic polymorphism to this phenotype, our data lay the foundation for genetic association studies that seek to elucidate the role of CD1a in human disease susceptibility. Previous studies have attempted to do this with CD1a coding region polymorphisms that are not associated with any functional deficiency. These studies have been underpowered and failed to replicate (42). Instead, we propose that future studies should focus on rs411089 and rs366316. For example, it has been postulated that IL-22 is important for the pathogenesis of psoriasis (43), and it was recently demonstrated that autoreactive CD1a-restricted T cells in the skin produce IL-22 (22). In principle, one could compare the SNP frequency in patients afflicted with psoriasis and compare this to the frequency observed in healthy controls.

### Table II. List of primers used to perform cloning and mutagenesis

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<td>T→C mutant</td>
<td>Forward</td>
<td>5'-CCAGAGGGGAAATGAGCACT-3'</td>
<td>55</td>
<td>18</td>
</tr>
<tr>
<td></td>
<td>Reverse</td>
<td>5'-CATTTAGCTAGCTAGCTG-3'</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>

Ta, Annealing temperature.
studies examining the skin lesions from patients with different genotypes would also be possible. Because CD1a also presents mycobacterial lipopeptides to T cells, similar studies could be performed in cohorts of patients with tuberculosis.

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Disclosures

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References