

Essential requirement of an invariant V α 14 T cell antigen receptor expression in the development of natural killer T cells

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ABSTRACT NK1.1⁺ T [natural killer (NK) T] cells express an invariant T cell antigen receptor α chain (TCR α) encoded by V α 14 and J α 281 segments in association with a limited number of V β s, predominantly V β 8.2. Expression of the invariant V α 14/J α 281, but not V α 1, TCR in transgenic mice lacking endogenous TCR α expression blocks the development of conventional T $\alpha\beta$ cells and leads to the preferential development of V α 14 NK T cells, suggesting a prerequisite role of invariant V α 14 TCR in NK T cell development. In V β 8.2 but not V β 3 transgenic mice, two NK T cells with different CD3 ϵ expressions, CD3 ϵ ^{dim} and CD3 ϵ ^{high}, can be identified. CD3 ϵ ^{high} NK T cells express surface V α 14/V β 8 TCR, indicating a mature cell type, whereas CD3 ϵ ^{dim} NK T cells express V β 8 without V α 14 TCR and no significant CD3 ϵ expression (CD3 ϵ ^{dim}) on the cell surface. However, the latter are positive for recombination activating gene (RAG-1 and RAG-2) mRNA, which are only expressed in the precursor or immature T cell lineage, and also possess CD3 ϵ mRNA in their cytoplasm, suggesting that CD3 ϵ ^{dim} NK T cells are the precursor of V α 14 NK T cells.

T lymphocytes and natural killer (NK) cells are distinct subsets of lymphoid cell lineage that develop from common precursors (1–3). NK cells do not possess T cell antigen receptors (TCRs) but express distinct types of NK receptors (4, 5). NK T cells are characterized by the expression of TCR composed mainly of $\alpha\beta$ heterodimers and CD16 and NK1.1, the latter two of which are “normally” NK markers (4, 5), and form a minor subset in the thymic CD4⁻CD8⁻ or CD4⁺CD8⁻ population (<0.5%) (6–13). In the periphery, NK T cells form a relatively major subset comprising 5% of splenic T and 40% of bone marrow T cells (13). Generally, murine splenocytes contain 2–3% NK cells (NK1.1⁺ TCR β ⁻), 1–2% NK T cells (NK1.1⁺ TCR β ⁺), and 40–50% conventional $\alpha\beta$ T cells (NK1.1⁻ TCR β ⁺). Contrary to the general rule that the interaction of TCR with major histocompatibility complex molecules leads to the development of conventional $\alpha\beta$ T lymphocytes, NK T cells are selected by a nonclassical major histocompatibility complex class I molecule (14–19), recently identified as CD1 in mice (20). It has been suggested that NK T cells are involved in tumor cell killing (11, 12, 21), controlling the T cell helper type 2 response (22, 23), acute bone marrow rejection (24, 25), and autoimmunity (26, 27).

Unique features of NK T cells include the expression of an invariant TCR α chain (TCR α) encoded by V α 14 and J α 281 segments with a one-base N region in association with limited V β s, mostly V β 8.2 (13, 28–30). This invariant V α 14 TCR α is not found in conventional $\alpha\beta$ T cells. We investigated the role of V α 14/V β 8 TCR in the development of NK T cells and found that V α 14 TCR expression in the absence of endogenous TCR α expression leads to the preferential development

of NK T cells but the developmental arrest of conventional $\alpha\beta$ T cells, indicating an essential role of invariant V α 14 TCR in the development of NK T cells. Furthermore, we found CD3 ϵ ^{dim} V β 8⁺, V α 14⁻ NK T cells of the precursor or immature cell type that express mRNA of recombination activating genes (RAG-1 and RAG-2) in cytoplasm. Thus, we defined CD3 ϵ ^{dim} V β 8⁺, V α 14⁻ NK T cells as NK T cell precursors.

MATERIALS AND METHODS

Mice. Specific pathogen-free C57BL/6 mice were purchased from the Shizuoka Experimental Animal Co. Ltd (Hamamatsu, Shizuoka, Japan). V α 14 TCR gene transgenic (V α 14 tg) mice were established using V α 14/J α 281 cDNA (pT α 2) (28). A 1.0-kb fragment of V α 14J α 281C α cDNA (pT α 104/46) was cloned into the *Sal*I site of p β APr-3-neo, which contains a 4.3-kb fragment of the human (h) β -actin promoter (p β APr-T α 2-neo). The 11.0-kb *Bgl*II/*Pvu*I fragment of p β APr-T α 2-neo was microinjected into C57BL/6 fertilized eggs and implanted into foster mothers. The resulting progeny were screened for the integration of V α 14 TCR transgenes (5.3 kb) by Southern blot analysis on *Eco*RI-digested tail DNA with probes for h β -actin promoter (4.3 kb fragment) and V α 14 cDNA. One (no. 12) out of five independent lines established was used for further experiments and mated with TCR α -deficient (TCR α ^{-/-}) mice (kindly provided by P. Mombaerts; ref. 31) to generate TCR α ^{-/-}/V α 14 tg mice by backcrossing for five generations. The (TCR α ^{+/-} × V α 14 tg)F₁ mice were selected and crossed with TCR α ^{+/-} mice to generate TCR α -deficient homozygous V α 14 tg (TCR α ^{-/-}/V α 14 tg) mice with a C57BL/6 background.

Several other TCR gene transgenic mice were obtained: V α 11 tg (B10.A) from M. Davis (32), V β 3 tg (B10.A) from M. Davis (32), V α 11/V β 3 tg (B10.A) derived from crossing V α 11 tg and V β 3 tg mice, V β 8.2 (V β HY) tg mice (C57BL/6) and V α HY/V β 8.2 tg (C57BL/6) from H. von Boehmer (33), V α 14/V β 8.2 tg mice (C57BL/6) obtained by mating with V α 14 tg and V β 8.2 (V β HY) tg mice, and TCR α ^{-/-}/V α 1 tg mice with a C57BL/6 background generated by mating V α 1 (V α DO11.10) tg mice with a C57BL/6 background from D. Loh (34) with TCR α ^{-/-} mice and further backcrossing for five to seven generations in S.K.'s laboratory.

Fluorescein-Activated Cell Sorter (FACS) Analysis. Splenocytes were incubated with 10 μ g/ml anti-CD16 (2.4G2) to block nonspecific Fc-mediated antibody binding, followed by incubation with various combinations of antibodies. For the

Abbreviations: NK, natural killer; RAG, recombination activating gene; TCR, T cell antigen receptor; TCR α and TCR β , TCR α and β chains; tg, transgenic; h β -actin, human β -actin; FACS, fluorescein-activated cell sorter.

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detection of V α 14 TCR expression, Cychrome-avidin, biotinylated anti-NK1.1 (PK136), fluorescein isothiocyanate-conjugated anti-TCR β (H57-598), and phycoerythrin-labeled anti-V α 14 (CMS-1) (35) were used; for the detection of CD3 ϵ in NK T cells, fluorescein isothiocyanate-anti-CD3 ϵ (2C11), phycoerythrin-anti-NK1.1, and biotinylated anti-TCR β mAbs together with Cychrome-avidin were used. To confirm specific staining with anti-TCR β or anti-V α 14, cells were preincubated with excess amounts of unlabeled antibodies and reacted with labeled antibodies. At least 10^5 cells, including small size cells, were gated and analyzed by EPICS-XL as described (13).

PCR. PCR was carried out with cDNAs derived from 5000 cells using primers specific for V α 14/C α , V β 8/C β , CD3 ϵ , RAG-1, RAG-2, and β -actin under the conditions described previously (13). PCR was performed at 94°C for 1 min, 60°C for 1 min, and 72°C for 1 min for 40 cycles. Oligonucleotides were 5'-GTACTGGTATCGGCAGGACAC-3' and 5'-GGTAGCCTTTTGTGTTTGC-3' for V β 8; 5'-CCCAAGTG-GAGCAGAGTCTAAGG-3' and 5'-CTGTCCTGAGAC-CGAGGATC-3' for V α 14; 5'-AACACTTCTGGGGCAT-CCTG-3' and 5'-TGATGATTATGGCTACTGCTG-3' for CD3 ϵ ; 5'-CCAAGCTGCAGACATTCTAGCACTC-3' and 5'-CAACATCTGCCTTCACGTCGATCC-3' for RAG-1; 5'-AGGGACATCTCCTACTAAG-3' for RAG-2; and 5'-GAG-AGGAAATCGTGTGA-3' and 5'-ACATCTGCTGGA-AGGTGGAC-3' for β -actin.

RNase Protection Assay. The RNase protection assay described previously (29) was performed using 32 P-labeled antisense probes generated by V α 14/J α 281/C α cDNA (pTsa2) and β 2 m cDNA (pMZ416). The radioactivity of the protected band was measured by automated densitometry (Bioimage Analyzer BAS 2000, Fuji) and expressed as a percentage of total C α or β 2 m bands.

RESULTS AND DISCUSSION

NK T cells are known to express only one invariant TCR α encoded by V α 14 and J α 281 gene segments with a one-base N region, indicating its essential requirement for NK T cells (28–30). To examine the role of invariant V α 14/J α 281 TCR in NK T cell development, we generated a V α 14/J α 281 transgenic (V α 14 tg) mouse strain (Fig. 1A and B). The expression of transgenic V α 14/J α 281 TCR was investigated by RNase protection (Fig. 1C) and FACS analysis (Fig. 1D). The transgenic V α 14 TCR mRNA was detected in all tissues, including thymus, spleen, and kidney, suggesting the unrestricted tissue expression of transgenic V α 14 TCR mRNA under the control of h β -actin promoter. The frequency of V α 14 TCR expression in lymphoid tissues was, however, about 9 times higher (3.4% and 3.7% in thymus and spleen, respectively) than in kidney (0.43%) (Fig. 1Ca), indicating normal lymphoid cell development in V α 14 tg mice. FACS profiles of V α 14 tg spleen (Fig. 1Dc) showed similar patterns to those of normal C57BL/6 spleen (Fig. 1Da), whereas V α 14 TCR expression was significantly increased in the V α 14 tg NK T cell population (Fig. 1Dd) compared with those in C57BL/6 NK T cells (Fig. 1Db) (31–64%). This result indicates that the transgene of the invariant V α 14 TCR gives rise to increased expression of invariant V α 14 TCR even though the absolute numbers of NK T cells (7.7×10^5) in V α 14 tg spleen are at normal levels (8×10^5).

Since allelic exclusion of the TCR α locus is usually incomplete, TCR α s other than transgenic TCR α are likely to be expressed in V α 14 tg animals. To avoid the contribution of endogenous TCR α , we mated V α 14 tg mice with TCR $\alpha^{-/-}$ mice to generate TCR $\alpha^{-/-}$ /V α 14 tg mice. Only V α 14⁺ NK T cells developed in these mice, but surprisingly, conventional $\alpha\beta$ T cells were absent (Fig. 2Ac and Ad). In fact, thymocyte development was completely disturbed, because only double-

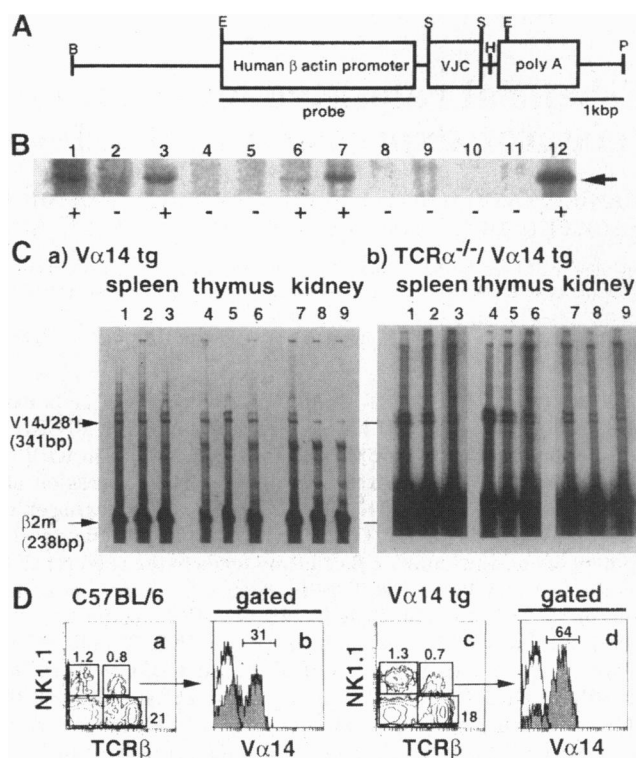


FIG. 1. Generation of V α 14 TCR gene transgenic mice and their expression. (A) Schematic representation of the V α 14 TCR construct. Restriction enzyme sites: B, *Bgl*II; E, *Eco*RI; S, *Sal*I; H, *Hind*III; P, *Pvu*I. (B) Detection of the transgenic h β -actin/V α 14 gene by Southern blotting on *Eco*RI-digested tail DNA. The data show the 5.3-kb band detected by an h β -actin probe. The V α 14 probe also detected the same band. No. 12 and its progeny were used for experiments. (C) Expression of invariant V α 14 TCR as detected by an RNase protection assay. The frequency of invariant V α 14 TCR is expressed as the percentage of β 2m in each sample (nos. 1–9): (a) 5.0%, 1.2%, and 4.0% (mean 3.4%) in the spleen; 3.4%, 6.1%, and 1.5% (mean 3.7%) in the thymus; 0.7%, 0.4%, and 0.2% (mean 0.43%) in the kidney in V α 14 tg mice; (b) 2.5%, 0.9%, and 0.7% (mean 1.4%) in the spleen; 8.4%, 4.8%, and 2.1% (mean 5.1%) in the thymus; 0.3%, 0.1%, and 0.3% (mean 0.23%) in the kidney in TCR $\alpha^{-/-}$ /V α 14 tg mice. (D) Cell surface expression of V α 14 TCR detected by FACS. (a) C57BL/6 spleen (1×10^8). (c) V α 14 tg spleen (1.1×10^8). (b and d) V α 14 staining patterns of NK T cells gated from Da and Dc, respectively. The numbers in parentheses represent total cell numbers in the legend and percentages in the FACS figures, respectively.

positive thymocytes with no TCR expression in the absence of CD4⁺ or CD8⁺ single-positive thymocytes were detected, indicating the severe developmental arrest of conventional $\alpha\beta$ T cells (Fig. 2Ab). TCR V β repertoire analysis also supports the present data and indicates that V α 14 TCR detected in TCR $\alpha^{-/-}$ /V α 14 tg mice are selectively associated with V β 8.2 similar to the major NK T cell repertoire in normal C57BL/6 mice (data not shown). The expression of invariant V α 14 TCR in thymocytes and spleen cells of TCR $\alpha^{-/-}$ /V α 14 tg mice was also confirmed by RNase protection assay, demonstrating that invariant V α 14 mRNA expression was 6 times (1.4% in spleen) and 20 times (5.1% in thymus) higher than in kidney (0.23%) (Fig. 1Cb). In contrast, TCR $\alpha^{-/-}$ /V α 1 tg mice (Fig. 2Ag) have conventional $\alpha\beta$ T cells but lack NK T cells. These results indicate that the expression of invariant V α 14/J α 281, but not other TCR α s such as V α 1, leads to the development of NK T cells and suppresses conventional $\alpha\beta$ T cell development. The essential requirement of invariant V α 14 TCR expression for NK T cell development was recently confirmed in mice lacking invariant V α 14 TCR expression generated by the homologous recombination technique. In these animals, no NK T cells were

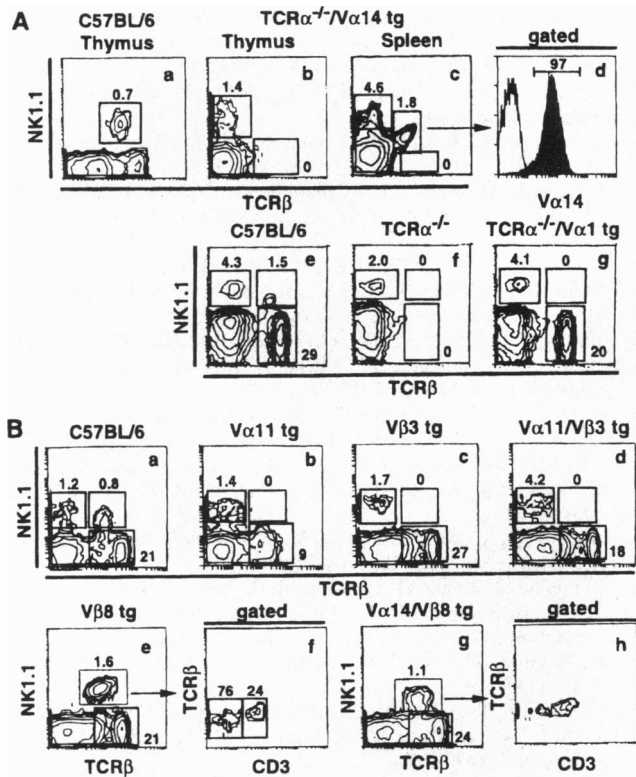


FIG. 2. FACS analysis of NK T cells in various TCR tg mice. (A) (a) C57BL/6 thymus (1.1×10^8). (b) C57BL/6 $TCR\alpha^{-/-}/V\alpha14$ tg thymus (0.85×10^8). Note that many of NK1.1⁺ cells detected in Fig. 2Aa are $\gamma\delta$ NK T cells that are not normally seen in C57BL/6 thymus but are present in $TCR\alpha^{-/-}$ mice. (c) C57BL/6 $TCR\alpha^{-/-}/V\alpha14$ tg spleen (1.1×10^8). (d) $V\alpha14$ TCR staining profile of NK T cells gated from Ac. (e) C57BL/6 spleen (0.8×10^8). (f) C57BL/6 $TCR\alpha^{-/-}$ spleen (1×10^8). (g) C57BL/6 $TCR\alpha^{-/-}/V\alpha1$ tg spleen (0.88×10^8). (B) (a) C57BL/6 spleen (1×10^8). (b) B10.A $V\alpha11$ tg spleen (1×10^8). (c) B10.A $V\beta3$ tg spleen (1.2×10^8). (d) B10.A $V\alpha11/V\beta3$ tg spleen (1×10^8). (e) C57BL/6 $V\beta8.2$ tg (1.3×10^8). (f) $CD3\epsilon$ staining patterns of NK T cells gated from Be. $CD3\epsilon^{high}$ and $CD3\epsilon^{dim/-}$ fractions were sorted out by FACS and used for PCR analysis shown in Fig. 4. (g) C57BL/6 $V\alpha14/V\beta8.2$ tg spleen (1.1×10^8). (h) $CD3\epsilon$ staining profiles of NK T cells gated from Bg. The numbers in parentheses represent total cell numbers in this legend and percentages in the figures, respectively.

observed, whereas other lymphoid lineage cells were normal (unpublished data). These findings also confirmed that NK T cells are an independent lineage distinct from other cell types and that $V\alpha14$ TCR is essential for the development of NK T cells.

Since $V\beta8.2$ is predominantly used in NK T cells, we examined NK T cell development in $V\beta8.2$ tg mice. As shown in Fig. 2Be, $V\beta8.2$ tg mice have NK T and T cells but lack NK cells. In contrast, $V\beta3$ tg animals have NK and T cells but lack NK T cells (Fig. 2Bc). It has been shown that $V\beta5$ tg mice also lack NK T cells (24). It is thus likely that $V\beta8.2$, but not $V\beta3$ or $V\beta5$, supports the development of NK T cells. This was also confirmed in $TCR\alpha/\beta$ double-transgenic mice. Mice expressing both $V\alpha14$ and $V\beta8.2$ have NK T cell populations similar to that of $V\beta8.2$ tg mice (Fig. 2Bg), but the majority of NK T cells in the double-transgenic mice become $V\alpha14^+$ $CD3\epsilon^{high}$ (data not shown; see Fig. 2Bh). On the other hand, $V\alpha11$ tg, $V\beta3$ tg, or $V\alpha11/V\beta3$ tg mice do not have NK T cells showing normal NK and T cell development (Fig. 2Bb, Bc, and Bd). Although the disappearance of NK cells in $V\beta8$ tg or $V\alpha14/V\beta8$ tg mice is intriguing, actual proof of this observation awaits further experiments. In any event, $V\beta8.2$ expression by itself is not sufficient to induce NK T cell development,

whereas both $V\alpha14/V\beta8.2$ TCR expression are required for full NK T cell development. RNase protection analysis also supports the above notion, because invariant $V\alpha14$ expression was always detected in $V\beta8.2$ tg and $V\alphaHY/V\beta8.2$ tg but not in $V\alpha1$ tg, $V\alpha11$ tg, $V\beta3$ tg, or $V\alpha11/V\beta3$ tg mice (Fig. 3). Therefore, the expression of invariant $V\alpha14/J\alpha281$ TCR and the development of NK T cells correlate perfectly, indicating that NK T cell development depends on invariant $V\alpha14/J\alpha281$ expression.

Interestingly, NK T cells in $V\beta8.2$ tg mice contain two populations: $CD3\epsilon^{high}$ and $CD3\epsilon^{dim}/CD3\epsilon^-$ (Fig. 2Bf). Thus, it is possible that the former is a mature cell type, whereas the latter is a precursor or immature cell type of the former. In fact, the transition from $CD3\epsilon^{dim}$ NK T cells to $CD3\epsilon^{high}$ NK T cells is quite likely, because the $CD3\epsilon^{dim}$ NK T cell fraction in $V\beta8.2$ tg mice, as shown in Fig. 2Bf, was greatly reduced, and the majority of NK T cells become $CD3\epsilon^+$ in $V\alpha14/V\beta8.2$ double-transgenic mice (Fig. 2Bh). We thus attempted to investigate whether $CD3\epsilon^{dim}$ NK T cells possess the molecular characteristics of an immature or precursor cell type. $CD3\epsilon^{high}$ and $CD3\epsilon^{dim}$ NK T cell populations in $V\beta8.2$ tg mice (Fig. 2Bf) were isolated by FACS and analyzed by PCR. The data shown in Fig. 4 clearly demonstrate that $CD3\epsilon^{dim}$ NK T cells have no $V\alpha14$ TCR mRNA, although they express small but significant levels of $CD3\epsilon$ mRNA in the cytoplasm, even though their cell surface expression is not enough to be detected by anti- $CD3\epsilon$ (left rectangle in Fig. 2Bf). In addition, $CD3\epsilon^{dim}$ NK T cells possess RAG-1 and RAG-2 mRNA, indicating their immature or precursor potential in this particular cell type (Fig. 4). It is, therefore, quite likely that $CD3\epsilon^{dim}$ NK T cells without $V\alpha14$ TCR expression are precursor for mature $V\alpha14^+$ NK T cells. In fact, both RAG-1 and RAG-2 expression were negative following their expression of $V\alpha14$ TCR in $CD3\epsilon^{high}$ NK T cells (Fig. 4).

Based on these characteristics, we define the $V\alpha14^- V\beta8^+ CD3\epsilon^{dim}$ NK T cell population as an NK T cell precursor. The results clearly suggest that the induction of $V\alpha14$ TCR, as well as the down-regulation of RAG expression, are essential for full NK T cell development. These events are strikingly similar to those observed in the transition from pro- $B\mu^-$ cells to large pre- $B\mu^+$ cells where RAG expression in pre- $B\mu^+$ cells becomes entirely negative along with the expression of the μ -heavy chain on the cell surface (36).

In summary, we present evidence that invariant $V\alpha14$ TCR expression in the absence of endogenous $TCR\alpha$ expression blocks the generation of conventional $\alpha\beta$ T cell development

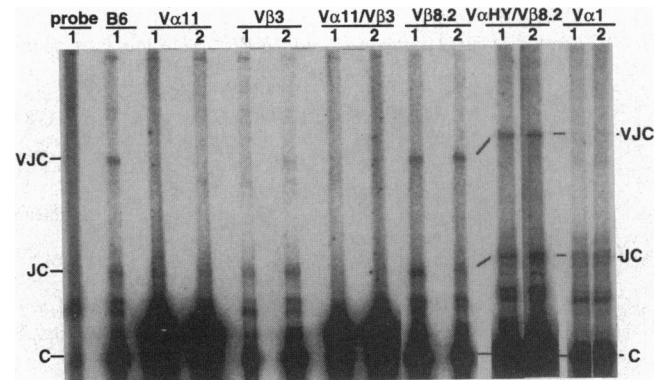


FIG. 3. RNase protection analysis of invariant $V\alpha14/J\alpha281$ TCR expression in various TCR tg mice. Total RNA from C57BL/6 (B6), $V\alpha1$ tg, $V\alpha11$ tg, $V\beta3$ tg, $V\alpha11/V\beta3$, $V\beta8.2$ tg, and $V\alphaHY/V\beta8.2$ tg mice were used. Lanes 1 and 2 represent two individual mice in each experiment. Anti-sense riboprobes detect $V\alpha14/J\alpha281/C\alpha$ (401 bp), $J\alpha281/C\alpha$ (275 bp), and $C\alpha$ (211 bp) protected bands, respectively. Note that invariant $V\alpha14$ TCR expression was detected only in $V\beta8.2$ tg and $V\alphaHY/V\beta8.2$ tg mice, but not in other mice.

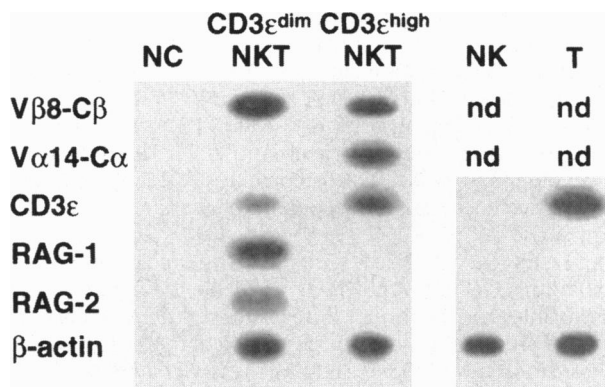


FIG. 4. Expression of TCR complex and RAG mRNA in CD3 ϵ^{dim} and CD3 ϵ^{high} NK T cells. Reverse transcription-PCR was performed on RNA from 4–5 $\times 10^5$ cells sorted from CD3 ϵ^{dim} (lane 2) and CD3 ϵ^{high} (lane 3) fractions of C57BL/6 V β 8.2 tg NK T cells shown in Fig. 2Bf, and RNA from 2 $\times 10^5$ $\alpha\beta$ T cells (lane 4) and 2 $\times 10^5$ NK cells of C57BL/6 spleen (lane 5). nd, not done; NC (lane 1), negative control.

and selectively drives the NK T cell-developmental pathway, indicating the essential role of V α 14 TCR in the development of NK T cells. In addition, the expression of V β 8.2 results in the generation of the precursor form of V α 14 NK T cells. The precursor NK T cells express small amounts of CD3 ϵ mRNA but large amounts of RAG-1/RAG-2 mRNA in the cytoplasm, whereas no significant V α 14 TCR or CD3 ϵ were detected on the cell surface. Interestingly, the down-regulation of RAG-1/RAG-2 expression in precursor NK T cells seems to be essential for the development of mature V α 14⁺ NK T cells. Although NK T cells seem to represent a lineage distinct from conventional T cells because of their extrathymic development before thymus formation during the very early stages of embryogenesis (d9.5) (37, 38), the molecular events that occur during NK T cell development are similar to those of other lymphoid cell lineages.

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