



HAL
open science

Genomic structure of the human pre-T cell receptor alpha chain and expression of two mRNA isoforms

Claude Saint-Ruf, Oskar Lechner, Jacqueline Feinberg, Harald von Boehmer

► **To cite this version:**

Claude Saint-Ruf, Oskar Lechner, Jacqueline Feinberg, Harald von Boehmer. Genomic structure of the human pre-T cell receptor alpha chain and expression of two mRNA isoforms. *European Journal of Immunology*, 1998, 28 (11), pp.3824-31. 10.1002/(SICI)1521-4141(199811)28:113.0.CO;2-9 . inserm-02177288

HAL Id: inserm-02177288

<https://inserm.hal.science/inserm-02177288>

Submitted on 8 Jul 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Genomic structure of the human pre-T cell receptor alpha chain and expression of two mRNA isoforms

Claude Saint-Ruf, Oskar Lechner, Jacqueline Feinberg, Harald von Boehmer

► **To cite this version:**

Claude Saint-Ruf, Oskar Lechner, Jacqueline Feinberg, Harald von Boehmer. Genomic structure of the human pre-T cell receptor alpha chain and expression of two mRNA isoforms. *European Journal of Immunology*, Wiley-VCH Verlag, 1998. inserm-02177288

HAL Id: inserm-02177288

<https://www.hal.inserm.fr/inserm-02177288>

Submitted on 8 Jul 2019

HAL is a multi-disciplinary open access archive for the deposit and dissemination of scientific research documents, whether they are published or not. The documents may come from teaching and research institutions in France or abroad, or from public or private research centers.

L'archive ouverte pluridisciplinaire **HAL**, est destinée au dépôt et à la diffusion de documents scientifiques de niveau recherche, publiés ou non, émanant des établissements d'enseignement et de recherche français ou étrangers, des laboratoires publics ou privés.

Genomic structure of the human pre-T cell receptor α chain and expression of two mRNA isoforms

Claude Saint-Ruf, Oskar Lechner, Jacqueline Feinberg and Harald von Boehmer

Institut Necker, INSERM Unité 373, Paris, France

The pre-TCR, which is minimally composed of the TCR β chain, the pre-T α chain, and the CD3 complex, regulates early T cell development. The pre-T α chain is a 33-kDa type I transmembrane glycoprotein with an extracellular part similar to the constant domain of the immunoglobulin supergene family. We have sequenced (11 kb) the human pT α gene, which like the murine pT α gene consists of four exons: exon 1 encodes the 5' untranslated region, the leader peptide and the first three amino acids of the mature protein, exon 2 the extracellular immunoglobulin (Ig)-like domain, exon 3 a 15-amino acid peptide including a cysteine required for heterodimerization with TCR β , exon 4 the transmembrane region, the cytoplasmic tail and the 3' untranslated sequence. The human pT α gene is located on chromosome 6p21.3, close to the HLA-A locus. Reverse transcription-PCR studies with human thymus and leukemic cells showed that alternative splicing produces a shorter pT α isoform, which lacks the Ig-like domain but contains the transmembrane elements and the extracytoplasmic cysteine and which could thus permit pairing with TCR β chain and association with CD3 molecules. The conserved splice sites suggest a yet ill-defined biological function of the short pT α protein.

Key words: pT α / Genomic structure / mRNA isoform / T cell development / Gene expression

| | |
|----------|---------|
| Received | 29/7/98 |
| Accepted | 11/8/98 |

1 Introduction

In the thymus T cells develop from precursor cells in discrete steps that are controlled by the pre-TCR as well as the $\alpha\beta$ TCR for antigen. The pre-TCR consists minimally of the TCR β chain and the covalently bound pre-TCR α chain associated with signal-transducing proteins of the CD3 complex [1]. The pre-TCR rescues developing T cells that harbor a productive TCR β rearrangement from programmed cell death and induces extensive cell division as well as differentiation. It is also essential for allelic exclusion of the TCR β locus through feedback inhibition of TCR β rearrangement (reviewed in [2]). Finally, it appears to play an important role in directing T cell development into the $\alpha\beta$ pathway [3].

Both murine [4] and human [5] pT α cDNA have been cloned. The deduced amino acid (aa) sequences revealed a type I transmembrane protein consisting of a hydrophobic signal peptide, an extracellular domain with a structure similar to the constant (C) domain of the

immunoglobulin (Ig) supergene family, hydrophobic transmembrane region, and a cytoplasmic tail. In contrast to the short (3 aa) cytoplasmic domains of the TCR α and TCR β chain, pT α has a prominent cytoplasmic tail (30 aa in mice and 114 aa in humans). Additionally, the pT α is not subjected to the rearrangement process and it is devoid of J-like sequences as well as V-like Ig domains [4, 6]. With the exception of the cytoplasmic domain, murine and human pT α cDNA are very homologous (70–80%). Murine pT α is located in the D/E1 region on chromosome 17. The human gene resides in the syntenic region p21.2-p12 on chromosome 6 close to the MHC.

In the present study we present data on the human pT α gene cloned from a human chromosome 6 cosmid library. To define some conserved regions potentially important for gene regulation the complete human pT α gene sequence was established and compared with the murine sequence. Analysis of pT α expression in human thymus and in leukemic human cell lines shows that a splice variant pT α isoform is expressed. This isoform, which lacks the Ig-like domain could also be found in mice and therefore may have an important function in T cell development.

[1 18643]

2 Results and discussion

2.1 Isolation of genomic clones encoding the pT α gene

A cosmid library of human chromosome 6 DNA was purchased from the Reference Library Database (RFLB) of the Max Planck Institute for Molecular Genetics (Berlin, Germany). Nizetic et al. [7] constructed the library from DNA digests of flow-sorted human chromosomes 6 of the 4x cell line which were ligated into lawris 4. DH5 alpha MCR (BRL) was used as host. Subsequently, a high-density colony filter (~ 36 864 clones) corresponding to this library, was hybridized with a human pT α cDNA probe. Ten clones were found to be pT α positive. One of them co-hybridizes with a probe designated Alu yac 7 (RFLD data), which is ALU PCR-derived genomic. This clone is HLA-A positive and located on 6p21-3 [8], thereby indicating the localization of the pT α gene. Previous *in situ* hybridization data already mapped it to the 6p21-6p12 region of the human genome [5].

Positive clones for pT α were mapped by restriction digestion and Southern blotting. Three of them, containing the complete pT α gene, were extensively studied. No difference was found regarding the organization of pT α in these three recombinants. A pT α restriction map is shown in Fig. 1. For two directional sequencing we subcloned inserts of 34 kb, 44 kb, and 46 kb, respectively into bluescript KS⁺ plasmids.

2.2 Sequence and organization of the human pT α gene

Different subclones were sequenced using the “abi-prism” system (PE Applied Biosystems, GB). We sequenced 11 kb starting 1500 bp upstream the ATG codon and ending 250 bp downstream the stop codon (se-

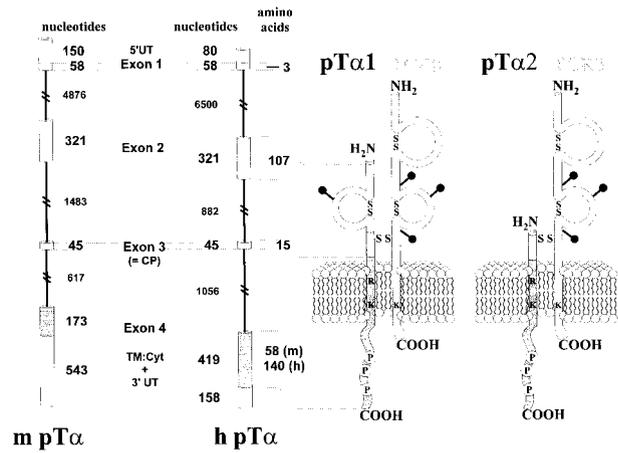


Figure 2. Genomic and protein organization of murine and human pT α

quence is available under accession number AF084941). Comparing this genomic sequence with pT α cDNA revealed the following exon/intron organization (Fig. 2).

Human pT α is encoded by four exons, which correspond, as in most other Ig superfamily genes, approximately to the different domains of the protein. The same organization has been observed for murine pT α . The first exon contains the 5' untranslated sequence, the leader peptide and the first three aa of the mature protein. In humans the following intron 1 is 6.5 kb long (5 kb in mice). It is particularly rich in repetitive DNA: 16 SINE elements (16 ALU sequences) and 3 LINE elements (2 LINE-2 and 1 LINE-1). Five simple repeats and 2 low complexity sequences have also been noticed. Exon 2 encodes 105 aa of the extracellular Ig-like domain, including the two cysteines that are thought to form the typical Ig intrachain disulfide bridge. It is followed by intron 2 (887 bp) containing one SINE element (mir) Exon 3 encodes 16 aa, which form the connecting peptide con-

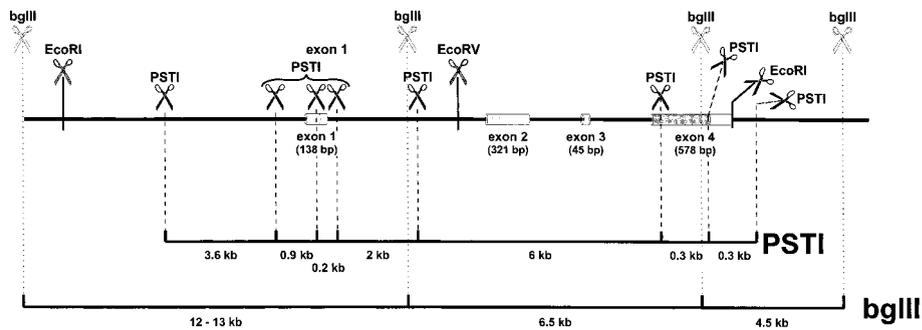


Figure 1. Restriction map of the human pT α gene

taining the cysteine residues for dimerization with the TCR β chain. Exon 2 and exon 3 have the same size in humans and mice. The following intron contains 1057 bp encompassing a SINE element (Alu Sg). Exon 4 encodes 139 aa, and contains the sequence for the approximately 20-aa long transmembrane region and the 3' untranslated region of \sim 160 nucleotides. This includes two positively charged aa (arginine, lysine) which are located at the same position in the murine pT α chain but also in the TCR α and TCR δ chain. These arginine and lysine are thought to be essential for the interaction of the TCR chains with negatively charged residues in the transmembrane regions of the CD3 complex [9]. The last 114 aa form the cytoplasmic tail. While more than 80 % aa identity can be observed between the murine and human Ig-like and transmembrane region, no significant homology could be found between the 114-aa human cytoplasmic tail and the 30 residues of the murine pT α cytoplasmic tail. We have suggested [5, 6] that the lack of identity between the human and murine cytoplasmic tails could reflect a divergence in gene structure. In fact, the organization of the pT α genome is very similar to the constant regions of TCR α and TCR δ genes. However, two differences can be found. First, only pT α is endowed with a leader sequence located far from the next coding sequence. This could be explained by the fact that pT α is expressed without a second, V region-like Ig domain. Second, the pT α transmembrane region, the cytoplasmic tail, and the 3' untranslated region are encoded by a single exon. In TCR α and TCR δ genes the 3' untranslated region is encoded by a separate exon. In mice the 3' untranslated region contains a B2 repetitive element which provides the polyadenylation site and thus can be considered as an integral part of the pT α gene. We have suggested that the specific structure of the murine pT α gene could be due to the presence of this transposon-like element in the 3' end of the gene [6]. Because human pT α has the same organization but has lost the B2 repetitive elements, this assumption is no longer valid.

2.3 Regulatory elements of the pT α gene

We sequenced (1.5 kb) upstream of the ATG start codon of the pT α gene. Usually promoter sequences are present within 100 bp upstream of the ATG start codon. While this region is well conserved between humans and mice (70 % of nucleotide identity) no TATA or CCAAT like regulatory elements, which are typical promoter motifs of many non-housekeeping genes, could be found. Furthermore, computer-based sequence analysis did not permit to define a potential promoter. Further analyses of this region by deletion and/or mutagenesis experiments will be necessary to define the promoter site and further regulatory elements.

Intron 1 is very large compared to other Ig-family genes (6.5 kb for the human and 5 kb for the murine gene). In the middle of this intron a single, 80-bp long sequence is highly conserved between humans and mice (80 % homology). Since intronic sequences are usually not conserved between species, except if they contain some regulatory elements, this sequence could play a role in the regulation of pT α . A detailed analysis using the TESS program (BCM Search Launcher) revealed potential binding sites for transcription factors AP1 and μ -EBP-C2. AP1 family members are known to play a critical role in regulating T cell gene expression in combination with other transcription factors [10]. Binding sites for μ -EBP-C2 have been found in intragenic enhancers of TCR β and IgH [11, 12]. Like in mice, the human pT α intron 1 is heavily loaded with short interspersed repetitive elements. About 4.5 kb of the 6.6 kb of human intron 1 are repeat sequences. The conservation of these sequences among humans and mice additionally suggests a role of intron 1 in the regulation of pT α expression. Since LINE elements carry an internal split promoter for RNA polymerase III, they are actively transcribed by this polymerase. They participate in host gene activity regulation by inserting into regulatory elements or by providing regulatory elements themselves [13, 14]. Therefore, it would be interesting to analyze whether this region plays an important role in the regulation of pT α expression. This could be helpful to understand the commitment of T cells to either the $\alpha\beta$ or the $\gamma\delta$ lineage since it appears that $\gamma\delta$ precursors but not $\gamma\delta$ T cells express the pT α gene [3].

2.4 Expression of human pT α and evidence for a splice-variant

We have used RT-PCR to analyze expression of human pT α in human thymus and in the human HPB-ALL, MOLT-4 and Jurkat cell line. Primers have been chosen in exon 1 and exon 4 in order to amplify the entire cDNA. Specific transcripts were found in the human thymus, in HPB-ALL and MOLT-4 cells, respectively. The Jurkat cell line was pT α negative. In all positive samples we observed two different bands (Fig. 3). One of the expected size of \sim 640 bp, and a smaller one of \sim 320 bp. Sequencing of these bands revealed that the larger one corresponds to the originally described form of pT α (as described in [5]), designated pT α 1. The smaller band represents a splice-variant of pT α , designated pT α 2.

The splice variant sequence, pT α 2, shows an open reading frame. The deduced primary sequence contains 231 aa. Comparison with pT α 1 revealed that pT α 2 lacks the major part of the Ig-like domain. During pT α 2 splicing, which uses at the same splice sites as pT α 1, the

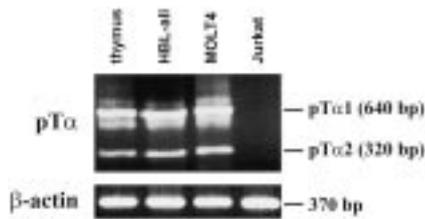


Figure 3. Expression of two different pT α splice variants. pT α expression was analyzed by RT-PCR in human thymus and three different human acute lymphoblastic cell lines: HBL-all, MOLT4, and Jurkat. Specific transcripts were not found in Jurkat cells. Two different bands could be observed: one of the expected size of \sim 640 bp, and a smaller one of \sim 320 bp. The control RT-PCR for β -actin is also shown below.

entire exon 2 is eliminated. The donor splice site of exon 1 and the acceptor splice site of exon 3 are used to yield pT α 2. Therefore, the protein encoded by this cDNA isoform is predicted to consist of the signal peptide followed by the first three aa of the extracellular domain and finally, just following the connecting peptide which is necessary for the binding to the TCR β chain, the transmembrane domain and the cytoplasmic tail. All these deduced domains are equal to those of pT α 1. The expected molecular mass of pT α 2 is of 18.4 kDa. In contrast to pT α 1, which contains one N-glycosylation site in humans and two in mice, pT α 2 has no potential N-glycosylation site. Both pT α 1 N-glycosylation sites are encoded by exon 2. Nevertheless numerous serines and threonines, which are potential targets for O-glycosylation, are present in pT α 1 and pT α 2. Therefore, it is possible that the two pT α splice forms are O-glycosylated, like many cell membrane glycoproteins (for instance CD8 or IL-2 are O-glycosylated or O-glycan sialylated, respectively [15]). As no consensus sequence(s) for O-glycosylation sites could be defined up to now, further analyses are needed to establish possible glycosylations.

2.5 Immunoprecipitation of the human pT α protein

The human cell lines HPB-ALL and Jurkat, which express and do not express the two pT α isoforms, respectively, were labeled with [3 H]leucine. Lysates were immunoprecipitated with R225 antibodies. These polyclonal rabbit antibodies were generated against the complete extracellular domain of murine pT α including the connecting peptide. The antibodies recognize the protein generated *in vitro* from human pT α 1 cDNA by an eukaryote-coupled transcription/translation system sup-

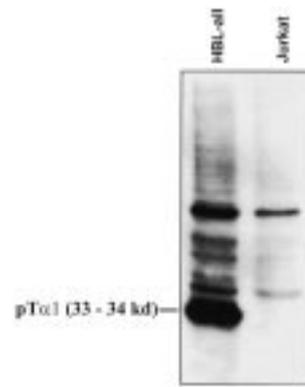


Figure 4. Immunoprecipitation of pT α 1 in the human acute lymphoblastic cell lines HBL-all and Jurkat.

plemented with dog pancreas microsomes (data not shown). Precipitates were analyzed by SDS-PAGE. A 33–34-kDa protein could be detected in precipitates from HPB-ALL but not from Jurkat cells (Fig. 4). This protein is likely to correspond to pT α 1. The same results were obtained under reducing and nonreducing conditions and suggest that in HPB-ALL cells pT α 1 is not linked to another protein. The human pT α 2 isoform could not be detected in these experiments. It is possible, however, that the R225 antibodies do not recognize this form. In contrast to the Ig-like domain, which shows 85 % homology between mice and humans and is only present in pT α 1, only 55 % homology exists between the murine and human 20 aa extracellular part which is shared by the two pT α isoforms. Thus, the R225 antibodies may not bind to the connecting peptide (compared to the Ig-like domain) of human pT α .

We were unable to precipitate pT α in biotinylated surface HPB-ALL cell extracts. In this cell line, which expresses the TCR $\alpha\beta$, pT α should not be expressed within a pre-TCR complex on the cell surface.

2.6 An additional pT α heterodimer in mice

Previous RT-PCR studies on pT α expression revealed two pT α forms in the murine thymus [16]. Since a corresponding smaller size mRNA could not be detected by Northern blotting we concluded that it was a PCR artifact. However, recently Barder et al. [17] reported the expression of mRNA corresponding to the two pT α isoforms. Prior sequence analysis had revealed that the murine splicing variant had exactly the same organization as human pT α [16].

To analyze whether pT α 2 protein could be detected cell surface biotinylation was performed with the SCB29 cell

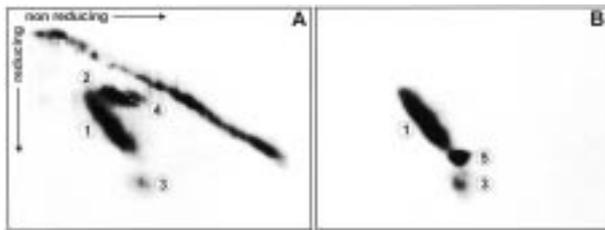


Figure 5. F23.1 (anti-V β 8 monoclonal antibody) immunoprecipitates of SCB29 cell lysates analyzed by nonreducing/reducing SDS-PAGE. (A) Blots from surface biotinylated cells. 1: pT α 1, 2: TCR β (pT α 1 associated); 3: a 20-kDa covalently TCR β -linked protein, which may represent pT α 2; 4: TCR β (associated with the 20-kDa, TCR β -linked protein). No other covalently TCR β -linked protein could be detected. (B) The blot shown in (A) was destained and probed with the polyclonal rabbit anti-murine pT α antiserum R225. Spots 1 and 3 correspond to spots 1 and 3 seen in blot A, representing pT α 1 and the putative pT α 2, respectively. An additional spot could be detected by the pT α -specific antibody. As this protein (spot number 5) could not be detected by cell surface protein biotinylation, it probably represents an intermediate, intracellular pT α protein with incomplete posttranscriptional modifications.

line [18]. After cell lysis, pre-TCR complexes were immunoprecipitated with an anti-TCR β antibody (F23.1) and analyzed by two-dimensional, reducing and nonreducing, diagonal gel electrophoresis. Gels were blotted and membranes labeled with streptavidin-horseradish peroxidase (HRP) to detect all precipitated proteins. Subsequently, the membrane was reprobed with a pT α -specific polyclonal antiserum (R225). Using the anti-TCR β antibody two complexes could be precipitated (Fig. 5A): the first, representing the major complex, consisted of the TCR β chain and the originally described, full-length pT α (pT α 1). The second, weakly detectable complex consisted of a protein with the same size as TCR β , linked to a second protein of 20 kDa (Fig. 5B). This latter protein was recognized by the polyclonal pT α antiserum R225. Since without glycosylation pT α could have an apparent molecular weight of 9 kDa we cannot be certain that a pT α 2 protein is indeed associated with the TCR β chain as has been claimed by Barder et al. [17]. The second heterodimer could also represent a degradation product of the pT α /TCR β heterodimer.

3 Concluding remarks

Recently, Irving et al. [19] have shown that thymocytes expressing a pre-TCR lacking the extracellular Ig-like domains of both pT α as well as TCR β develop normally. They generated RAG $^{-/-}$ transgenic mice expressing a truncated form of the TCR β and the pT α chain, which

had their (normal) extracellular domain replaced by a “flag” or “myc” epitope, but still had the cysteine residue necessary for heterodimerization. Thymocyte development could be restored in these transgenic mice. The truncated pT α construct used to generate these transgenic mice is very similar to the variant pT α isoform found in mice and humans but these mice obviously contained also endogenous pT α . Nevertheless, these results were interpreted to indicate that pre-TCR complex without extracellular Ig-like domains could be sufficient to drive the transition from the double-negative to the double-positive stage without binding to an extracellular ligand. Irving et al. [19] observed that in transgenic RAG $^{-/-}$ mice, that expressed only the truncated TCR β Myc transgene, the modified pre-TCR (composed by the truncated β chain and the endogenous pre TCR α chain) was inefficiently expressed on the cell surface. Based on these results they proposed that only a symmetrical pre-TCR complex can be stable or properly assembled. Following this idea, a pre-TCR complex with pT α 2 should not be stable. For the moment we can only speculate about the possible role of this differential splicing form. It is possible that pT α 2 could compete with pT α 1 for CD3 and TCR β binding, forming an inactive or differentially signaling complex, thus providing a regulatory element in pre-TCR assembly.

4 Materials and methods

4.1 Cell lines and tissues

Three human acute lymphoblastic leukemia cell lines, kindly provided by Dr. MacIntyre (Hôpital Necker, Paris, France), were used for our experiments: the mature, TCR $^{+}$ and CD3 $^{+}$ T cell lines HBL-all and Jurkat, and the $\gamma\delta$ T cell line MOLT4 [20, 21]. These cell lines were cultured in RPMI 1640/10 % FCS (Gibco-BRL, Gaithersburg, MD). The immature, pre-TCR-positive T cell line SCB29 [1] was cultured in IMDM/10 % FCS (Gibco). A thymus from a 3-month-old child was purchased from Hôpital Saint-Louis (Paris, France).

4.2 Isolation, mapping and sequencing of genomic DNA

High-density colony filters corresponding to a cosmid library of human chromosome 6 (no. 109 L4/FS6; Reference Library Database, Max Planck Institute for Molecular Genetics, Berlin; [7]) were prehybridized overnight at 42 °C in 50 % formamide, 4 \times SSC, 50 mM sodium phosphate (pH 6.8–7.2), 1 mM EDTA (pH 8.0), 10 % dextran sulfate, 1 % SDS, 50 μ g/ml denatured salmon sperm DNA and 10 \times Denhart's solution [22]. Hybridization was

performed in the same solution and under the same conditions with an [α - 32 P]dCTP random priming labeled (High-Prime, Boehringer Mannheim), human pT α cDNA probe [5]. For detection of positive clones, filters were washed three times in 0.1 % SSC at 65 °C and exposed to an X-ray film (Kodak). The pT α cosmids-containing bacterial clones DHR-5 α -MCR were supplied by the Max Planck Institute for Molecular Genetics. Cosmid DNA was purified according to Birnboim and Doly [23].

DNA inserts were mapped by Southern blotting: endonuclease-digested cosmid DNA samples were subjected to electrophoresis and transferred with 0.4 M NaOH to Hybond N+ membranes (Amersham). Filters were prehybridized and hybridized in 5 \times SSC, 5 \times Denhart 1 % SDS at 65 °C. Sequences of the human cDNA corresponding to the different pT α domains (leader peptide, Ig-like domain, and cytoplasmic tail) were used as probes for subsequent 32 P labeling. For rehybridizations probes were removed by incubating membranes for 10 min at 95 °C in 0.5 % SDS. DNA inserts were cut by enzyme restriction and subcloned into a Bluescript-KS⁺ vector (Stratagene, La Jolla, CA). DNA subclones were sequenced with an ABI PRISM dRhodamine Terminator Cycle Sequencing Ready Reaction Kit (PE Applied Biosystems, Warrington, GB) and by automated sequencing ABI PRISM 310 Genetic Analyzer (PE Applied Biosystems).

4.3 RT-PCR

Total RNA was isolated using the RNeasy Mini kit (Qiagen, Hilden, Germany). Reverse transcription was carried out using Superscript II reverse transcriptase kit (Gibco). Subsequent PCR was carried out in a total volume of 50 μ l, containing 1 mM deoxynucleoside triphosphates (dNTP), 0.5 μ M of each primer, 5 μ l 10 \times buffer (500 mM KCl, 100 mM Tris-HCl, pH 8.3, 15 mM MgCl₂ and 0.01 % (w/v) gelatin, in a volume of 1.5 ml), 2 μ l cDNA from the RT step, and 2 U AmpliTaq[®] DNA polymerase, LD (PE Applied Biosystems).

After a 3-min denaturation step at 94 °C, 40 cycles consisting of 45 s at 94 °C, 1 min at a primer-specific annealing temperature (T_A), and 1 min at 72 °C were performed in a Gene Amp PCR System 9700 thermal cycler (PE Applied Biosystems). Amplified DNA fragments were analyzed on a 2 % agarose gel in 1 \times TAE buffer. The PCR primers used for human pT α (T_A = 60 °C) were CTGCAGCTGGGTCCTGCCTC and AGTCTCCGTGCCGGGTGCA. Primers for human β -actin (T_A = 55 °C) were ACACTGTGCCCATCTACGAGGG and ATCATG-GAGTTGAAGGTAGTTTCG.

4.4 Protein analysis

L-[4,5- 3 H]-leucine metabolic and cell surface biotinylation were performed as described previously [24]. Subsequently, cells were lysed for 1 h in Triton lysis buffer (20 mM Tris/HCl, 150 mM NaCl, 2 % Triton X-100, 1 mM MgCl₂, pH 8) or digitonin lysis buffer (10 mM triethanolamine, 150 mM NaCl, 1 % digitonin, 1 mM EDTA) supplemented with 5 mg/ml aprotinin, 5 mg leupeptin, 100 mM PMSF and 10 mM iodoacetamide. Nuclei were removed by a 10 min centrifugation at 12 000 \times g at 4 °C. The remaining supernatant was precleared four times by a 2–6-h incubation with normal rabbit or mouse serum and protein G-Sepharose CL-4B (pG; Pharmacia, Uppsala, Sweden) in Triton or digitonin lysis buffer.

Proteins were immunoprecipitated by a 3-h incubation at 4 °C with pG-coupled R225 polyclonal antiserum (rabbit anti-murine pT α extracellular domain; [25]) or F23.1 monoclonal antibody (mouse anti-murine TCR β -V β 8). Unbound proteins were removed by washing four times with NET-TON buffer (650 mM NaCl, 5 mM EDTA, 50 mM Tris-HCl, 0.5 % Triton X-100, 0.05 % NaN₃, 1 mg/ml ovalbumin) and twice with NET-T (NET-TON with 0.15 M NaCl and without ovalbumin). Proteins were eluted from beads with reducing or non-reducing sample buffer (10 % glycerol, 2.3 % SDS, 62.5 mM Tris-HCl, pH 6.8, 0.05 % w/v bromophenol blue \pm 10 mM mercaptoethanol) by boiling for 5 min and subsequent addition of iodoacetamide (60 mM final concentration).

Proteins were run in a one-dimensional 12 % polyacrylamide gel or in two-dimensional diagonal SDS-polyacrylamide gels (nonreducing 8 % polyacrylamide gel in the first and reducing 12 % polyacrylamide gel in the second dimension) as described previously [1]. For visualization of radioactive proteins gels were fixed, incubated in Amplify solution (Amersham), dried and analyzed by autoradiography.

After electrophoresis, samples were transferred onto polyvinylidene difluoride membranes by semi-dry blotting. Membranes were blocked in the following solution: PBS, 4 % Tween 20, 2 % fetal calf serum 10 % non-fatty milk powder. Blots were incubated with streptavidin-HRP conjugate (Southern Biotechnology, Birmingham, AL) for 30 min, at room temperature in PBS 4 % Tween 20. HRP was detected by incubation with ECL detection solution (Amersham) and exposure to an X-ray film (Kodak). Blots were destained by incubation in PBS/0.1 % sodium azide for reprobing. Subsequently, blots were incubated in PBS 4 % Tween 20 with the pT α -specific R225 rabbit antiserum (1/1000), washed three times in PBS/4 % Tween 20 and incubated for 1 h with HRP goat anti rabbit IgG (1:20000 dilution; Southern Biotechnology). HRP detection was performed as described above.

Acknowledgments: Oskar Lechner is a recipient of a Marie Curie Training Grant from the European Commission. Harald von Boehmer is supported by the Institut Universitaire de France, by the Juvenile Diabetes Foundation (USA), and by the Koerber Foundation (Germany). This work was supported in part by the Institut National de la Santé et de la Recherche Médicale, Paris, and by the Faculté Necker Enfants Malades, Descartes Université, Paris.

5 References

- 1 Groettrup, M., Ungewiss, K., Azogui, O., Palacios, R., Owen, M. J., Hayday, A. C. and von Boehmer, H., A novel disulfide-linked heterodimer on pre-T cells consists of the T cell receptor beta chain and a 33 kd glycoprotein. *Cell* 1993. **75**: 283–294.
- 2 von Boehmer, H. and Fehling, H. J., Structure and function of the pre-T cell receptor. *Annu. Rev. Immunol.* 1997. **15**: 433–452.
- 3 Aifantis, I., Buer, J., von Boehmer, H. and Azogui, O., Essential role of the pre-T cell receptor in allelic exclusion of the T cell receptor beta locus. *Immunity* 1997. **7**: 601–607.
- 4 Saint-Ruf, C., Ungewiss, K., Groettrup, M., Bruno, L., Fehling, H. J. and von Boehmer, H., Analysis and expression of a cloned pre-T-cell receptor gene. *Science* 1994. **266**: 1208–1212.
- 5 Del Porto, P., Bruno, L., Mattei, M. G., von Boehmer, H. and Saint-Ruf, C., Cloning and comparative analysis of the human pre-T-cell receptor alpha chain gene. *Proc. Natl. Acad. Sci. USA* 1995. **19**: 121058–12109.
- 6 Fehling, H. J., Laplace, C., Mattei, M. G., Saint-Ruf, C. and von Boehmer, H., Genomic structure and chromosomal location of the mouse pre-T-cell receptor alpha gene. *Immunogenetics* 1995. **42**: 275–281.
- 7 Nizetic, D., Monard, S., Young, B., Cotter, F., Zehetner, G. and Lehrach, H., Construction of cosmid libraries from flow-sorted human chromosomes 1, 6, 7, 11, 13, and 18 for reference library resources. *Mamm. Genome* 1994. **5**: 801–802.
- 8 Shortle, V. P., Malaspina, P., Fox, M., Dooley, J. S., Volz, A., Ziegler, A., Trowsdale, J., Morrison, K. M. and Edwards, Y. H., A cosmid library specific for human chromosome regions 6p21.3 and 6q27. *Mamm. Genome* 1993. **4**: 493–498.
- 9 Cosson, P., Lankford, S. P., Bonifacino, J. S. and Klausner, R. D., Membrane protein association by potential intramembrane charge pairs. *Nature* 1991. **351**: 414–416.
- 10 Leiden, J. M. and Thompson, C. B., Transcriptional regulation of T-cell genes during T-cell development. *Curr. Opin. Immunol.* 1994. **6**: 231–237.
- 11 Peterson, C. L. and Calame, K., Proteins binding to site C2 (μ E3) in the immunoglobulin heavy-chain enhancer exist in multiple oligomeric forms. *Mol. Cell Biol.* 1989. **9**: 776–786.
- 12 McDougall, S., Peterson, C. L. and Calame, K., A transcriptional enhancer 3' of C beta 2 in the T cell receptor beta locus. *Science* 1988. **24**: 205–208.
- 13 Georgiev, G. P., Mobile genetic elements in animal cells and their biological significance. *Eur. J. Biochem.* 1984. **145**: 203–220.
- 14 Berger, M. A., Dave, V., Rhodes, M. R., Bosma, G. C., Bosma, M. J., Kappes, D. J. and Wiest, D. L., Subunit composition of pre-T cell receptor complexes expressed by primary thymocytes: CD3 δ is physically associated but not functionally required. *J. Exp. Med.* 1997. **186**: 1461–1467.
- 15 Hounsell, E. F., Davies, M. J. and Renouf, D. V., O-linked glycosylation structure and function. *Glycoconj. J.* 1996. **13**: 19–26.
- 16 Bruno, L., Rocha, B., Rolink, A., von Boehmer, H. and Rodewald, H. R., Intra- and extrathymic expression of pre-T cell receptor α gene. *Eur. J. Immunol.* 1995. **25**: 1877–1882.
- 17 Barber, D. F., Passoni, L., Wen, L., Geng, L. and Hayday, A. C., Cutting edge: The expression *in vivo* of a second isoform of pT α : implications for the mechanism of pT α action. *J. Immunol.* 1998. **161**: 11–16.
- 18 Groettrup, M., Baron, A., Griffiths, G., Palacios, R. and von Boehmer, H., T cell receptor (TCR) β chain homodimers on the surface of immature but not mature alpha, gamma, delta chain deficient T cell lines. *EMBO J.* 1992. **11**: 2735–2746.
- 19 Irving, B. A., Alt, F. W. and Killeen, N., Thymocyte development in the absence of pre-T cell receptor extracellular immunoglobulin domains. *Science* 1998. **280**: 905–908.
- 20 Minowada, J., Ohnuma, T. and Moore, G. E., Rosette-forming human lymphoid cell lines. I. Establishment and evidence for origin of thymus-derived lymphocytes. *J. Natl. Cancer Inst.* 1972. **49**: 891–895.
- 21 Fitzgerald, T. J., Neale, G. A., Raimondi, S. C. and Goohra, R. M., Rhom-2 expression not always correlates with abnormalities on chromosome 11 at band p13 in T cell acute lymphoblastic leukemia. *Blood* 1992. **80**: 3189–3197.
- 22 Sambrook, J., Fritsch, E. F. and Maniatis, T. (Eds.), *Molecular cloning: A laboratory manual*. Cold Spring Harbor Laboratory Press, Cold Spring Harbor 1989.
- 23 Birnboim, H. C. and Doly, J., A rapid alkaline extraction procedure for screening recombinant plasmid DNA. *Nucleic Acids Res.* 1979. **7**: 1513–1523.

- 24 **Groettrup, M. and von Boehmer, H.**, A role for a pre-T-cell receptor in T-cell development. *Immunol. Today* 1993. **14**: 610–614.
- 25 **Ungewiss, K.**, *Cloning and expression of a pre-T cell receptor gene*. PhD thesis, Univ. Basel, Switzerland 1996.

Correspondence: Claude Saint-Ruf, INSERM Unité 373, 156, rue de Vaugirard, F-75730 Paris, France
Fax: +33-1-4061-5590
E-mail: Saintruf@infobiogen.fr