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Identification of a Novel Ly49 Promoter That Is Active in Bone Marrow and Fetal Thymus

Ali Saleh,* Andrew P. Makrigiannis,* Deborah L. Hodge,* and Stephen K. Anderson††


The analysis of several Ly49 genes has identified a tissue-specific promoter adjacent to the previously defined first exon. The current study reveals the presence of an additional Ly49 promoter (Pro-1) and two noncoding exons upstream of the previously defined promoter (Pro-2). DNA sequences homologous to Pro-1 are present 4–10 kb upstream of Pro-2 in all Ly49 genes examined, and Pro-1 transcripts were detected from the Ly49a, e, g, a, and v genes. Pro-1 activity can be detected in bone marrow, embryonic thymus, freshly isolated liver NK cells, and the murine LNK cell line, but it does not function in adult thymus, sorted NK-T cells, spleen NK cells, or the EL-4 T cell line, even though these cells express Ly49 proteins. Luciferase reporter assays identified a Pro-1 transcriptional orientation. Of the 16 genes currently identified in the Ly49 gene family of class I MHC receptors represent the functional analogs of the human killer cell Ig-related receptor gene family. Although they constitute structurally distinct protein families, the C-type lectin-related Ly49 proteins and the killer cell Ig-related receptor proteins associate with identical signaling molecules to achieve either activation or inhibition of NK cells in response to specific MHC class I ligands. The Ly49 gene cluster has been mapped in the C57BL/6 (B6) mouse genome (1–3), and the genes are arranged in tandem with an identical transcriptional orientation. With the exception of the Ly49 h, p, and n cluster of highly related activators, the Ly49 genes are not grouped with respect to activating/inhibitory function or gene homology. Of the 16 Ly49 genes currently identified in the B6 genome, Ly49a–j, and q have been shown to produce mRNAs with a complete coding region, Ly49k, m, and n represent transcribed pseudo genes, and the remaining two genes (Ly49i and v) do not appear to produce transcripts in the B6 strain (4–8) (S. K. Anderson, unpublished observations).

The activation of Ly49 genes during murine NK cell development presents an interesting system for the study of selective gene expression. It has been proposed that a stochastic process controls the activation of Ly49 gene transcription, because the proportion of NK cells that express two Ly49 proteins is roughly equivalent to the product of the proportion of NK cells expressing the individual receptors (9). Single cell RT-PCR analysis of Ly49 expression has shown that the majority of NK cells express from one to four different receptors per cell and NK cells with five or more Ly49 proteins are extremely rare, supporting the theory that the Ly49 genes are activated by a probabilistic mechanism (10).

The promotor region responsible for the expression of Ly49a in mature NK/NK-T cells has been cloned, and the role of cis-acting elements in gene activation and cell-specific transcription has been studied (11–13). The trans-acting T cell-specific factor-1 has been shown to be required for the acquisition of Ly49A expression during development (13). The activating transcription factor-2 binds to a 13-bp element adjacent to the predicted TATAAA of Ly49a, and it is the major factor responsible for Ly49a transcription in EL-4 cells (12). A study of the 5′ region of the Ly49 gene identified a core promotor that is preferentially transcribed in a Ly49-expressing cell line, EL-4 (14). Surprisingly, sequence elements immediately upstream from the core promotor were found to inhibit activity, and no enhancers were detected in the upstream region analyzed. An inhibitory upstream element was also detected in a functional analysis of the Ly49c and j promoters (15). The lack of detectable enhancer elements immediately upstream of these promoters suggests that additional control elements may exist elsewhere. The current knowledge of Ly49 promotor structure and function has not provided any insight with respect to the mechanisms responsible for the stochastic activation of Ly49 genes.

Extensive screening of a 129/J liver NK cell cDNA library resulted in the identification of several novel Ly49 genes, including an unusual cDNA clone of Ly49g containing an alternative first exon (16). This result indicated the presence of an alternative Ly49 promotor. This study describes the isolation and characterization of the novel promotor from several Ly49 genes.

Materials and Methods

Cell lines

EL-4 and P815 cell lines were cultured in RPMI 1640 supplemented with 10% FBS, 100 U/ml penicillin, and 100 U/ml streptomycin. The LNK cell line (17) was cultured in RPMI 1640 containing 2-ME, nonessential amino acids, 10% FBS, 100 U/ml penicillin, 100 U/ml streptomycin, sodium pyruvate, L-glutamine, HEPES, and IL-2 (8000 IU/ml).

Cell isolation

Mouse NK cells were purified from livers or spleens of 129/J or B6 mice. Liver NK cells were isolated as previously described (18). Routinely, 75–
80% of the resulting cells were NK-1.1+. Spleen cells were sorted for DX5+ CD3+ NK cells or DX5- CD3- NK-T cells on a MoFlo Cell Sorter (Cytomation, Ft. Collins, CO). Bone marrow cells were isolated from the femurs and tibias of B6 mice. After lysis of RBCs, the remaining cells were washed with PBS and counted. Total liver and thymus cell suspensions were isolated from day-15 B6 embryos. Animal care was provided in accordance with the procedures outlined in “A Guide for the Care and Use of Laboratory Animals” (National Institutes of Health, publication no. 86-23, 1985).

RT-PCR analysis of promoter use

Cellular poly(A)+ RNA was isolated using the QuickPrep mRNA kit (Amersham Pharmacia Biotech, Piscataway, NJ). Oligo(dT)-primed cDNA was synthesized with the Superscript CDNA synthesis kit (Invitrogen, Carlsbad, CA). One microliter of cDNA was amplified using 35 cycles of 94°C for 30 s, 58°C for 30 s, and 72°C for 30 s with specific primers using Platinum PCR Supermix (Invitrogen). The antisense primer used to detect promoter (Pro)-1 activity was from a conserved region of exon 4 at position 261 of the Ly49 coding sequence (5′-TACCTTGTCCATGTTGCTGAG-3′). A degenerate antisense primer spanning the Ly49 termination codon (5′-CSTRTTGGGARATYAAATSAGGAG-3′) was used to amplify and clone the complete coding region. The −1a exon forward primers were 5′-GCAAG GTCCTCCTCAGTGAAGC and 5′-TTGACGCTGTGCAATGATAG, and the exon 1 forward primer was 5′-GAGGTGTGATCTACCTGAGG.

RNase protection assays

The RNase protection assay (RPA) was performed according to the manufacture’s protocol using an RPA kit (RPA II; Ambion, Austin, TX). To localize the transcription initiation site of the Ly49g alternative promoter in EL-4 cells, an antisense Ly49g RNA probe was generated from the Ly49g Pro-1 clone in pCR2.1-TOPO linearized with HindIII. In vitro transcription was performed according to the manufacturer’s protocols using the T7 MAXScript (Ambion) in vitro transcription kit. The [α-32P]RNA probe was separated on a 10% denaturing polyacrylamide gel and the full-length 500-bp probe was excised and eluted by overnight incubation at 37°C in gel elution buffer (Ambion). Approximately 2 × 106 cpm of the gel-purified Ly49g-specific probe was added to 1 μl of poly(A)+ mRNA from either LNK or EL-4 cells in each reaction mixture. The protected mRNA products were separated on a 6% denaturing polyacrylamide gel. The gel was dried and exposed for 72 h on a PhosphorImager cassette (Molecular Dynamics, Sunnyvale, CA). The image was visualized using PhosphorImager SI analysis and ImageQuaNT (Molecular Dynamics).

Generation of luciferase reporter plasmids

The Ly49i-Pr1 construct was generated by PCR from a 5-kb PstI fragment of the Ly49i promoter region (14) using a reverse primer within the predicted exon −1a (5′-AACCTGTCATAGTCACAGCC) and a T7 primer from the vector. The 330-bp PCR product was subcloned into the pcR-XL-TOPO vector. A 400-bp PCR product was used to subclone into the pcR-XL-TOPO vector and inserted into the pcGL3-basic vector (Promega, Madison, WI). To generate the Ly49i-3′-Pro1 construct, Ly49i-Pro1 was digested with Smal and BstZI to remove the 5′ region of the promoter, and the remaining vector was religated. The Ly49i-5′-Pro1 construct was generated by digestion of Ly49i-Pro1 with BstZI and HindIII to remove the 3′ region, and the remaining vector was religated using Klenow to fill in the HindIII site. To generate a Ly49i construct similar to the Ly49i-altpro construct, PCP was performed on a B6 BAC clone (RPCI-23 416H5) with primers corresponding to the 5′ and 3′ ends of Ly49i-altpro (forward, CCTGTATCATGTTTATTACACTCC; reverse, GGGAGGATTGTCATATCGCT). The PCR product was subcloned into pCR2.1-TOPO and then transferred to pGL3-basic using SacI and XhoI, resulting in the Ly49i-altpro luciferase construct. The Ly49i-altpro promoter region was isolated from this PCP clone by digestion with SacI and XhoI and inserted into the pcGL3-basic vector. To generate the Ly49j-Pro1 construct, a 5′-TTCCCTTGACTCATCGTCTTG; reverse 5′-CAGTCGACACCTGAGCAGT) and cloned into pCR2.1-TOPO. The Ly49j-Pro1 core was transferred to pGL3-basic using HindIII and XhoI, resulting in the Ly49-Pro1 luciferase construct. The Ly49-Pro2 construct was generated by ligating a XbaI-EcoRV fragment of the Ly49a promoter region (12) into pGL3-basic. The Ly49a-2kb construct was generated by PCR from a B6 BAC clone (RPCI-23 416H5) using the following primers: forward, CAACTTATTAGAGTCAGGC; reverse, CCATCGAGAGAATCA CTC. Ly49a-2kb-Pro1 was generated by inserting the Ly49-Pro1 core in front of the 2-kb region using SacI and XhoI. All constructs were verified by sequencing with specific primers. Sequence analysis was performed with the SeqWeb package at the Frederick Cancer Research and Development Center supercomputing center (Frederick, MD).

Cell transfection and luciferase assays

A total of 4 × 105 P815 cells in RPMI medium without serum were transduced with 10 μg of the individual reporter constructs by electroporation using a GenePulser (Bio-Rad, Richmond, CA). All constructs were verified by sequencing with specific primers. Sequence analysis was performed with the SeqWeb package at the Frederick Cancer Research and Development Center supercomputing center (Frederick, MD).

Results

Identification of novel 5′ exons in the Ly49 gene family

The studies of Ly49 promoter function reported to date have focused on the region preceding the 5′ end of CDNAs isolated from mature NK cells. The isolation of a variant of Ly49g from 129/J liver NK cells that contained a novel 5′ untranslated region suggested that an additional promoter existed. A search of GenBank with the novel sequence yielded significant matches to a region 5′ of the Ly49a promoter and two regions upstream of the Ly49i promoter. This result indicated the presence of an additional promoter as well as an additional noncoding exon upstream of the Ly49g promoter. Three B6 BAC clones were identified (GenBank accession nos. AC087336, AC090127, and AC090563) that contained the intergenic sequences preceding the Ly49a, c–f, h–k, m, and n genes. Sequences corresponding to the predicted novel exons were found in all Ly49 genes examined; however, this sequence was less homologous in the activating Ly49j, k, and l genes, but the splice acceptor sequence of the putative exon c–f was significantly different from that of the inactivating Ly49h, i, and j genes.

Differences in the sequence preceding the Pro-1 region of the activating Ly49j genes was found to be significantly different from that of the inhibitory Ly49h, whereas the region upstream of the previously described Pro-2 is highly conserved among all Ly49s (19). The Pro-1 sequence was compared against the available rat genomic Ly49 sequences (GenBank accession no. AC103500; Fig. 1B). The Pro-1 region was conserved to the same extent as the sequences surrounding exons (>80%), while intron sequences were less conserved (60%), suggesting that Pro-1 represents an important functional element that has been conserved between the two species.
Detection of Ly49 mRNAs containing exon –1a

To survey cell lines and tissues for Pro-1 activity, an oligonucleotide primer from a conserved region of exon –1a was used in conjunction with an antisense primer from a conserved region of exon 4 to perform RT-PCR on mRNA isolated from bone marrow, thymus, spleen NK, liver NK, NK-T cells, the LNK cell line, and the EL-4 cell line. Fig. 2A shows the results of an RT-PCR experiment performed with the exon –1a forward primer as well as a control exon 1 forward primer on mRNAs isolated from 6- to 8-wk-old B6 mice. Purified liver NK cell mRNA generated Ly49 PCR products corresponding to spliced transcripts containing exon –1a or exon 1, whereas purified NK-T cell mRNA produced only Pro-2-derived PCR products. Transcripts derived from Pro-1 were detected in bone marrow and liver NK cells, but not in thymus or spleen NK cells. Several PCR products were cloned and sequenced from each reaction to verify that the bands observed represented Pro-1 or Pro-2 transcripts. In the experiment shown in Fig. 2A, all cloned Pro-1 PCR products represented Ly49g transcripts. Previous PCR cloning experiments have shown a bias toward Ly49g amplification (16); therefore, it is possible that Pro-1 transcripts for other inhibitory Ly49 genes are present, but they are not readily isolated using the PCR approach. To demonstrate the existence of a Pro-1 transcript for the Ly49a and o genes, Pro-1 forward and exon 4 reverse primers specific for Ly49a/o were synthesized and...
used to clone the Ly49alo Pro-1 transcripts from liver and LNK mRNA. Analysis of the EL-4 and LNK cell lines demonstrated that Pro-1 is used in LNK but not EL-4 cells. EL-4 represents a mature Ly49/H11001 NKRP1/H11001 CD3/H11001 NK-T cell tumor (20), whereas the LNK cell line represents a Ly49/H11002 CD3/H11002 IL-2R/H9252/H11001 CD16/H11001 CD94/H11001 cell that lacks NK activity (17). The Ly49g Pro-1 PCR product from LNK (BALB/c derived) was sequenced, and it was identical to the 129/J Ly49g alternative transcript. The Pro-2 transcript amplified from LNK was from the Ly49a gene. However, the Ly49a Pro-1 transcript contains exon 1 and includes the Pro-2 primer site, indicating that Pro-2 may not be active in the LNK cell line because no Pro-2 Ly49g transcript was detected, and the Ly49g Pro-1 transcript does not contain exon 1. Fig. 2B shows the results of RT-PCR on mRNAs derived from day-15 embryonic liver and thymus. Products containing either exon 1 or exon -1a were detected; however, the exon -1a products were less intense. Exon -1a-containing PCR products generated from thymus were cloned into the pCR2.1 vector and sequenced. All of the clones analyzed corresponded to transcripts from the alternative promoter of Ly49e. This is in agreement with the previous report of Ly49E expression in fetal thymus (21). In addition, all clones of Ly49e contained exon -1a but not exon -1b, as predicted by the absence of a consensus splice acceptor preceding exon -1b in the Ly49e gene.

To determine whether Pro-1 was active at a time when most Ly49 protein expression is initiated, mRNAs isolated from 1- to 2-wk-old B6 mice were analyzed. Fig. 2C demonstrates significant Pro-1 activity in the bone marrow of neonatal mice.

Characterization of Pro-1-derived transcripts

Pro-1 transcripts containing the complete Ly49 coding region were isolated by PCR with the exon -1a primer and a degenerate reverse primer located 3' of the Ly49 termination codon. Products from 129/J and B6 liver NK cell mRNA were cloned into the pCR2.1 vector and 10 clones were sequenced from each strain. A summary of the observed cDNAs derived from Pro-1 is shown in Fig. 3. Both strains produced several cDNAs corresponding to Ly49 that contained exons -1a and -1b, but skipped exon 1, splicing directly to exon 2. The B6- and 129/J-derived transcripts of Ly49v lacked exon -1b and used an exon 1 splice acceptor close to the Pro-2 start site. Pro-1-derived transcripts of Ly49v isolated from 129/J NK cells contained both exons -1a and -1b; however, exon 1 was also found in all Ly49v clones due to the use of a splice acceptor 175 bp upstream from the previously described Pro-2 initiation site in the Ly49a gene (11). Pro-1 transcripts of

FIGURE 2. Detection of Pro-1 and Pro-2 transcripts by PCR. A, Purified mRNA from B6 mouse tissues and cell lines was subjected to RT-PCR with either an exon 1 or exon -1a primer. Arrows indicate the positions of the expected amplification products from either the Pro-1 or Pro-2 transcripts. B, Total thymus or liver mRNA from day-15 embryos was subjected to RT-PCR as described in A. C, Total thymus, liver NK, spleen NK, or bone marrow mRNA from 1-wk-old mice was subjected to RT-PCR as described in A.
Ly49a could not be isolated with the exon -1a primer used for PCR analysis, so an additional primer near the 3' end of exon -1a was used to successfully amplify the Pro-1 Ly49a transcript. Exon -1b of Ly49a was 117 bp larger than the Ly49g and v exon -1b due to the use of an upstream splice acceptor site. The Ly49a exon 1 splice acceptor site was the same as that used by the Ly49v Pro-1 transcripts, and this provides an explanation for the previous identification of Ly49a cDNAs that extend 5' of the reported Pro-2 start site (22, 23). The Ly49a, e, g, o, and v Pro-1 transcripts contain the Pro-2 region, preventing specific detection of Pro-2 transcripts if Ly49a, o, or v Pro-1 transcripts are present. Of the five Ly49v clones sequenced, three represented alternatively spliced products lacking a complete open reading frame. Three clones did not contain exon 3, and one of these also contained a novel alternative exon contained in intron 6, as determined by comparing the Ly49v sequence with the partial B6 Ly49v sequence contained in GenBank (accession no. AC090563). The novel exon (6b) contains an in-frame stop codon, resulting in a truncated Ly49 coding region. The Pro-1 transcripts of Ly49a, e, g, v, and alt-v have been deposited in GenBank and can be found under accession numbers AY078436, AF419251, AF419249, AF419250, and AF444273, respectively. To determine whether full-length transcripts from the promoter in intron 2 (Pro-3) could be detected, a forward primer from intron 2 was used in conjunction with an exon 7 antisense probe. Fully spliced Ly49g and v cDNAs derived from Pro-3 were detected in spleen NK cell mRNA (data not shown).

Identification of the transcription start site of the Ly49 alternative promoter

Cloning and sequencing of cDNAs produced from Pro-1 indicated that the Ly49g gene was actively transcribed from this alternative promoter in LNK cells. To determine the transcription initiation site, an RNA probe encompassing the Pro-1 region of Ly49g was synthesized and used to perform an RPA on mRNA purified from LNK cells. Fig. 4 shows the region of the Ly49g gene contained within the probe, as well as the protected fragments observed. Protected fragments of 158 and 161 bp were detected in LNK mRNA, but not in mRNA from EL-4 cells which lack detectable alternative promoter activity. This result indicates the presence of two transcription start sites 13 and 16 bp upstream of the 5' end of the alternative Ly49g cDNA isolated from 129/J NK cells. The region protected by the antisense probe and the location of the predicted start sites are indicated in Fig. 1B. To rule out the possibility of additional upstream start sites, RT-PCR was performed.
with a series of 5’ primers spanning the predicted start site. Primers upstream of the predicted initiation region were unable to amplify Pro-1 cDNA, indicating that there are no additional upstream start sites (data not shown).

Comparison of Pro-1 and Pro-2 activity in the EL-4 and LNK cell lines

To locate and characterize sequence elements required for Pro-1 activity in LNK cells, several luciferase reporter constructs were generated. The regions cloned and the reporter constructs generated are shown in Fig. 5A. Examination of the region preceding exon –1a in the Ly49i gene revealed a potential TATAA-related element (CATAAAA) 25 nt upstream from the 5’ end of the region with homology to the Ly49g cDNA. A (CATAAAA) sequence is also found 29 bp upstream from the Pro-2 initiation site of the Ly49a promoter (11). To test this region for promoter activity, a 250-bp fragment containing the predicted Pro-1 element of Ly49j was cloned into the pGL3 luciferase reporter vector. Transfection of this construct (Ly49j-Pro1) into EL-4 and LNK cells revealed the presence of a promoter that displayed strong activity in the LNK cell line and no detectable activity in EL-4 cells (Fig. 5B), consistent with the PCR results shown in Fig. 2. Removal of the 5’ half of the Ly49j-Pro1 construct yielded a 140-bp fragment that retained the same relative promoter activity, localizing the core promoter region. A Ly49j luciferase construct similar to Ly49j-Pro1 was tested and no activity was found. The CATAAAA element is not present in Ly49j, and the region encompassing the transcriptional start site has been deleted. Although the Ly49g Pro-1 region does not contain a CATAAAA element, a TATAAA element is located 25 nt upstream from the predicted transcription initiation sites. A luciferase construct containing the Ly49g alternative promoter region also possessed LNK-specific transcriptional activity. A luciferase construct containing the previously characterized Ly49a promoter (Ly49a-Pro2) was used as a control, and it was active in EL-4 but not LNK cells. An additional construct containing 2 kb upstream of the Ly49a Pro-2 core promoter (Ly49a-2kb) was tested and shown to contain the same inhibitory activity observed in the Ly49c, i, and j promoters. The lack of Pro-2 activity in LNK cells is contrary to the observed Pro-2 transcripts detected by PCR in Fig. 2; however, the Ly49a Pro-1 transcript contains the Pro-2 start site, resulting in a false positive result for Pro-2 because Ly49a Pro-1 transcripts are present. Cloning of the Pro-2 PCR band indicated that it corresponded to the Ly49a transcript. To determine whether Pro-1 was capable of activating Pro-2 transcription, the core Pro-1 element without the exon –1a splice donor was added to the extended Ly49a construct (Ly49a-2kb+Pro1). The exon –1a splice donor was not included in the Ly49a-2kb+Pro1 construct to avoid the production of spliced transcripts that could result in luciferase activity driven by Pro-1. Pro-1 transcripts produced from this construct would contain a long noncoding region that would presumably inhibit luciferase transactivation. Transfection of this construct into LNK cells did not result in significant luciferase activity, which may be due to the inability of the Pro-2 core to function in LNK cells coupled with inefficient translation of the unspliced Pro-1 transcript. To reliably test for the ability of Pro-1 transcription to overcome the inhibitory effects of the region preceding Pro-2 it will be necessary to identify a cell line that is permissive for both Pro-1 and Pro-2.

Discussion

The Ly49 promoter regions previously described (Pro-2) are highly conserved among all Ly49 family members, and several have been shown to contain a core promoter preceded by an inhibitory region, suggesting that additional control regions might exist. The current study has identified a novel promoter (Pro-1) that is preferentially expressed in bone marrow and fetal thymus, both sites of initiation of Ly49 expression (24, 25). Therefore, Pro-1 is a good candidate for a regulatory element involved in the process of selective Ly49 gene activation. Pro-1 activity might be restricted to a small subset within the populations tested because PCR was the only method that efficiently detected Pro-1-derived transcripts, and the identification of the Pro-1 start site in LNK cells required long exposures of products generated by the highly sensitive RPA assay. Also, LNK cells do not express detectable levels of Ly49G protein, even though Pro-1 Ly49g transcripts containing a complete open reading frame were detected by PCR. In addition, the scarcity of Pro-1 transcripts was suggested by the identification of only one Pro-1-derived clone of >100 independent Ly49 cDNAs analyzed from 129/J liver NK cells (16). This suggests that either Pro-1 is a very weak promoter or only a small percentage of cells express Pro-1 transcripts. The latter possibility is supported by the detection of similar Pro-1 and Pro-2 strength in the reporter assays performed in LNK and EL-4 cells. An extensive study of the start sites of Ly49 genes (19) did not detect any Pro-1 transcripts in adult spleen-derived NK cells, in agreement with our inability to detect Pro-1 activity in these cells. The observed rarity of Pro-1 transcripts together with the detection of Ly49g Pro-1 activity in bone marrow and Ly49e Pro-1 activity in fetal thymus suggests that Pro-1 is transiently activated in cell populations that are initiating Ly49 expression. It is interesting to note that the Pro-1 region of Ly49j does not have significant activity in luciferase reporter assays, and the percentage of NK cells expressing Ly49J (5%) is significantly lower than the percentage of NK cells expressing Ly49I (37%) (10). If Pro-1 is involved in the initial activation of
Ly49 gene expression, the difference in Pro-1 activity between Ly49i and j may explain the different probability of activation of these two highly related genes. Pro-1 activity would be expected to suppress transcription of Pro-2, due to transcriptional interference (26), because the Pro-1 transcript reads through the Pro-2 region. However, there may not be concurrent activity of Pro-1 and Pro-2 because luciferase assays indicated that Pro-2 was specific for EL-4 cells and Pro-1 was specific for LNK cells. The positive PCR result with the Pro-2 primer in LNK cells was due to the presence of Ly49a Pro-1 transcripts in LNK, because we were unable to detect Ly49g Pro-2 transcripts and the Ly49a Pro-1 transcript encompasses the Pro-2 start site, unlike the Ly49g Pro-1 transcript, which skips exon 1. Therefore, the Pro-2 PCR primer set only reliably indicates Pro-2 activity in tissues that do not have any Pro-1 activity. The role of Pro-1 transcripts may be to open the Pro-2 region, making it accessible to transcription factors required for subsequent activation. This would provide an explanation for the presence of an inhibitory region preceding Pro-2. Pro-2 may lack elements required to make the promoter accessible; therefore, it would be dependent on transcription from Pro-1 for its initial activation. The stochastic nature of Ly49 gene activation may be related to the window of opportunity between the loss of Pro-1-specific transcription factors and the appearance of Pro-2-specific transcription factors. Once activated, Pro-2 appears to function as a constitutive NK cell promoter, because there is no evidence for modulation of Pro-2 activity in mature NK cells. Whether or not Pro-1 transcription is controlled by a probabilistic mechanism is currently under investigation.

The 5′ untranslated region of Pro-1 transcripts is significantly longer than that of Pro-2 transcripts, suggesting possible differences in their translation efficiencies. Transfection of full-length Ly49g Pro-1 or Pro-2 cDNAs into 293T cells failed to show any differences in the surface expression of Ly49g (data not shown). One potential effect of the Pro-1-derived 5′ region may relate to the production of alternatively spliced products. Three of five Ly49g clones isolated were missing exon 3, and one clone contained a novel alternative exon (6b) that disrupted the open reading frame. Perhaps the presence of the Pro-1 noncoding region enhances the production of alternatively spliced Ly49g mRNAs. Our laboratory has been unable to identify any Ly49g protein products resulting from cDNAs lacking the third exon (27), suggesting that the primary role of Pro-1 transcription may be to activate the gene, and Ly49g protein expression from this promoter is down-regulated by alternative splicing.

Studies of the Ly49 promoter used by mature NK cells (Pro-2) have not provided an explanation for the stochastic activation of Ly49 genes. The discovery of an upstream Ly49 promoter (Pro-1) that is primarily active in tissues where Ly49 expression is initiated suggests that further study of this novel promoter may lead to an understanding of the mechanisms underlying the seemingly random activation of Ly49 genes. Generation of Ly49 transgenic mice with mutations in the Pro-1 region will enable a direct evaluation of the role of Pro-1 in the stochastic process of Ly49 gene activation.

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