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Activated Human T Cells Accomplish MHC Class II Expression Through T Cell-Specific Occupation of Class II Transactivator Promoter III

Tjadine M. Holling, Nienke van der Stoep, Edwin Quinten, and Peter J. van den Elsen

Activated human T cells express HLA-DR, HLA-DQ, and HLA-DP on their surface, but the regulation and functioning of MHC class II molecules in T lymphocytes are poorly understood. Because the MHC class II transactivator (CIITA) is essential for MHC class II expression, we have investigated transcriptional activation of CIITA in activated T cells. In this study, we show that in human activated CD4+ T cells, CIITA promoter III (CIITA-PIII) drives the expression of CIITA. The in vivo genomic footprint analysis revealed activated T cell-specific occupation of CIITA-PIII. Subsequent EMSA analysis of several promoter regions showed differences in banding pattern among activated T cells, naive T cells, primary B cells, and Raji B cells. Activating response element (ARE)-I is shown to interact with the acute myeloid leukemia 2 transcription factor in nuclear extracts derived from both T and B cells. Interestingly, the acute myeloid leukemia 3 transcription factor was bound in nuclear extracts of T cells only. The ARE-2 sequence is able to bind CREB/activating transcription factor family members in both T and B cells. In addition, a yet unidentified Ets family member was found to interact with site C in activated T cells, whereas in B cells site C was bound by PU.1 and Pip/IFN regulatory factor 4/IFN consensus sequence binding protein for activated T cells. In Jurkat T cells, both ARE-1 and ARE-2 are crucial for CIITA-PIII activity, similar to Raji B cells. The differential banding pattern in in vivo genomic footprinting and transcription factor binding at the ARE-1 and site C between T cells and B cells probably reflects differences in CIITA-PIII activation pathways employed by these cell types. The Journal of Immunology, 2002, 168: 763–770.

Major histocompatibility complex class II molecules play a central role in the control of the adaptive immune response by, among others, binding and presenting immunogenic peptides to CD4+ Th cells (1). Only a limited number of cell types express MHC class II molecules; professional APCs, such as B cells, macrophages, Langerhans cells, and dendritic cells, display constitutive expression of MHC class II, while nonprofessional APCs, such as fibroblasts and T cells, acquire MHC class II expression under certain circumstances.

Much of our understanding on the transcriptional control of MHC class II and class I gene expression has been derived from studies with cells obtained from patients with a MHC class II deficiency, also referred to as bare lymphocyte syndrome (2–5). In bare lymphocyte syndrome patients, the genetic defect resides in the genes encoding transcriptional regulatory proteins required for transcriptional activation of MHC class II and class I promoters, i.e., in the genes encoding the MHC class II transactivator (CIITA) and the individual components of the regulatory factor X (RFX) complex (6–10). RFX manifests its role in transcriptional binding to the X1 box of the SXY regulatory module within the promoters of MHC class II genes (11). As such, RFX is crucial for the formation of a multimeric transcription factor protein/DNA complex with the CREB/activating transcription factor (ATF) proteins and the heterotrimeric complex NF-Y, which bind to the conserved X2- and Y-box promoter elements, respectively (12–14). CIITA functions as a coactivator by interacting with almost all of the components of this multimeric transcription factor complex bound to the SXY regulatory module, and together these regulatory proteins form a stable enhanceosome that drives transcription of MHC class II genes (15–19). This is achieved through interaction of the NH2-terminal activation domain of CIITA with components of the basal transcription initiation apparatus and by facilitation of chromatin remodeling through interactions with general coactivators that possess histone acetyltransferase activities (20–23).

Whereas the DNA-binding components of the enhanceosome (including RFX) are ubiquitously expressed, CIITA is only constitutively expressed in professional APCs and is induced in nonprofessional APCs. The expression of CIITA is controlled by four separate promoters, each coding for distinct first exons (24). CIITA promoter (CIITA-P) is the promoter used in dendritic cells, and CIITA-PII is expressed at insignificant levels and is as yet functionally poorly understood. CIITA-PIII is constitutively expressed in B lymphocytes and can drive CIITA expression after IFN-γ stimulation in a number of different cell types, including endothelial cells and fibroblasts (25). While the B cell-specific expression of CIITA requires a small region directly upstream of the initiation codon, the IFN-γ induction requires an additional region located ~5 kb upstream of the transcriptional start site (25).
CIITA-PIII accomplishes CIITA expression in activated T cells

CD4+ T cells is driven by CIITA-PIII only. Notably, despite the shared usage of CIITA-PII, differences in CIITA-PIII occupation were observed between activated T cells and Raji B cells. Furthermore, EMSA studies showed differences in banding pattern in activated T cells and Raji B cells. This probably reflects the difference in CIITA activation pathways employed by T cells (induced expression) and Raji B cells (constitutive expression).

Materials and Methods

Cell culture

The Jurkat cell line was purchased from the American Type Culture Collection (Manassas, VA; Jurkat clone E6-1, TIB-152) and cultured in RPMI 1640 (Life Technologies, Breda, The Netherlands) supplemented with 10% heat-inactivated FBS (Greiner, Alphen a/d Rijn, The Netherlands), 100 U/ml streptomycin, 100 U/ml penicillin, and 2 mM L-glutamine.

Naive CD4+ T cell isolation and stimulation

Peripheral blood was obtained from normal healthy donors by venipuncture procedure, and PBMCs were isolated using a Ficoll gradient (Pharmac - Leiden University Medical Center, Leiden, The Netherlands). To obtain naive and in vivo activated CD4+ T cells, PBMCs were stained with FITC-coupled HLA-DR (1:8) and PE-coupled CD4 (1:32) Abs (both from BD Biosciences, Mountain View, CA) in PBS containing 5% heat-inactivated FBS (Greiner) for 30 min at 4°C. CD4+ DR− (naive CD4+ T cells) and CD4+ DR+ (in vivo activated CD4+ T cells) cells were separated and collected using the FACSVantage SE (BD Biosciences). To increase cell numbers, the in vivo activated T cells were, after isolation, further propagated with 10 µg/ml PHA and irradiated allogenic PBMCs (3000 rad) in RPMI 1640 (Life Technologies) supplemented with 10% human serum, 10 U/ml IL-2, 100 U/ml streptomycin, 100 U/ml penicillin, and 2 mM L-glutamine. To obtain in vitro activated CD4+ T cells, naive CD4+ T cells were, after isolation, stimulated once with 1 µg/ml anti-CD3, 1 µg/ml anti-CD28 (both from Central Laboratory of The Netherlands Red Cross Blood Transfusion Service, Amsterdam, The Netherlands), and irradiated allogenic PBMCs (3000 rad), and further propagated in RPMI 1640 (Life Technologies) supplemented with 10% human serum, 10 U/ml IL-2, 100 U/ml streptomycin, 100 U/ml penicillin, and 2 mM L-glutamine.

Isolation of human primary B cells

Primary B cells were isolated from human spleen using Dynabeads CD19 positive B (Dynal Biotech, Oslo, Norway), and after positive selection the beads were removed from the cells by DETACHABead CD19 (Dynal Biotech) according to the manufacturer’s instructions.

RNA isolation and RT-PCR analysis

Total RNA was isolated from the different T cell populations using the RNazol extraction method (Cinna/Biotech Laboratories, Houston, TX). RNA samples (2 µg) were transcribed into cDNA using avian myeloblas- tosis virus reverse transcriptase (Promega, Madison, WI). The cDNA was then amplified using nucleotide primers specific for CIITA-PII, CIITA-PIV, and GAPDH: CIITA-PI, sense, 5′-GGTGGACCG GAGTTCCAGGACTG-3′; CIITA-PII, sense, 5′-GATCTTCTCACA TATGCGGGTTCGTT-3′; CIITA-PIV, sense, 5′-AGTCGCGGGAGG GAGACGGCACC-3′; CIITA-PIV, antisense, 5′-CATACTGTGCT GATTCGGGATATTG-3′; GAPDH, sense, 5′-GTCGAGTACACG GATTG-3′, and GAPDH antisense, 5′-ATGACGCGCCTTCTCCTC-3′. One microliter of cDNA was amplified in 1× PCR buffer II (Roche Diagnostics, Mannheim, Germany), 0.3 mM NucleixPlus PCR nucleotide mix (Amer sham Pharmacia Biotech, Piscataway, NJ), 0.4 µM of both sense and antisense primers, 2.5 U AmpliTaq DNA polymerase (Roche), and MgCl2 (Roche) in a total volume of 50 µl. The final concentration of MgCl2 was for 1.25 mM CIITA-PI, 1.5 mM CIITA-PIII, 1.5 mM CIITA-PIV, and 4 mM GAPDH. The PCR conditions used for CIITA-PI, CIITA-PII, PIPII, and CIITA-PIV were as follows: denaturation for 1 min at 94°C, annealing for 1 min at 61°C, and extension for 1 min at 72°C for a total of 35 cycles; the PCR conditions used for GAPDH were as follows: denaturation for 1 min at 94°C, annealing for 1 min at 60°C, and elongation for 1 min at 72°C for a total of 25 cycles. The PCR products were visualized on an ethidium bromide-stained agarose gel, and colors were reversed for reasons of clarity.

IVG analysis

Dimethyl sulfate treatment of cells, preparation of genomic DNA, and ligation-mediated PCR were performed as described by Mueller and Wold (39), with minor modifications (40). Three CIITA locus-specific primers and 2.5 µM of methylated genomic DNA were used to amplify cleaved fragments from the noncoding strand of CIITA-PIII: P3.31, 5′-GCAAC GCAATTGTGAGGAAATCCC-3′; P3.32, 5′-GCCACGCTCGAAGAC ACAGCCTATACAC-3′; P3.33, 5′-GCAACGACCTCATTACAGC CTCACA-3′. Electrophoretic mobility shift assay

Nuclear extracts. Purified nuclear extracts from naive CD4+ T cells, in vivo and in vitro activated CD4+ T cells, Raji B cells, and primary B cells were obtained as described by Kaminuma et al. (41). In vivo and in vitro activated T cells and primary B cells were derived as described above; naive CD4+ T cells were isolated from Ficoll-purified PBMCs using the human CD4+ T cell enrichment columns (R&D Systems, Minneapolis, MN), according to the manufacturer’s instructions.

EMSA. Two microliters of nuclear extracts, containing approximately 4 µg/µl nuclear proteins, were incubated in the following binding buffer: 10 mM HEPES (pH 7.9), 60 mM KCl, 10% v/v glycerol, 1 mM EDTA, 10 mM Na3PO4, 1 mM DTT, 3 mM MgCl2, 1 µg of poly(dI-dC), and 1 µg of sonicated salmon sperm ssDNA, with 2 ng of 32P-labeled dsDNA probe for 30 min at room temperature. The samples were run on a 6% polyacrylamide gel in 0.25× Tis-borate-EDTA buffer at 200 V for 150 min. The following oligonucleotides were used as probes: CRE consensus, sense 5′-AGAGATTTGC TGACGTACGAGAAGATCAG-3′ and antisense 5′-CTCAGTGTATCCGAC-3′; wt-PII-ARE-2, sense 5′-GAGTTTTTGTGTG-3′, and antisense 5′-CATACTGTGCT GATTCGGGATATTG-3′; and antisense 5′-ACAAGTGAGGGATCATC GAAATCCC-3′; wt-PIII-ARE-2, sense 5′-GAGGAGGCTTAA GGAGGCTTGGTTCGTT-3′, and antisense 5′-AAATTATACCAACC TCTTAAAGGCTCCT-3′; site C, sense 5′-CATTCCACTTCTCAGTGAC-3′ and antisense 5′-TGATCGGCTACAGGATAT-3′; and antisense 5′-TAATTTACAGGACTGTCTGCC-3′; the changed
nucleotides are underlined. Due to the limited amount of in vivo activated T cell nuclear extract, we performed the EMSA with site A and site B oligonucleotides only with nuclear extract from in vitro activated T cells, as these elements were found not to be critical for CIITA-PII activation in Jurkat T cells.

Supershift assays were performed by incubating nuclear extract and oligonucleotide for 30 min on ice, after which 1 μg of Ab was added and incubation was continued for an additional 60 min on ice. The following Abs were used for supershift assays: ATF/CREB (sc-270) reactive with ATF-1 p35, CREB-1 p43, and cAMP responsive element modulator-1; CREB-1 (sc-271) reactive with CREB-1 p43; ATF-1 (sc-243) reactive with ATF-1 p-35; P U.1 (sc-6059); all obtained from Santa Cruz Biotechnology, Santa Cruz, CA), acute myeloid leukemia (AML1) (PC284); AML2 (PC286); AML3 (PC287) (all obtained from Oncogene Research Products, San Diego, CA).

**Reporter and expression constructs**

The pGL3-CIITA-PIII reporter construct was generated by cloning a 668-bp region of pGL2-CIITA-PIII, which contains the sequence −545 to +123 (obtained by J. P.-Y. Ting, University of North Carolina, Chapel Hill, NC) into the pGL3-basic luciferase reporter plasmid (Promega). The pGL3-CIITA-PIV construct was previously described by van den Elsen et al. (42). Several 5′ truncations of CIITA-PIII were generated. The −145 to +123 bp or the −113 to +123 bp fragment of CIITA-PIII was created by PCR using the GL2 primer (Promega) and either the pIII-145 sense primer (5′-AAATTTTACCATCTAGACTTAAGCCC-3′) or the pII-113 sense primer (5′-AGATCTGAAACAGAGATCTGGCGTCGTCGCTG-3′) and pGL3-CIITA-PIII as template. The PCR products were subsequently cloned into the pGL3-basic luciferase reporter plasmid (Promega). Mutations in ARE-1, ARE-2, and site C were introduced by site-directed mutagenesis using overlapping extension PCR (43). Mutation primers for the PU.1 site in site C are described above. Mutation primers for the AML site at ARE-1 were as follows: AMLM sense, 5′-CTTAAAGGAGAAGCTTAATTTAAGCTTCTCCCTTAAG-3′. Mutation primers for ARE-1 were as follows: ARE-1M sense, 5′-GGCCCTTAAGCTTAGTGGAAATT-3′; ARE-1M antisense, 5′-AAATTTTACCATCTAGACTTAAGCCC-3′. Mutation primers for the CRE site in the ARE-2 binding site were as follows: ARE-2M sense, 5′-GAGTITTITTGGACCCGGGTCATCTGGTTCT-3′; ARE-2M antisense, 5′-GAAACAAAGAAGGGCGGTGCTAAAATACTC-3′, the changed nucleotides underlined. All constructs were verified by DNA sequencing at the Leiden Genome Technology Center (Leiden, The Netherlands).

**Transient transfections**

The human T lymphocyte cell line Jurkat was transfected by electroporation (Gene Pulser; Bio-Rad, Richmond, CA) at 250 V and 960 μF, and harvested after 72 h. Electroporations were performed with 8 × 10⁶ cells and 10 μg of luciferase pGL3-reporter construct together with 2.5 μg of SV40-Resilla pGL3-reporter construct (Promega) as an internal control. Luciferase and Resilla luciferase activity were measured using the Dual Luciferase Assay kit according to the manufacturer (Promega) and normalized for transfection efficiency with the Resilla luciferase activity.

**Results**

**CIITA promoter usage in activated CD⁴⁺ T cells**

First we have investigated which of the CIITA promoters is used to drive CIITA expression in CD⁴⁺ HLA-DR⁺ T cells. Two populations of CD⁴⁺ HLA-DR⁺ T cells were obtained, which we designated in vivo activated CD⁴⁺ T cells and in vitro activated CD⁴⁺ T cells. In vivo activated CD⁴⁺ T cells were obtained by gating CD⁴⁺ HLA-DR⁺ from PBMC, and to increase cell numbers these cells were propagated in vitro using PHA, IL-2, and irradiated allogenic PBMCs. In vitro activated CD⁴⁺ T cells were derived from CD⁴⁺ HLA-DR⁻ gated PBMC and stimulated in vitro using CD3 and CD28 Abs, IL-2, and irradiated allogenic PBMCs. To detect which CIITA promoter was used in activated T cells, a RT-PCR with primer sets specific for CIITA-PI, CIITA-PIII, and CIITA-PIV was applied. The results of these analyses showed that both the in vivo and the in vitro activated CD⁴⁺ T cell populations employ CIITA-PIII only (Fig. 1). This implies that CIITA-PII is thus not exclusively used in B cells but is also the principal promoter employed in activated T cells.

![CIITA-PI, CIITA-PIII, and CIITA-PIV](image)

**FIGURE 1.** CIITA-PIII is used for CIITA mRNA transcription. RT-PCR analysis was performed on cDNA derived from human naive CD⁴⁺ T cells or in vivo and in vitro activated CD⁴⁺ T cells with CIITA-PI-, -PIII-, and -IV-specific primers. In activated T cells, CIITA-PIII transcripts were found. As a positive control for CIITA-PI, cDNA of human dendritic cells was used; for CIITA-PIII, cDNA of PBMC was used; and for CIITA-PIV, cDNA of IFN-γ-stimulated melanoma cells was used. GAPDH primers were used as a control for equal cDNA loading.

In vivo promoter occupation of CIITA-PIII in activated T cells

To compare promoter occupation between naive and activated T cells, and between activated T cells and Raji B cells, in vivo genomic footprinting (IVGF) analysis was employed to visualize the protein/DNA interactions on CIITA-PIII. The lower strand from nucleotide −250 to +10 of the CIITA-PIII promoter was analyzed using dimethyl sulfate as a modifying agent. Analysis of equal amounts of methylated genomic DNA by IVGF analysis showed clear differences in promoter occupation between naive and activated T cells (Fig. 2A, summarized in Fig. 2B). In the screened region, naive T cells have no protection, as its footprint pattern is comparable with that of Jurkat DNA, in which the proteins were removed before methylation (see Fig. 2A, in vitro methylated DNA).

In activated T cells, many protected guanine residues were found. Five of these protected areas were already described for the B cell line Raji (31). Similar to Raji B cells, a strong protection is seen at the ARE-1 in activated T cells (nucleotide −132 to −143). Although strong protection is seen in both activated T cells and Raji B cells at the ARE-1 binding site, several differences in the protection pattern were also found. In Raji B cells, all guanine residues in the ARE-1 binding site are protected, while in activated T cells the guanine at position −134 is not protected. Notably, the guanine residues downstream of the ARE-1 site (−124 to −89) are completely or partially protected in activated T cells. Furthermore, in activated T cells, a strong hypermethylation is seen in an area devoid of guanine residues directly downstream of the ARE-1 site; however, the significance of this nonguanine enhancement is not clear.

A second strong hypermethylation in activated T cells is seen at the ARE-2. Again the protection pattern at the ARE-2 site differs between activated T cells and Raji B cells; nucleotide −64 is enhanced in activated T cells, while this guanine residue is partially protected in Raji B cells. Furthermore, the guanine at position −61 is enhanced in Raji B cells, while in activated T cells this guanine is neither enhanced nor protected. A third region with strong protection in activated T cells is seen between site A (nucleotide −13 to −25) and site B (−38 to −45). At site A, a cluster of four protected guanine residues is found in activated T cells, while in Raji B cells only two guanine residues are partially protected. Moreover, directly downstream of site B, protected guanine residues were detected in activated T cells. Also, we found a few protections or enhancements of promoter DNA...
upstream of the ARE-1 binding site and at site C. Overall, the CIITA-PIII in activated T cells shows more protected guanine residues outside the described Raji B cell binding regions, and within these areas the protection pattern differs between activated T and Raji B cells.

Transcription factor binding to CIITA-PIII in T cells

The IVGF analysis showed that the protection pattern at several CIITA-PIII binding sites differs between activated T cells and Raji B cells. This difference in protection pattern might be due to the binding of different transcription factors to these regulatory elements in activated T and Raji B cells. To determine which transcription factors bind to the different regulatory elements, EMSA with DNA sequences of these elements was utilized. Naive T nuclei possess low numbers of nuclear proteins (approximately seven times fewer proteins than activated T cells), which makes it difficult to observe qualitative differences. Therefore, equal amounts of nuclear proteins were used in the assays described below instead of equal numbers of cells.

ARE-1

Incubation of an oligonucleotide containing the ARE-1 binding site and nuclear extract from naive T cells, in vivo activated T cells, primary B cells, or Raji B cells revealed a complex, complex 1, specifically present in activated T cells (Fig. 3, lane 6, arrow 1), and a complex, complex 2, specifically present in naive T cells and Raji B cells (Fig. 3, lanes 1 and 11, arrow 2). This complex was difficult to detect in primary B cells. No differences were found in banding pattern between in vivo and in vitro activated T cells (not shown). The ARE-1 site displayed a high homology with the binding site for proteins of the AML/core-binding factor (CBF)/H9251/Runx family. In a supershift assay, addition of the AML1 Ab did not reveal the presence of AML1 in the complex (Fig. 3, lanes 3, 8, 13, and 17), whereas AML2 and AML3 were readily detected. Addition of AML2 Ab shifted complex 1 in activated T cells (Fig. 3, lane 9, from arrow 1 to arrow 2*). Moreover, in naive T cells and Raji B cells, complex 2 is also shifted with this Ab (Fig. 3, lanes 4 and 14, from arrow 2 to arrow 2*). These two different AML2 complexes might reflect the presence of an isoform of AML2 or an additional factor in the complex. Inclusion of the AML2 Ab also resulted in the formation of an additional complex in primary B cells. Interestingly, addition of the AML3 Ab to the binding reaction resulted in the formation of a large complex in naive and activated T cells, but not with primary B cells or Raji B cell nuclear extract (Fig. 3, lanes 5, 10, 15, and 19, arrow 3*). However, it is not clear which DNA-protein complex is shifted by the AML3 Ab. Thus, AML3 binds the ARE-1 site in naive and activated T cells, but not in B cells, and a specific AML2/ARE-1 complex is formed in activated T cells.

ARE-2

Next, an oligonucleotide spanning the ARE-2 binding site was used to test transcription factor binding to this site. Three specific complexes compared with Jurkat T cell in vitro methylated DNA. Open arrowheads indicate protected residues in activated T cells, while filled arrowheads indicate hypermethylation. Earlier described regions are indicated on the left. B, Schematic representation of DNA-protein interactions in T and Raji B cells. Earlier described regions are boxed. Open triangles (protection) and filled triangles (hypermethylation) indicate found DNA-protein interactions in activated T cells. Open circles (protection) and filled circles (hypermethylation) indicated found DNA-protein interactions in Raji B cells. Gray circles indicate residues earlier reported to be protected in Raji cells (31).

FIGURE 2. IVGF of CIITA-PIII reveals differences in DNA-protein interactions between activated T cells and B cells. A, The IVGF analysis of the noncoding strand of CIITA-PIII in naive T cell, in vivo and in vitro activated T cell, and Raji B cell in vivo methylated genomic DNA was
were seen using the nuclear extracts of naive T cells, in vivo activated T cells, Raji B cells (Fig. 4, lanes 1, 5, and 9, indicated by arrows), and in vitro activated T cells and primary B cells (not shown). The ARE-2 sequence shows homology with binding sites for members of the CREB/ATF family of transcription factors, and in Raji B cells it has been shown that CREB/ATF can bind to ARE-2 (N. van der Stoep, E. Quinten, and P. J. van den Elsen, unpublished observations). Also in T cells, Abs recognizing CREB/ATF proteins were able to supershift the complexes (Fig. 4, bracket). The upper complex can be supershifted with an Ab specific for CREB-1 (Fig. 4, lanes 2, 6, and 10), while the lower complex supershifts with a specific ATF-1 Ab (Fig. 4, lanes 4, 8, and 12). All three complexes can be supershifted with an Ab broadly reactive with CREB and ATF members (Fig. 4, lanes 3, 7, and 11).

**Sites A and B**

The site A sequence formed a complex (Fig. 5A, arrow 1) with a factor predominantly present in in vitro activated T cells. A more slowly migrating complex (Fig. 5A, arrow 2) can be seen using Raji B cell nuclear extracts, but not in an activated T cell extract. This later complex was previously suggested to be a NF-1 (related) transcription factor (31). Indeed, an oligonucleotide containing the consensus NF-1-binding sequence was able to eliminate the upper complex in Raji B cells (Fig. 5A, arrow 2), but not the lower complex in T cells (Fig. 5A, arrow 1; data not shown).

Site B is able to form several complexes in in vitro activated T cells, which differ from those in naive T cells and in Raji B cells (Fig. 5B, bracket). The sequence of site B displays weak homology with an octamer factor-binding site. However, it was shown previously that only very weak binding of octamer-binding transcription factor-1 could be detected at site B (31). Because site B has no further apparent homology with any transcription factor-binding site known to date, it remains unclear which proteins bind to site B in activated T cells and Raji B cells.

**Site C**

Incubation of a nuclear extract from in vivo and in vitro activated T cells with an oligonucleotide containing the sequence of site C resulted in the formation of a specific activated T cell complex (Fig. 6, lane 2, arrow 1; and data not shown), which is not detectable in nuclear extracts from naive T cells or Raji B cells (Fig. 6, lanes 1 and 3). Furthermore, in Raji B cells, two specific complexes are formed (Fig. 6, lane 3, arrows 2 and 3). Site C has a high homology, with the binding site of transcription factors belonging to the Ets family. An oligonucleotide containing site C with a mutated Ets binding site was not able to form both complex 1 in activated T cells and complex 3 in Raji B cells (Fig. 6, lanes 7 and 10), indicating that these complexes are formed by Ets motif-binding factors. Because the Ets protein containing complex 1 is
formed only in activated T cells, mutation of this Ets binding site results in the same banding pattern with naive and activated T cell nuclear extract. Furthermore, in Raji B cells, we now demonstrate that the Ets family member PU.1 and its activating partner Pip/IFN regulatory factor 4/IFN consensus sequence binding protein acting that the Ets family member PU.1 and its activating partner Pip/IFN nuclear extract. Furthermore, in Raji B cells, we now demonstrate results in the same banding pattern with naive and activated T cell formed only in activated T cells, mutation of this Ets binding site.

**CIITA-PIII activity in Jurkat T cells**

To correlate protein/DNA interactions with CIITA-PIII transcriptional activity in T cells, several 5' truncated promoter constructs and mutant promoter constructs were generated and transiently transfected in the Jurkat T cell line (Fig. 7). The activity of these truncated and mutant CIITA-PIII promoter constructs was compared with the activity of a wild-type CIITA-PIII promoter fragment encompassing nucleotides −545 to +123. The activity of CIITA-PIII-145, lacking site C, was about 75% of the wild-type CIITA-PIII promoter activity. Mutation of the PU.1 site in wild-type CIITA-PIII site C results in a decreased CIITA-PIII activity to 60%, which is comparable with the reduction in activity seen with CIITA-PIII-145. Deletion of the promoter region containing both site C and ARE-1 in CIITA-PIII-113 caused a dramatic drop in promoter activity to 18%. When in wild-type CIITA-PIII the AML-binding sequence at ARE-1 was mutated, promoter activity decreased to 38% (not shown). Moreover, mutation of the entire ARE-1 site in wild-type CIITA-PIII completely abolished CIITA-PIII activity. Also, mutation of the CRE site at the ARE-2 annihilated CIITA-PIII activity, revealing that both ARE-1 and the ARE-2/CRE site are of crucial importance for CIITA-PIII promoter activity in Jurkat T cells.

**Discussion**

To gain more insight into MHC class II expression in T lymphocytes, we have investigated the regulation of the MHC CIITA in activated human T cells. Naive T cells do not express MHC class II molecules on their cell surface, and the lack of CIITA transcripts in this T cell population (Fig. 1). Moreover, naive T cells displayed an almost bare CIITA promoter occupancy, as analyzed by IVGF (Fig. 2A). This lack of transcription factor binding might relate to the low amount of nuclear protein per naive T cell. However, when in the EMSA analysis equal amounts of nuclear protein were used, different banding patterns were observed in naive T cells and activated T cells with ARE-1, and site A, B, and C oligonucleotides (Figs. 3, 5, and 6). Thus, naive and activated T cells not only differ from each other with respect to the amount of nuclear protein per cell, but also differ qualitatively with respect to the proteins able to interact with the various regulatory elements.

It was found that of the four CIITA promoters, only CIITA-PIII is used to drive CIITA expression in both in vivo and in vitro activated T cells. CIITA-PIII is thus, besides by B cells, also employed by activated T cells. However, B cells have constitutive CIITA expression, while in activated T cells CIITA expression is induced, suggesting the presence of alternative activation pathways of CIITA-PIII. In accordance, IVGF analysis revealed differences in promoter occupation between activated T cells and Raji B cells. A prominent difference was seen in promoter occupation at the ARE-2 site. For Raji B cells, it has already been shown that the ARE-2 element is a binding site for members of the CREB/ATF family of transcription factors. We now show that in activated T cells CREB/ATF family members also can bind the ARE-2 element of CIITA-PIII. Although the promoter occupancy differs at the ARE-2 site between activated T cells and Raji B cells, EMSA analysis did not reveal any differences in the specific banding pattern between these cell types. On the one hand, it
is possible that the conditions used in our EMSA analysis did not support the formation of protein/DNA complexes that occurs in activated T cells in vivo. On the other hand, the IVGF analysis showed that CIITA-PIII upstream of ARE-2, in contrast to Raji B cells, is highly occupied in activated T cells. Factors binding to this region might interact with CREB/ATF at the ARE-2 site, causing differences in protection pattern in the genomic footprint compared with Raji B cells, or, alternatively, occupation of this region leads to a conformational change of the DNA and to a change in methylation pattern. Besides in activated T cells and Raji B cells, in primary B cells and naive T cells CREB/ATF binding was also demonstrated with the ARE-2 sequence. Yet, because the IVGF analysis revealed that the ARE-2 is not occupied in naive T cells, these data suggest that in naive T cells CREB/ATF is already present in very low amounts in the cell but is recruited to ARE-2 following T cell activation. This might be achieved through the activities of coactivators and/or, as discussed above, by the increased amounts of CREB/ATF in the nuclei of activated T cells.

Also, differences in promoter occupation between B and T cells were found at the ARE-1 site. The ARE-1 site in CIITA-PIII was proposed to be the binding site of a transcriptional enhancer factor-2-like transcription factor, as suggested by competition with a transcriptional enhancer factor-2 consensus oligonucleotide (31). Using specific Abs, we now show that the ARE-1 sequence can be bound by AML2, and that the binding pattern differs among activated T cells and naive T cells, primary B cells, or Raji B cells. It suggests that in activated T cells ARE-1 is bound by an AML2 isoform or, alternatively, that AML2 is complexed at ARE-1 with additional factors in naive T cells and Raji B cells. Notably, we also show that binding of AML3 to the ARE-1 site was specific for T lymphocytes because no AML3 Ab supershift is observed with nuclear extracts of Raji B cells or primary B cells.

All members of the AML family are capable of forming a heterodimer with the partner subunit CBFβ and form the CBF complex. Cooperative binding of CBF and Ets-1 to their separate binding sites has been demonstrated (45, 46), and this cooperative binding is relatively independent of the orientation and distance between the two binding sites (45). In this respect, it is of interest to note that CIITA-PIII contains both a CBF and an Ets binding site. An AML binding site has been located next to ARE-1, and site C has been shown to be capable of binding Ets family members (PU.1 in Raji B cells, and an Ets-like protein in activated T cells). The CIITA-PIII activity in activated T lymphocytes and Raji B cells might be the result of cooperative binding of these Ets and AML transcription factors. However, this cooperative binding of these factors may not be of crucial importance for CIITA-PIII activation because mutation of the Ets motif at site C and the AML site at ARE-1 has only moderate effects on CIITA-PIII activity. However, mutation of the entire ARE-1 sequence totally annihilates promoter activity, showing that ARE-1 is conclusive for CIITA-PIII activity in T cells. Also, CREB/ATF transcription factor binding is of crucial importance for CIITA-PIII activation, because deletion of the CRE site in ARE-2 totally diminishes CIITA-PIII activity in T cells.

Previously, it has been shown that also in Raji B cells, mutation of the ARE-1 sequence results in a strong reduction of CIITA-PIII activity (31). In Raji B cells the CIITA-PIII activity is reduced to 25%, while in Jurkat T cells the same mutation completely abolishes CIITA-PIII activity, suggesting a more potent role of the ARE-1 binding site in T cells than in B cells. Mutation of the ARE-2 binding site in CIITA-PIII results in complete loss of promoter activity in both Raji B cells (31) and Jurkat T cells, indicating that this site is equally important for both T and B cell CIITA-PIII activity. Considerable difference is seen between B and T cells when site C is mutated. In Raji B cells there is an increase of promoter activity to ~130% (31), while in Jurkat T cells there is a reduction to 60% of the wild-type promoter activity. It should be noted that the mutation in site C, as described in this study, specifically affects the PU.1 binding site and therefore differs from that designed by Ghosh et al. (31), which affects the complete nucleotide sequence of site C.

Although it is a recognized fact that activated human T lymphocytes express MHC class II molecules on their membrane, the precise function of these molecules on T cells is not yet fully established. It has been demonstrated that MHC class II molecules expressed on activated T cells are capable of Ag presentation. However, there are some controversies concerning MHC class II expression and Ag presentation by T cells. On the one hand, it is reported that activated T cells act as professional APCs, in that they deliver costimulatory signals to other T cells (38). Also, the expression of CD80/B7-1 at the surface of activated T cells implies that T cells can stimulate bystander T lymphocytes. On the other hand, it has been suggested that activated T cells provide down-regulatory signals for the immune response by inducing anergy in activated T cells and cytotoxicity in resting T cells (47). Besides potential APC activity, it is also reported that MHC class II molecules can transduce signals into T lymphocytes, which results in protein kinase C membrane translocation and inositol phosphate accumulation (48). Moreover, simultaneous triggering of CD3 and MHC class II molecules also leads to an increase in CD3-mediated T blast proliferation (48). Thus, MHC class II expression on T cells indirectly affects the activity of bystander T lymphocytes but can also provide signals that further enhance T cell proliferation and activity.

Recent findings have shown that CIITA, besides its central role in the transcriptional regulation of Ag presentation, either directly or indirectly, also affects the transcriptional expression patterns of other genes. For instance, it has been demonstrated that CIITA modulates IL-4 expression through interference with the general coactivator CREB binding protein (49). In addition, it has been reported that CIITA is capable of suppressing the Fas:Fas ligand pathway by inhibiting transcription of the Fas ligand gene through its promoter (50), and that expression of CIITA in Jurkat T cells enhances HIV-1 replication and transcriptional activity of the HIV long terminal repeat (51). All these data suggest additional functions of CIITA in the regulation of T cell-mediated control of the immune response.

In conclusion, CIITA-PIII is the principal CIITA promoter employed by human activated T cells to drive expression of CIITA. While the IVGF analysis of naive T cells showed no transcription factor binding on CIITA-PIII, several DNA/protein interactions were found to be specific for activated T cells compared with Raji B cells. In accordance, using band shift assays, differences in factor binding were found among activated T cells, naive T cells, primary B cells, and Raji B cells at established regulatory sites. Some of these DNA binding factors were identified as CREB/ATF, AML/Runx, and Ets family members.

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References


