Genetic Control Of Natural Killing and In Vivo Tumor Elimination by the *Chok* Locus

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Summary

The molecular mechanisms underlying target recognition during natural killing are not well understood. One approach to dissect the complexities of natural killer (NK) cell recognition is through exploitation of genetic differences among inbred mouse strains. In this study, we determined that interleukin 2–activated BALB/c-derived NK cells could not lyse Chinese hamster ovary (CHO) cells as efficiently as C57BL/6-derived NK cells, despite equivalent capacity to kill other targets. This strain-determined difference was also exhibited by freshly isolated NK cells, and was determined to be independent of host major histocompatibility haplotype. Furthermore, CHO killing did not correlate with expression of NK1.1 or 2B4 activation molecules. Genetic mapping studies revealed linkage between the locus influencing CHO killing, termed *Chok*, and loci encoded within the NK gene complex (NKC), suggesting that *Chok* encodes an NK cell receptor specific for CHO cells. In vivo assays recapitulated the in vitro data, and both studies determined that *Chok* regulates an NK perforin–dependent cytotoxic process. These results may have implications for the role of NK cells in xenograft rejection. Our genetic analysis suggests *Chok* is a single locus that affects NK cell–mediated cytotoxicity similar to other NKC loci that also regulate the complex activity of NK cells.

Key words: natural killer cell • natural killer gene complex • cytotoxicity • tumor

Natural killer (NK) cells are bone marrow–derived lymphocytes, distinct from T and B cells, that are capable of lysing certain tumor cells without prior sensitization (1, 2). Because of this capacity, termed natural killing, NK cells serve as a first line of defense against certain intracellular pathogens and perhaps developing tumor cells (3, 4). Although the phenomenon of natural killing has been studied intensely for many years and underlies the functional definition of NK cells, the molecular mechanisms underlying target recognition during natural killing are not well understood. Despite some descriptions of natural killing as being nonspecific, it is not random. In general, NK cells do not lyse normally dividing cells, and their susceptible targets are classically tumor cell lines, among which there is marked differential sensitivity (5). NK cells do not rearrange T cell antigen receptor genes nor do they express surface Ig (6). Therefore, NK cells must possess a recognition mechanism to discriminate between appropriate targets and normal cells that is distinct from the antigen-specific receptors of T and B cells.

Recent studies on the inverse correlation between target cell expression of MHC class I and target cell susceptibility to NK cell lysis have provided major insight into NK cell recognition. In the "missing-self hypothesis," Kärre postulated that NK cells are chronically inhibited by MHC class I. Accordingly, if a cell lacks expression of MHC class I or expresses an aberrant form, the inhibitory influence is lost, permitting the NK cell to lyse the target (7–9). The identification of MHC class I–specific inhibitory receptors in rodents (Ly-49) and humans (killer cell inhibitory receptor [KIR][1] and CD94/NKG2) provides a molecular basis for this hypothesis. Receptors in all three of these families contain immunoreceptor tyrosine-based inhibitory motifs (ITIMs) in their cytoplasmic domain, which have been shown

[1]*Abbreviations used in this paper:* B6, C57BL/6; CHO, Chinese hamster ovary; AGM1, asialo ganglio-*N*-tetraosylceramide; ITIM, immunoreceptor tyrosine-based inhibitory motif; KIR, killer inhibitory receptor; MCMV, murine cytomegalovirus; NKC, NK gene complex; RI, recombinant inbred; SDP, strain distribution pattern.

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to recruit cytoplasmic tyrosine phosphatases like SHP-1 upon receptor cross-linking and subsequent ITIM phosphorylation (10–15). Therefore, these MHC class I–specific inhibitory receptors on NK cells may explain the original observations regarding the inverse relationship between target cell expression of MHC class I and susceptibility to lysis that led to Kärre's hypothesis.

However, the known inhibitory receptors do not explain all aspects of NK cell specificity. For example, mouse NK cell clones have varying reactivity against a panel of tumor targets yet do not express members of the Ly-49 family (16). Moreover, in addition to the inhibitory receptors, NK cell recognition appears to involve activation receptors, giving rise to a two-receptor model for NK cell activation. This model predicts that the fate of a target cell is determined by the integration of signals transduced by inhibitory and activation receptors which are simultaneously expressed on a single NK cell (17, 18). Studies using mAbs specific for NK cell surface structures have led to the description of candidate activation receptors. Cross-linking these receptors with specific mAbs stimulates NK cells to kill targets that are otherwise inefficiently lysed. In rodents, these molecules include NKR-P1, CD69, Ly-6, 2B4, and Ly-49D (19–22). Although mAbs have helped identify candidate receptors, the role of these molecules in natural killing and in in vivo NK cell function remains unclear.

Recent studies by Ryan et al. took a mutagenesis approach in order to define the role of NKR-P1A in natural killing. An NKR-P1–deficient mutant of the rat RNK-16 line demonstrated natural killing of YAC-1 cells but not other mouse tumor targets (23). Transfection of the mutant RNK cells with rat NKR-P1A restored lysis of only the xenogeneic IC-21 target. Although these studies strongly suggest that NKR-P1A molecules are target-specific receptors that activate natural killing, the NKR-P1–deficient NK clones were able to lyse other targets, suggesting other routes for activation of natural killing. Hence, there must be other receptors, perhaps some yet to be described, that can influence NK cell recognition.

The current panoply of NK cell receptors is further complicated by the expression of multiple receptors on an individual NK cell and on overlapping NK cell subsets. The resultant heterogeneic NK cell receptor repertoire renders it difficult to analyze the contribution of individual receptors in natural killing. One approach to dissect the complexities of NK cell recognition is to exploit genetic differences among inbred strains of mice. Additionally, the availability of recombinant inbred and congenic strains of mice as well as the current wealth of informative genetic markers makes it possible to rapidly identify novel loci controlling NK cell function.

In the present study, we demonstrate that NK cells from two distinct inbred mouse strains possess differential cytotoxic capacity against Chinese hamster ovary (CHO) target cells. This is an intrinsic phenomenon, manifested in freshly isolated NK cells as well. We have exploited this differential cytotoxicity to identify a genetic locus, termed *Chok*, responsible for NK cell–mediated cytotoxicity of tumor cells. This locus is linked to the NK gene complex (NKC), and also influences the capacity to clear tumor cells in vivo through a perforin-dependent mechanism, consistent with the hypothesis that *Chok* encodes a recognition structure specific for certain targets.

Materials and Methods

Mice. All mouse strains, except the BALB.B6-*Cmv1*^{r}, B6.BALB-*Cmv1*^{s}, and the intra-NKC recombinant strains, were obtained from The Jackson Laboratory (Bar Harbor, ME), including C57BL/6J (B6), BALB/cJ, C57BL/6ByJ, BALB/cByJ, CB6F1/J, C57BL10/J, B10.D2, BALB.B, NZB/B1NJ, NZW/LacJ, NOD/LtJ, DBA/2J, 129/J, C3HeB/FeJ, AKR/J, A/J, SJL/J, ST/J, CE/J, C57L/J, C57BR/cdJ, C58/J, C57BL/6-*Pfp*^{tm1Sdz}, and seven mice of the recombinant inbred panel derived from C57BL/6ByJ and BALB/cByJ parental strains, CXB-1 through -7. The BALB.B6-*Cmv1*^{r} mouse is a congenic strain in which the murine cytomegalovirus (MCMV) resistance allele, *Cmv1*^{r}, as well as other NKC-linked loci from C57BL/6J strain have been transferred onto the BALB/c genetic background as described previously (24). The B6.BALB-*Cmv1*^{s} congenic strain supports high splenic MCMV titers since it carries the susceptible BALB/c allele, *Cmv1*^{s} (25). This strain also contains other BALB/c-derived NKC loci on the B6 genetic background (25). All mouse strains were maintained in a pathogen-free facility at Washington University.

Cell Lines. CHO cell lines (CHO as well as Lec1 and LEC11 mutants) were a gift from Dr. P. Stanley (Albert Einstein College of Medicine, Bronx, NY). The derivation of the mutants has been described previously (26). All three lines were cultured in MEM-α (GIBCO BRL, Gaithersburg, MD) supplemented with ribonucleosides, deoxyribonucleosides, and 10% FCS (Harlan Sprague Dawley, Inc., Indianapolis, IN) without any antibiotics. The BHK.vp16 hamster kidney line was provided by Dr. P. Hippenmeyer (Monsanto, St. Louis, MO [27]). All other cell lines were obtained from the American Type Culture Collection (Rockville, MD). Cells were grown in either RPMI 1640 medium (GIBCO BRL) supplemented with l-glutamine (300 μg/ml), penicillin (100 U/ml), streptomycin (100 μg/ml), 50 μM β-mercaptoethanol, and 10% FCS or in DME (GIBCO BRL) supplemented with l-glutamine (300 μg/ml), penicillin (100 U/ml), streptomycin (100 μg/ml), 50 μM β-mercaptoethanol, sodium pyruvate (1 mM), nonessential amino acids (0.1 mM), and 10% FCS.

IL-2 and Antibodies. Human rIL-2 was purchased from Chiron Corp. (Emeryville, CA). mAbs used in this study include GK1.5 (rat IgG2b, anti–murine CD4), J11D (rat IgM, anti–murine B cells, neutrophils, erythrocytes, and immature thymocytes), M5/114.15.2 (rat IgG, anti–MHC II), MAR 18.5 (mouse IgG2a, anti–rat κ Ig), 53-6.72 (rat IgG2a, anti–murine CD8), H57-957.1 (hamster IgG, anti–murine TCR-α/β), 2.4G2 (rat IgG, anti–mouse FcγRII/III), PK136 (mouse IgG2a, anti-NK1.1), AF6-88.5.3 (mouse IgG2a, anti–H-2K^b), 145-2C11 (hamster IgG anti-CD3ϵ), anti-2B4 (mouse IgG2b, anti-2B4), 12A8 (rat IgG2a, anti–Ly-49D and –Ly-49A), 4E5 (rat IgG, anti–Ly-49D), 3D10 (mouse IgG1, anti–Ly-49H), and mouse IgG1 isotype control. All antibodies were either ascites preparations or purified mAb from hybridoma culture supernatants, except for anti-2B4 which was purchased from PharMingen (San Diego, CA). All mAb-producing hybridomas were obtained from American Type Culture Collection, with the exception of 12A8 and 4E5, a gift from L. Mason and J. Ortaldo (National Cancer Insti-

tute, Frederick, MD), and 3D10 developed in our lab.[2] In addition, rabbit anti-asialo ganglio-*N*-tetraosylceramide (AGM1) antiserum was obtained from Wako Bioproducts (Richmond, VA), and FITC-conjugated and unconjugated goat $F(ab')_2$ fragments anti–mouse Ig as well as affinity-purified rabbit anti–mouse Ig were purchased from Cappel, Inc. (Malvern, PA).

IL-2–activated NK Cell Preparation. Splenocyte suspensions were prepared in HBSS (GIBCO BRL) containing 10% FCS; RBCs were lysed using Tris-buffered ammonium chloride (0.14 M NH_4Cl and 0.017 M Tris, pH 7.2). Washed cells were incubated on a nylon wool column for 1 h at 37°C. Nylon wool nonadherent cells were cultured in complete RPMI medium supplemented with 1,000 U/ml of rIL-2 at 2–4 $\times$ 10^6 cells/ml. On day 3 or 4, adherent cells were harvested with Ca^{2+}/Mg^{2+}–free PBS containing 0.2% EDTA (GIBCO BRL) and incubated (2×10^7 cells/ml) with the mAbs (0.5% ascites preparations) 53-6.72 and H57-957.2 on ice in HBSS plus 3% FCS for 30 min. The cells were washed and incubated (10^7 cells/ml) with 10 μg/ml affinity-purified rabbit anti–mouse Ig and 100 μg/ml rabbit complement (Cedarlane Labs, Inc., Westbury, NY) for 45 min at 37°C. Surviving cells were separated from dead cells using a Lympholyte-M density gradient (Cedarlane Labs, Inc.). These cells were then washed and expanded for 4–6 d in culture with IL-2–supplemented medium. Assays were performed with adherent cells harvested on days 7–9.

Freshly Isolated NK Cell Preparation. Mouse spleens were harvested and splenocyte suspensions were depleted of RBCs as described above. Nylon wool nonadherent spleen cells (2×10^7/ml) were incubated with ascites preparations (0.5% final dilution) of mAbs GK1.5, 53-6.72, J11D, and M5/114.15.2 on ice for 30 min. The cells were washed and plated onto T-75 flasks precoated with goat $F(ab')_2$ anti–mouse Ig at 10 μg/ml. After 1 h at 4°C, the nonadherent cells were resuspended at 10^7 cells/ml. Purified MAR 18.5 protein was added (10 μg/ml final) together with rabbit complement (100 μg/ml final; Cedarlane Labs, Inc.) and cells were incubated at 37°C for 45 min. The live cells were rescued using a Lympholyte-M density gradient. These cells were analyzed by FACS® and used in cytotoxicity assays.

Cell Surface Expression of Molecules. Cell surface markers on IL-2–activated NK cells were evaluated using FACS® analysis for each cytotoxicity assay. Typical analysis examines the expression of several cell surface molecules, including CD16 (2.4G2, rat IgG anti-FcγRII/III), 2B4 (2B4, mouse IgG anti-2B4), NK1.1 (PK136, mouse IgG anti-NK1.1), and CD3ε (2C11, hamster IgG anti-CD3ε). Typically, our IL-2–activated NK cells constitute a cell population that is >90% $CD3^-CD16^+$ and $2B4^{+/-}$, $NK1.1^{+/-}$ (depending on the strain). Cells were incubated with saturating concentrations of the appropriate mAbs on ice for at least 30 min. The cells were then washed twice and incubated with FITC-conjugated goat $F(ab')_2$ anti–mouse Ig at 10 μg/ml final concentration. The FITC-conjugated goat $F(ab')_2$ anti–mouse Ig second step reagent cross-reacts with both the rat 2.4G2 and the hamster 2C11 mAbs. Stained cells were analyzed on FACScan® with CellQuest® software (Becton Dickinson, San Jose, CA). Dead cells were excluded by propidium iodide staining.

Natural Killing. The standard ^{51}Cr-release assay was used to establish NK lytic function. Tumor targets ($2–4 \times 10^6$) were radiolabeled with ^{51}Cr (50 or 100 μCi) in RPMI without FCS for 90 min. Effector cells were plated onto 96-well round-bottomed plates at various cell densities in order to achieve E/T ratios usually of 20:1, 6.7:1, and 2.2:1. Radiolabeled target cells (10^4 cells/well) and effectors were incubated for 4 h in a 37°C humidified CO_2 incubator. Subsequently, 100 μl of the supernatants was collected and assayed for ^{51}Cr release. For antibody blocking experiments, mAbs were added at saturating levels to effectors and incubated for 15–30 min at room temperature before the addition of labeled target cells. The mAb 12A8 was used at 1:100 final concentration of an ascites preparation, and the purified mAb 4E5 at 10 μg/ml final concentration. Both the 3D10 (anti–Ly-49H) and its isotype control were used at a final concentration of 10 μg/ml. Specific cytotoxicity was calculated according to the standard formula:

$$\% \text{ specific lysis} = 100 \times (\text{exp} - \text{spont})/(\text{max} - \text{spont}),$$

where experimental (*exp*) release represents the radioactivity from the experimental wells, maximum (*max*) release represents counts from detergent-lysed targets, and spontaneous (*spont*) release represents background release from wells with targets alone.

Lung Clearance Assay. Target cells (8×10^6) were incubated with 50 μg of 5-fluoro-2′-deoxyuridine (Sigma Chemical Co., St. Louis, MO) in 2 ml of complete DME for 15 min at 37°C. ^{125}I-labeled 5-iodo-2′-deoxyuridine ([^{125}I]dUrd; Amersham Pharmacia Biotech, Inc., Piscataway, NJ) was added (5 μCi), and cells were incubated for an additional 90–120 min at 37°C. Subsequently, the cells were washed in PBS. Mice were injected intravenously with 3×10^5 cells/200 μl PBS. 4 h after injection, the lungs were removed, rinsed with PBS, and soaked in 70% ethanol for at least 1 h. ^{125}I activity in the lungs and in the inoculum (200 μl) was measured using a gamma counter. Results were determined by expressing the residual ^{125}I activity measured in the lungs as a percentage of the total activity in the inoculum as follows:

$$\text{percent retention in lung} = (\text{average lung cpm}/\text{average inoculum cpm}) \times 100.$$

Thus, percent retention is an indirect measure of number of surviving cells in the lungs. All experiments were done with groups of at least three mice. For in vivo NK cell depletion, 50 μl of anti-AGM1 antiserum diluted in 200 μl vol of PBS was injected intravenously (tail vein) 3 d before the lung clearance assay. In the case of PK136 (anti-NK1.1) or the isotype-matched AF6-88.5.3 (anti-K^b), 100 μg of purified mAb was injected intraperitoneally 2 d before the assay.

Results

Strain-determined Differences in Natural Killing. We evaluated the target cell repertoires of NK cells derived from two distinct inbred mouse strains, C57BL/6J (B6) and BALB/cJ, to screen for genetic loci that influence NK cell target specificity (Table 1). B6 IL-2–activated NK cells displayed efficient lysis of most murine tumor targets as well as several hamster cell lines, with the exception of BB88 and WR19L. For most targets, BALB/c-derived NK cells displayed a similar target specificity profile, suggesting that the intrinsic killing capacity of BALB/c NK cells was comparable to that of B6-derived effector cells. However, several targets were killed less efficiently by BALB/c-derived NK cells compared with B6-derived NK cells. This strain-determined difference in capacity for target lysis was most pronounced in killing of CHO targets as well as two variants of this line, Lec1 and LEC11. At E/T ratios >20:1,

[2]Smith, H.R.C., and W.M. Yokoyama, manuscript in preparation.

Table 1. *Strain-determined Lysis of a Panel of Tumor Targets*

				C57BL/6J			BALB/cJ		
				E/T ratios					
Cell line	Type		*n*	20	6.7	2.2	20	6.7	2.2
Hamster		Strain							
CHO	Fibroblast	Chinese	4	76	56	29	8	3	2
Lec1	Fibroblast	Chinese	1	78	69	44	9	8	6
LEC11	Fibroblast	Chinese	1	86	70	54	8	8	6
V79-4	Lung	Chinese	1	71	61	42	45	32	18
CHL/IU	Lung	Chinese	1	70	68	63	64	56	40
AHL-1	Lung	Armenian	1	50	40	24	35	33	12
BHK.vp16	Kidney	Syrian or Golden	1	62	59	41	68	55	32
Murine		H2							
YAC-1	Thymoma	a	4	93	89	76	82	72	52
RAW264.7	Macrophage	d	1	100	100	26	82	75	39
SP2/0	Myeloma	d	1	100	93	74	90	78	56
PU51R	Macrophage	d	1	93	82	49	87	66	40
MPC11	Plasmacytoma	d	1	56	31	19	52	31	15
MOPC315	Plasmacytoma	d	1	45	26	25	43	24	30
WEHI7.1	Thymoma	d	1	69	55	38	60	59	37
WR19L	Lymphoma	d	1	30	12	2	20	13	2
BB88	Leukemia	b	1	9	1	0	15	0	0
IC-21	Macrophage	b	1	89	61	37	57	36	25
B16S	Melanoma	b	1	71	69	28	54	54	39
BLKSVHD2	Fibroblast	b	1	60	47	31	50	41	30
EL-4	Thymoma	b	1	50	37	26	29	15	8
C1498	Lymphoma	b	1	72	65	49	71	47	25
RMA-S	Lymphoma	b	1	65	50	29	48	35	20

Lysis of various tumor targets by B6- and BALB/c-derived NK cells was determined in triplicate using the standard ^{51}Cr-release cytotoxicity assays at E/T ratios of 20:1, 6.7:1, and 2.2:1. Tumor killing is expressed as percent specific cytotoxicity. For each target used the cell type is indicated. Additionally, for hamster targets, the strain is specified; for murine targets, the H2 haplotype is indicated.

maximal YAC-1 killing by both effector populations is apparent, demonstrating that BALB/c effectors are potent killers for sensitive targets (Fig. 1 *A*). Despite this, the strain-determined difference in killing capacity of CHO targets was maintained at E/T ratios as high as 80:1, at which the BALB/c NK cells manifested only minimal lysis of CHO (Fig. 1 *A*). Furthermore, the difference in CHO cytotoxicity was not overcome by longer ^{51}Cr-release assays. Similar differences were apparent in 4-, 8-, or 24-h assays (data not shown), suggesting that the observations were not due to varying kinetics of killing. The differential susceptibility of CHO targets was not dependent on differences in species origin of the target, since other hamster lines, BHK (Syrian or Golden) and AHL-1 (Armenian), as well as Chinese hamster–derived V79-4 and CHL/IU cells were lysed equivalently by both effector populations (Table 1). Thus, compared with B6-derived effector cells, IL-2-activated BALB/c NK cells manifest a qualitative difference in ability to kill CHO targets.

In general, IL-2–activated NK cells display a broader target spectrum as well as higher lytic efficiency compared with freshly isolated NK cells (1, 28, 29). Therefore, it was possible that the differences in CHO killing were due to differential NK cell sensitivity to activation by IL-2. However, freshly isolated B6 NK cells killed CHO, whereas those from BALB/c did not (Fig. 1 *B*). Although less potent killers, freshly isolated effectors displayed the same differential killing capacity with regard to CHO cell targets. These results demonstrate that an intrinsic capacity unrelated to IL-2 activation controls NK cell–mediated CHO killing.

Inheritance of Strain Difference in CHO Cell Killing and Independence from Host MHC Haplotype. To characterize the

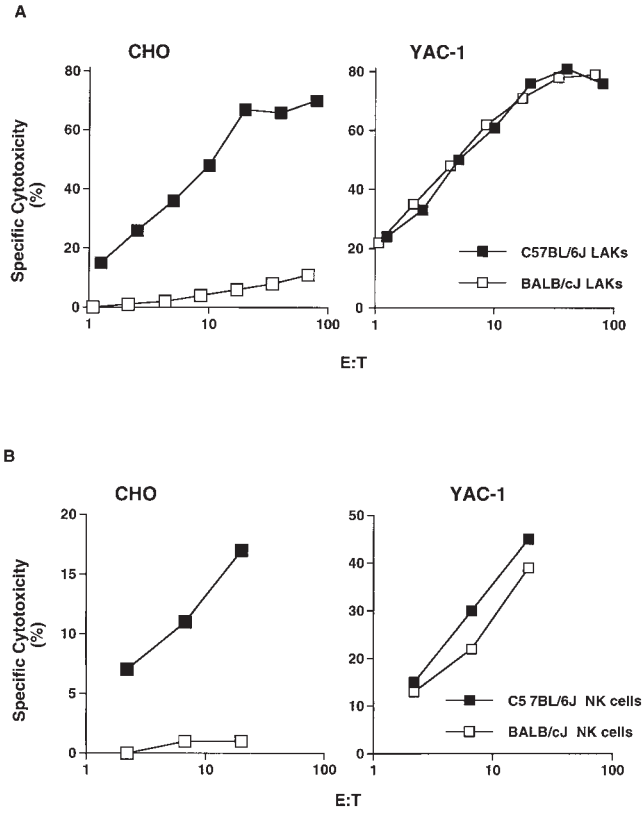


Figure 1. Strain-determined differences in CHO killing by NK cells. (*A*) Standard chromium-release assays were performed using B6 and BALB/c IL-2–activated NK cells (LAKs) against CHO and YAC-1 target cells at indicated E/T ratios. (*B*) Cytotoxicity assays against CHO or YAC-1 targets using freshly isolated NK cells from B6 and BALB/c.

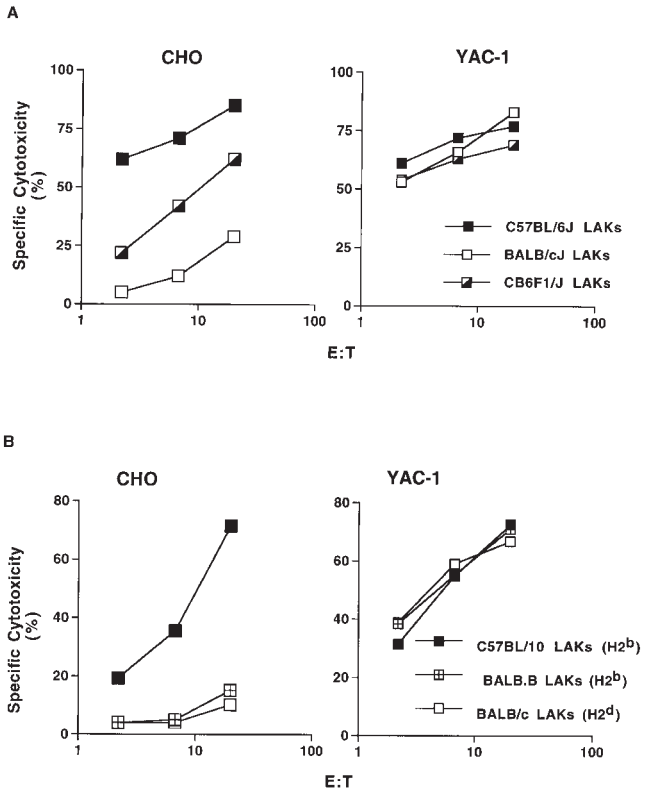


Figure 2. Inheritance of strain difference in CHO cell killing and independence from host MHC haplotype. (*A*) Lytic capacity of IL-2–activated NK cells from the (BALB/c × C57BL/6)F_1 strain was compared with that of parental B6 and BALB/c IL-2–activated NK cells against the CHO and YAC-1 targets. (*B*) No association between H2 haplotype and capacity to lyse CHO. IL-2–activated NK cells derived from C57BL/10, BALB/c, and BALB.B were compared for their capacity to lyse CHO and YAC-1 targets.

inheritance pattern of this trait, cytotoxicity against CHO cells was compared using effector cells from (BALB/c × B6)F_1 hybrid mice and the parental strains (Fig. 2 *A*). Interestingly, the F_1 NK cells reproducibly exhibited an intermediate level of cytotoxicity against the CHO target, suggesting a gene dosage effect of an incomplete dominant or codominant inheritance pattern.

Previous studies on the Ly-49A NK cell receptor indicated that its expression and function are influenced by host MHC haplotype (30–33). Since BALB/c mice are $H2^d$ while B6 are $H2^b$, we ascertained if CHO cell lysis is influenced by host MHC haplotype by using H2 congenic mouse strains on C57BL or BALB background. NK cells derived from C57BL background (C57BL/10, $H2^b$; or B10.D2, $H2^d$) exhibited significantly greater cytotoxicity against CHO cells than did NK cells from H2 congenic mouse strains with BALB/c background (BALB.B, $H2^b$; or BALB/c, $H2^d$) regardless of MHC haplotype (Fig. 2 *B*, and data not shown). These results argue against an influence of the host MHC on the capacity of effector cells to lyse CHO targets.

Panel of Inbred Mouse Strains Assessed for CHO Cytotoxicity. We next assessed NK cells from several inbred mouse strains to determine if this differential CHO susceptibility is restricted to the B6 and BALB/c backgrounds (Table 2). For each strain tested, the cytotoxicity against the prototypical NK target, YAC-1, was determined in parallel to CHO. Effector NK cells always retained cytolytic activity versus YAC-1, and in no case was CHO killing more efficient than YAC-1 killing. Since there are differences in general capacity to mediate cytotoxicity as indicated by YAC-1 killing, we normalized for the strain differences in overall killing efficiency by determining lysis as a ratio of CHO to YAC-1 killing. We chose a minimum value of 0.5 as a measure of efficient (B6-like) CHO killing for each of the strains tested. Among the 17 additional strains examined, only 4, C57BL/10, NZB/B1NJ, NZW/LacJ, and NOD/LtJ, possessed NK cells that displayed CHO cytotoxic capacity similar to B6 NK cells. NK cells derived from the remaining strains were not able to lyse CHO cells, thus displaying a phenotype similar to BALB/c.

The NK1.1 and 2B4 molecules were both considered as candidates for mediating the differential CHO lysis because they are selectively expressed on NK cells, can activate NK cells (18, 20, 21, 34), and exhibit strain-specific expression on B6- but not BALB/c-derived NK cells (35–37). However, there was no correlation between expression of either epitope by FACS® analysis and the capacity to lyse CHO

Table 2. *CHO Cytotoxicity and Expression of 2B4 and NK1.1 Antigens by NK Cells Derived from a Panel of Inbred Mouse Strains*

Strain	H2 haplotype	NK1.1 expression	2B4 expression	CHO percent lysis	YAC-1 percent lysis	CHO/YAC-1 ratio
C57BL/6J	b	+	+	55	71	0.8
C57BL/10SnJ	b	+	+	36	55	0.7
B10.D2	d	+	+	51	70	0.7
NZB/B1NJ	d	+	−	32	36	0.9
NZW/LacJ	z	+	−	45	67	0.7
NOD/LtJ	g	−	−	45	46	1.0
BALB/cJ	d	−	−	4	59	0.1
BALB.B	b	−	−	5	55	0.1
DBA/2J	d	−	−	16	77	0.2
129/J	b	−	−	6	39	0.2
C3HeB/FeJ	k	−	−	1	58	0.0
AKR/J	k	−	−	17	69	0.2
A/J	a	−	−	8	53	0.2
SJL/J	s	−	−	2	30	0.1
ST/bJ	k	+	−	1	30	0.0
CE/J	k	+	−	4	27	0.1
C57L/J	b	+	+	10	52	0.2
C57BR/cdJ	k	+	+	7	24	0.3
C58/J	k	+	+	5	79	0.1

IL-2–activated NK cells derived from each indicated strain were assessed for their capacity to mediate CHO and YAC-1 lysis. Percent specific lysis values at a 6.7:1 E/T ratio are shown in the table; similar results were obained at other E/T ratios (data not shown). To normalize for strain differences in overall killing efficiencies, the CHO/YAC-1 ratio was determined. We arbitrarily set a value for CHO/YAC-1 $\geq$ 0.5 as an index of efficient CHO lysis. The IL-2–activated NK cells derived from each strain tested were also characterized (usually on the same day of the cytotoxicity assay) for their expression of NK1.1 and 2B4 antigens by flow cytometric analysis.

(Fig. 3, and Table 2). For example, NK cells from C57L/J, C57BR/cdJ, and C58/J strains, which express both NK1.1 and 2B4 epitopes, did not lyse CHO. Conversely, NK cells from NOD/LtJ strain that lack expression of either epitope displayed efficient lysis of CHO targets. Furthermore, murine NK cell clones generated in our laboratory from p53-deficient B6 mice (16) express NK1.1 and 2B4 but do not kill CHO cells despite efficient killing of YAC-1 targets (data not shown). Therefore, these data show that natural killing of CHO cell targets is not unique to the B6 strain and cannot be correlated with expression of the NK1.1 or 2B4 antigen. These data also independently confirm that MHC haplotype is not correlated with CHO killing.

Linkage of Chok to NKC-encoded Genes. To further characterize the genetic basis for CHO cell killing, we used seven recombinant inbred (RI) mouse strains derived from BALB/cBy and C57BL/6By progenitor inbred strains (Fig. 4 *A*). Since each RI line is homozygous for either the BALB/c or B6 allele for CHO killing, we expected to see phenotypes that mirrored those of the progenitor strains. Indeed, NK cells derived from CXB-1, -2, and -6 were all B6-like (Fig. 4 *B*) since they lysed CHO cells efficiently. The remaining strains, CXB-3, -4, -5 and -7, were BALB/c-like (Fig. 4 *C*) and did not lyse CHO despite efficient lysis of YAC-1. We observed a clear segregation of phenotypes into high or low levels of killing, and roughly 50% of the RI strains displayed either phenotype, consistent with the interpretation that a single chromosomal locus determines killing of CHO targets. We have termed this locus *Chok* for CHO killing.

A comparison of the strain distribution pattern (SDP) for *Chok* with SDPs for other genes previously typed in the CXB RI strains revealed complete concordance between *Chok* and *Ly49a*, *Nkrp1*, and *Cmv1* loci, all of which have been mapped within the NKC on distal mouse chromosome 6 (Fig. 4 *B*). Although this analysis was limited to a small set of RI strains, these results strongly suggest that *Chok* is NKC linked.

To confirm the chromosomal location of *Chok*, we examined the BALB.B6-*Cmv1*^{r} congenic strain that possesses the *Cmv1*^{r} allele as well as other NKC loci from B6, backcrossed onto the BALB/c background (24). NK cells derived from BALB.B6-*Cmv1*^{r} mice displayed efficient lysis against both YAC-1 and CHO cell targets (Fig. 5 *A*). We

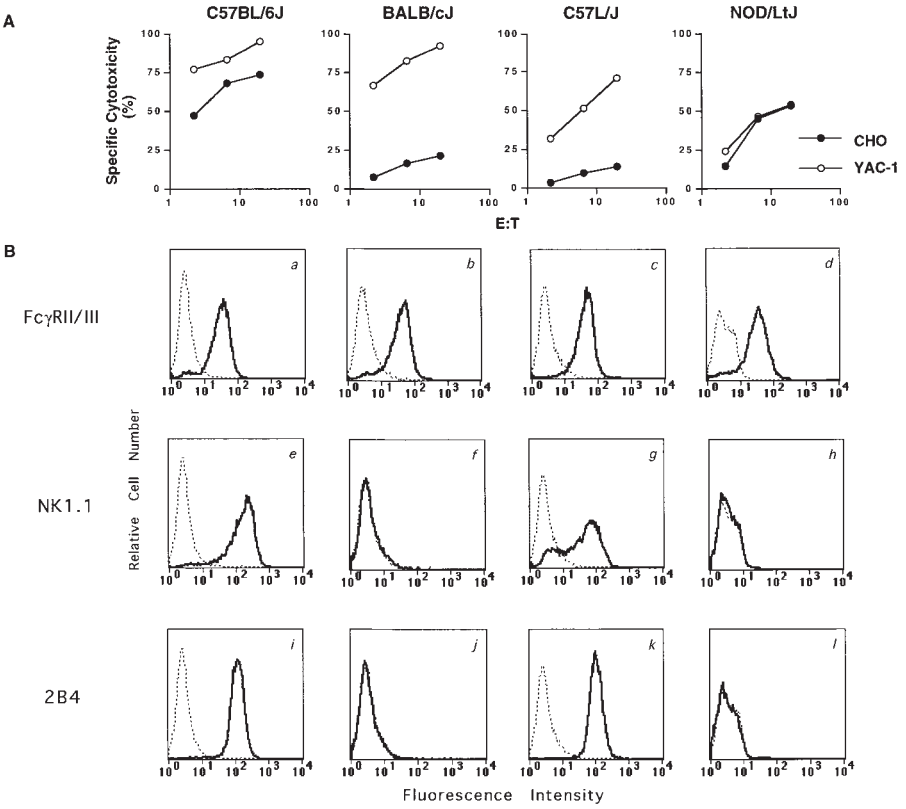
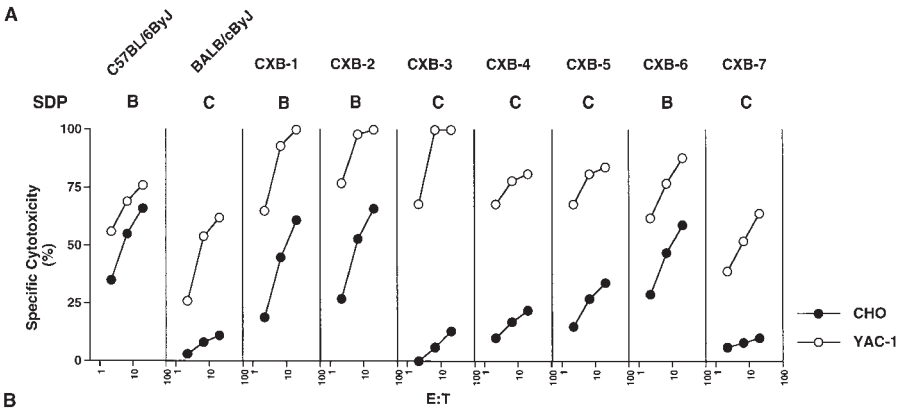


Figure 3. No correlation between expression of 2B4 and NK1.1 activation antigens and capacity to lyse CHO cells. (*A*) IL-2–activated NK cells from B6, BALB/cJ, C57L/J, and NOD/LtJ were analyzed for their capacity to lyse CHO and YAC-1 targets. (*B*) Flow cytometric analysis of IL-2–activated NK cells from B6, BALB/cJ, C57L/J, and NOD/LtJ strains. NK cells from each of the strains were incubated with mAbs specific for FcγRII/III (*a–d*), NK1.1 (*e–h*), or 2B4 (*i–l*) followed by FITC-conjugated goat $F(ab')_2$ anti–mouse Ig. *Solid lines*, specific staining; *dotted lines*, staining by secondary antibody alone. The 2.4G2 mAb is specific for both FcγRII and FcγRIII, even though mouse NK cells express only FcγRIII (reference 73).

have recently established a reverse congenic strain, designated B6.BALB-*Cmv1*^{s}, carrying the BALB/c *Cmv1*^{s} allele and other BALB/c-derived NKC loci on the B6 genetic background (25). Consistent with the localization of *Chok* to the NKC, NK cells derived from B6.BALB-*Cmv1*^{s} could not lyse CHO, indicating that these animals possess the BALB/c allele for *Chok* (Fig. 5 *A*). These results formally establish linkage of *Chok* to the NKC.



	CXB (BALB/cBy x C57BL/6By)						
	1	2	3	4	5	6	7
Locus							
Chok	B	B	C	C	C	B	C
Chromosome 6							
Cmv-1	B	B	C	C	C	B	C
Nk1.1	B	B	C	C	C	B	C
Nkrp1	B	B	C	C	C	B	C
Ly49	B	B	C	C	C	B	C
Prp	B	B	C	C	C	B	C
Chromosome 1							
2b4	C	B	C	B	B	C	C

Figure 4. The SDP of CHO killing among the CXB RI mouse strains demonstrates linkage to the NKC. (*A*) IL-2–activated NK cells derived from seven CXB RI strains as well as the progenitor strains, C57BL/6ByJ and BALB/cByJ, were assessed for their capacity to mediate CHO and YAC-1 lysis. The SDP is summarized using the symbols *B* and *C* to indicate the alleles inherited from the C57BL/6By and BALB/cBy progenitor strains, respectively. (*B*) Linkage of *Chok* to NKC-encoded loci on chromosome 6. The SDP observed for the *Chok* locus is compared with SDPs of other genes previously typed using the same CXB-RI panel (references 35, 37, 47, 48, 74, and 75). The symbols *B* and *C* represent alleles inherited from the progenitor C57BL/6By and BALB/cBy strains, respectively.

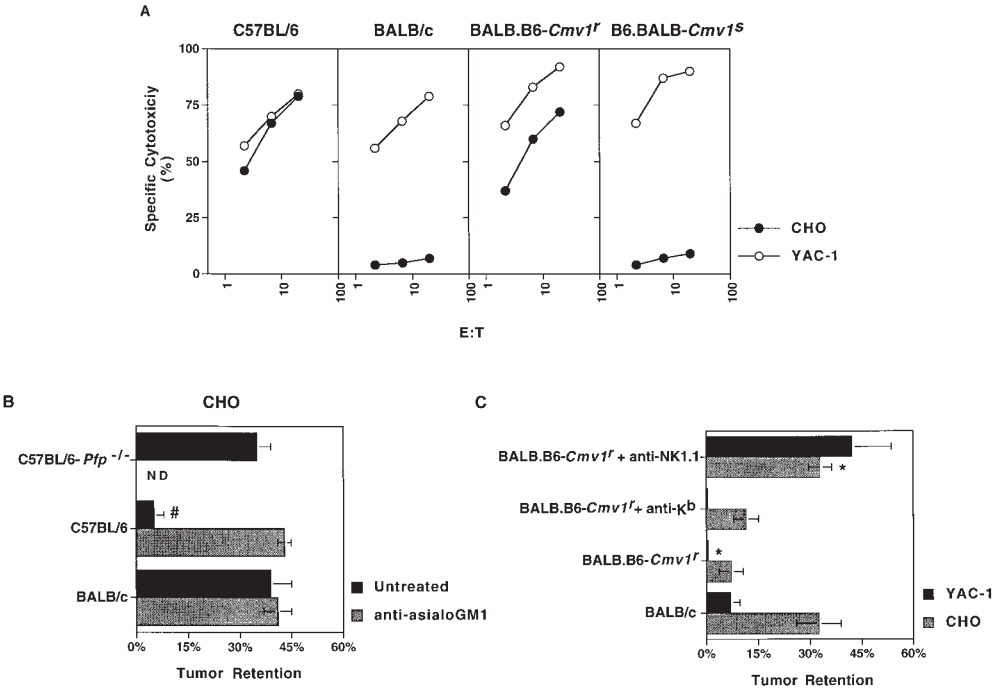


Figure 5. NK cells from BALB.B6-*Cmv1*^{r} as well as B6.BALB-*Cmv1*^{s} confirm *Chok* linkage to the NKC, and *Chok* regulates NK-mediated in vivo elimination of tumor targets through a perforin-dependent pathway. (*A*) Cytotoxicity assays against CHO and YAC-1 targets were performed using IL-2–activated NK cells derived from B6, BALB/c, and the NKC-congenic, BALB.B6-*Cmv1*^{r}, and B6.BALB-*Cmv1*^{s} mouse strains. (*B*) ^{125}I-radiolabeled CHO cells were injected into tail veins of perforin-deficient B6, BALB/c, or B6 mouse strains untreated or treated with anti-AGM1 antiserum 3 d before the assay. Each bar represents the mean percent retention of six mouse lungs except where $^{\#}n = 5$. (*C*) Lung clearance of [^{125}I]UdR-labeled YAC-1 or CHO targets was assessed in BALB/c and BALB.B6-*Cmv1*^{r} congenic mice, untreated or treated with 100 μg of either anti-NK1.1 mAb or an isotype-matched control anti-K^b mAb, intraperitoneally 2 d before the assay. Each bar represents the mean percent retention of four mouse lungs except where $^*n = 3$. In all experiments, mice were killed and lungs were harvested 4 h after inoculation.

Antibodies against Ly-49D and Ly-49H Do Not Block CHO Lysis. Since linkage of the *Chok* locus to the NKC suggests that *Chok* may encode an NK cell recognition receptor involved in tumor killing, we evaluated this region for genes that encode known receptors for which there are specific monoclonal reagents. Two members of the Ly-49 family of receptors, Ly-49D and Ly-49H, lack an ITIM in their cytoplasmic tail and have been shown to activate NK cells (22, 38).[2] To determine if either of these receptors plays a role in CHO lysis, we examined the effect of antibodies against these molecules in our killing assays. There are two previously characterized anti–Ly-49D reagents: 12A8, which also recognizes Ly-49A, and 4E5, which is monospecific for Ly-49D (22, 39). Neither antibody had an effect on CHO lysis by either B6 or BALB/c NK cells (Fig. 6 *A*). To examine the role of Ly-49H, we made use of an antibody recently developed in our laboratory that is specific for the Ly-49H molecule.[2] Inclusion of this reagent, mAb 3D10, in our assay also did not alter the levels of CHO lysis by B6 NK cells (Fig. 6 *B*). Thus, anti–Ly-49D and anti–Ly-49H do not block CHO killing.

Chok Regulates Rapid Elimination of CHO Cells In Vivo. To determine if *Chok* could play a role in NK-mediated activity in vivo, we performed lung clearance assays in B6 and BALB/c hosts. Intravenously inoculated ^{125}I-radiolabeled CHO cells were efficiently eliminated (within 4 h) from the lungs of B6 mice as demonstrated by the low residual radioactivity measured (5 ± 3%; Fig. 5 *B*). Treatment of B6 mice with anti-AGM1 antiserum 3 d before the assay resulted in an eightfold increase in radiolabel retention, consistent with a role for NK cells in tumor clearance from the lung. In contrast, untreated BALB/c mice retained high levels of radioactivity (39 ± 6%) similar to those detected in the lungs of anti-AGM1–treated B6 mice (41 ± 4%; Fig. 5 *B*). In BALB/c mice, anti-AGM1 treatment abolished the clearance of YAC-1 targets, but had no effect on CHO clearance, indicating that BALB/c NK cells were functionally intact yet incapable of recognizing the CHO targets (data not shown, and Fig. 5 *B*). Thus, the in vivo lung clearance assay results parallel the findings of the in vitro cytotoxicity assay.

To ascertain if this strain-determined difference in CHO elimination in vivo maps to the NKC, we compared the lung clearance capacity of BALB/c and the congenic BALB.B6-*Cmv1*^{r} mouse strains. CHO cells were effectively eliminated in the congenic BALB.B6-*Cmv1*^{r} strain but not in BALB/c mice despite efficient clearance of YAC-1 tumor cells in both strains (Fig. 5 *C*). The clearance of YAC-1 and of CHO cells was abrogated in the BALB.B6-*Cmv1*^{r} mouse strain by prior injection of anti-NK1.1 mAb but not by injection of an isotype-matched control antibody, anti-K^b. It is noteworthy that the retention of radiolabeled CHO cell targets in the lungs of BALB/c mice (32.5 ± 6.5%) is about fivefold greater than the level retained in the BALB.B6-*Cmv1*^{r} (7.1 ± 3.5%) lungs and is very similar to the retention detected in the lungs of NK-depleted BALB.B6-*Cmv1*^{r} mice (33 ± 3.4%). These results strongly suggest that the B6 allele of *Chok* in the congenic strain also plays a role in NK-mediated tumor clearance of CHO targets in vivo.

Perforin Dependence of Chok Phenotype. In addition to the membranolytic pathway involving granule exocytosis and

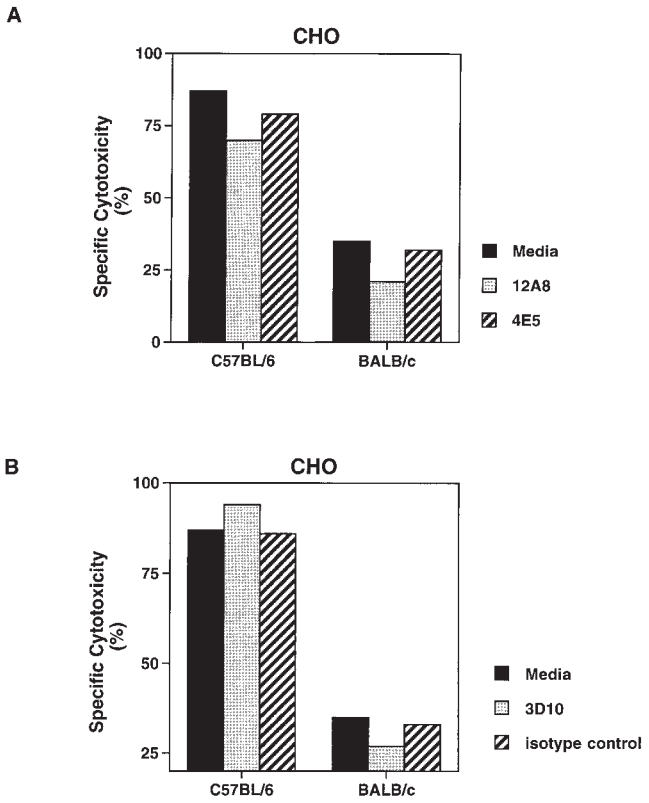


Figure 6. Antibodies against Ly-49D or Ly-49H do not block CHO lysis. (*A*) Cytotoxicity assays against CHO targets were performed using IL-2–activated NK cells derived from B6 and BALB/c in the presence or absence of anti–Ly-49D mAbs. (B) Neither mAb 3D10 (anti–Ly-49H) nor the isotype control had an effect on B6 NK–mediated CHO lysis.

release of pore-forming protein (perforin) and granzymes, NK cells are also capable of Fas ligand–mediated cytotoxicity (40, 41). To investigate the effector mechanisms used by B6 NK cells to kill CHO targets both in vitro and in vivo, we made use of the perforin-deficient B6 (B6-*Pfp*$^{-/-}$) mouse strain. Importantly, in vitro analysis revealed that B6-*Pfp*$^{-/-}$ NK cells could not lyse either YAC-1 or CHO in the standard 4-h chromium-release assay (data not shown), in agreement with previous characterization of natural killing in these animals (42). Furthermore, we demonstrated that the B6-*Pfp*$^{-/-}$ mice were unable to clear the CHO cells as reflected in the high level of radiolabel retention (35 $\pm$ 4%; Fig. 5 *C*). This tumor retention is very similar to that observed in the B6 group treated with anti-AGM1 antiserum, and is about sevenfold greater than in wild-type B6 mice. Taken together, these results indicate that natural killing of CHO targets in vitro and NK-mediated elimination of CHO cells in vivo are perforin dependent, consistent with differential susceptibility to NK cell recognition and subsequent initiation of the granule exocytosis pathway.

Discussion

In this study, we determined that the capacity of NK cells from different strains of mice to kill CHO targets is due to a single genetic locus, *Chok*. Although resistance or susceptibility of CHO cells to NK lysis may have been due to differences in downstream signaling events or mediators of cytolysis, our observations strongly support a differential recognition event. BALB/c-derived NK cells were able to kill YAC-1 and most other targets as efficiently as B6-derived NK cells; however, they could not lyse CHO cell targets. Moreover, this differential capacity to kill CHO was extended to our in vivo tumor clearance model and was determined to be perforin dependent, suggesting that activation of granule exocytosis was required. Therefore, we postulate that this strain-specific cytotoxicity of CHO is due to significant differences in NK cell specificity of target recognition.

In support of the hypothesis that *Chok* encodes a phenotypically defined recognition structure, B6 and BALB/c NK cells express different alleles for several target recognition molecules, including 2B4, a putative activation receptor (37). Importantly, we have localized *Chok* to the NKC by assessment of RI strains, a finding verified by examination of the BALB.B6-*Cmv1*^{r} and the B6.BALB-*Cmv1*^{s} congenic mouse strains. The genetic analysis formally eliminates many known candidate genes, including 2B4. These studies highlight the power of genetic analysis and specifically, the utility of our RI and congenic mouse strains, in evaluation of candidate molecules in NK cell activation.

The known NKC genes encode NK receptors that have similar structure (type II integral membrane protein orientation, disulfide-linked dimers, and C-type lectin homology) and that regulate NK cell functions. The expression of these molecules is generally restricted to NK cells (18, 35) and includes the mouse NKR-P1 and Ly-49 families, as well as CD94 and NKG2, and CD69, which also have been described in humans and rats (43–46). The NKC also contains several other functional loci controlling NK cell activity, including *Cmv1*, which determines the NK cell–mediated clearance of MCMV, and *Nka*, which mediates lymphocyte alloreactivity (47–50). Inasmuch as several of these molecules are also known to influence NK cell specificity and recognition, we postulate that *Chok* encodes one of the known NKC-encoded molecules or represents a novel but structurally related molecule responsible for NK cell recognition of CHO target cells.

Molecules encoded in the NKC either activate or inhibit NK cells. With this dichotomy in mind, we propose two alternative hypotheses to account for the strain-determined difference in cytotoxicity against CHO. The B6-derived NK cells may possess an activating receptor, encoded by *Chok*, that interacts with the CHO target and mediates its lysis. BALB/c mice may either lack this gene (null) or express an allele that is incapable of CHO recognition. Alternatively, the BALB/c allele of an inhibitory receptor may recognize its ligand on the CHO cell, preventing NK cell activation. In this case, B6 NK cells may either lack this receptor or possess an allelic form that is incapable of CHO recognition. The intermediate killing of CHO targets by F_1 hybrid mice provides some support for the activation receptor hypothesis, because NK cell inhibitory receptors

tend to strongly dominate over NK cell activation. However, the available data do not permit unequivocal discrimination between these possibilities, and it remains possible that *Chok* is related to either type of NK cell receptor.

Cd69 and the *Nkrp1* family of genes encode activation receptors on rodent NK cells (20, 23). However, CD69 can be excluded as a candidate for the gene product of *Chok* because it is not expressed on resting NK cells (51, 52). The *Nkrp1* family includes *Nkrp1c*, which encodes the most specific serologic marker of NK cells in B6 mice (NK1.1), and which displays both strain-specific expression and allelic polymorphism between the B6 and BALB/c strains (36). However, there was discordance between NK1.1 expression on NK cells and capacity to lyse CHO targets (Table 2, and Fig. 3). Also, our B6-derived NK cell clones, which express NK1.1, were not able to lyse CHO targets (data not shown). Furthermore, attempts to block CHO killing by B6 IL-2–activated NK cells using the anti-NK1.1 mAb were not successful (data not shown). Thus, other known genes that reside in this region may potentially have a role in the *Chok* phenotype (e.g., the Ly-49 family).

The NKC-encoded Ly-49 family of inhibitory receptors displays several levels of polymorphism. At least nine distinct cDNAs (A–I) have been cloned from the B6 strain, and there is evidence implicating multiple alleles for each *Ly49* gene among inbred strains. At least three members, Ly-49A, Ly-49C, and Ly-49G, are expressed on distinct but overlapping NK cell subsets and are inhibitory receptors specific for MHC class I molecules (53–57). In mouse strains expressing its MHC class I ligand, Ly-49A expression is downmodulated, thus establishing a mechanism whereby host MHC can influence the NK cell receptor repertoire, and presumably effector function (30–32, 58, 59). The level of Ly-49A expression appears to alter the capacity of the inhibitory effect, consistent with a role for host MHC in modulating NK cell cytotoxicity. Although our studies of H2 congenic strains demonstrated that CHO killing is independent of MHC haplotype, we cannot exclude the possibility that an inhibitory Ly-49 molecule is involved, since ligands for the majority of Ly-49 receptors have not been described. Similarly, NKR-P1B contains an ITIM and is probably inhibitory, but its ligand is not known. Furthermore, for most of these receptors, specific serologic reagents are not available.

On the other hand, both the Ly-49D and Ly-49H receptors lack ITIMs and can enhance NK cell lytic function in redirected lysis assays with an anti–Ly-49D or anti–Ly-49H mAbs (22, 38).[2] However, anti–Ly-49D and anti–Ly-49H mAbs do not affect CHO killing by B6 NK cells (Fig. 6). Nonetheless, these results do not rule out involvement of either of these receptors, since mAbs used in our study may not bind epitopes necessary for target recognition. Finally, recent studies have identified the mouse orthologues of the human CD94 and NKG2 molecules. The genes for these molecules also reside in the mouse NKC near the *Ly49* gene cluster (32), as predicted by the localization of the human genes to a syntenic region on human chromosome 12p13 (60, 61). To date, however, the expression patterns of these molecules and their functional role in NK cell activity in mice are unknown, and specific monoclonal reagents are lacking.

It is very possible that Chok may be the product of a novel gene, since the mouse NKC spans at least 2.1 million bases (50). Currently, there are cDNA cloning data on only 15 genes (9 Ly49, 3 NKRP1, CD69, NKG2D, and CD94) of an estimated 84 genes, assuming a conservative 1 gene per 25 kb. Thus, Chok could be the product of any one of the aforementioned candidate known genes, or the product of a novel gene. But whether the gene responsible for the Chok phenotype is a known or novel gene, allelic polymorphism of this NKC-encoded locus affects the natural killing of a tumor target and operates in vivo and in vitro through a perforin-dependent mechanism. Hence, the identification of the *Chok* gene product will further our insight of a known molecule or lead to the discovery of an important and as yet unidentified molecule.

If *Chok* encodes a recognition structure on NK cells, what is the nature of its putative ligand on CHO cells? Given that some NK cell receptors encoded in the NKC, such as Ly-49 inhibitory molecules, are known to interact with MHC class I molecules, hamster MHC class I molecules may be potential target ligands for the *Chok* gene product. However, V79-4 and CHL/IU are Chinese hamster cell lines that were killed efficiently by BALB/c effector populations. Since MHC polymorphism is comparatively limited in hamsters, it is unlikely that an MHC class I structure represents a ligand for Chok. Moreover, given that MHC ligands inhibit only a subset of NK cells bearing the cognate inhibitory receptor(s), it is unlikely that CHO cells would inhibit all BALB/c NK cells. Therefore, we currently favor the interpretation that the differential killing of CHO is not due to a direct inhibitory influence of target cell MHC class I molecules.

Since many of the known molecules encoded within the NKC are C-type lectins, it is possible that a carbohydrate moiety expressed by CHO targets may be involved in the interaction between CHO and NK cells. However, our studies using glycosylation mutant variants of the parental CHO cells strongly suggest that the ligand for Chok is independent of complex N-linked oligosaccharides. Lec1 mutants lack demonstrable *N*-acetylglucosaminyltransferase I activity and therefore have no detectable complex type N-linked oligosaccharides, whereas the LEC11 line expresses an $\alpha(1,3)$ fucosyltransferase not normally expressed by the CHO parental cells (26). Both mutant cell lines displayed susceptibility to B6 but not to BALB/c NK–mediated lysis, similar to what was observed for the parental CHO targets (Table 1). Although these results contradict studies using human NK cells, in which a role for N-linked oligosaccharides has been proposed (62–64), our data indicate that complex N-linked carbohydrates and fucose do not affect the susceptibility of CHO targets to lysis by murine NK cells. These data are consistent with the hypothesis that the product of *Chok* recognizes a noncarbohydrate ligand on CHO cells.

In addition to providing insight into the molecular basis for specific target recognition of CHO cells, our studies have important implications with regard to the general phenomena of natural killing of tumor targets. We examined a large panel of tumor targets, representing different MHC haplotypes, tissue origins, and species. Despite this, only CHO targets manifested a dramatic difference in killing by NK cells from the two mouse strains. If *Chok* influences natural killing through a putative activation receptor, and BALB/c lacks a functional *Chok* gene product, then BALB/c NK cells must utilize other recognition systems, since they can efficiently kill other targets. Therefore, on B6 NK cells, the putative receptor that triggers CHO killing may be coexpressed with receptor systems for other targets. Any or all of such receptors could be stimulated by a given target. Experimental strategies to dissect NK recognition that are based on a "one receptor per NK cell" model, such as those using specific mAb blockade of a single NK cell receptor, may be flawed because of the capacity of NK cells to be activated through other receptor pathways. This notion is supported by studies documenting the expression of more than one inhibitory receptor on an NK cell and on overlapping NK cell subsets (59). Yet, the *Chok* phenotype was revealed in studies of whole populations of heterogenous NK cells, indicating its dominant role in certain situations. Thus, the capacity to study the effect of a genetic locus that controls natural killing in isolation will aid in dissection of NK cell recognition.

Finally, xenotransplantation has received considerable interest in treating end organ failure in humans, particularly since there is a general shortage of suitable human tissue. The first major obstacle in xenotransplantation is hyperacute rejection, which is mediated by xenoreactive "natural antibodies" and complement (65). Blockade of this humoral response delays but does not abrogate rejection (65, 66). This delayed xenograft rejection is characterized by a cellular infiltrate consisting of mainly NK cells and macrophages (66, 67). Evidence is now mounting that human NK cells are active participants in delayed xenograft rejection (68). Furthermore, other studies revealed that depletion of rat NK cells led to prolonged hamster cardiac graft survival (67). Since these experiments were performed in the absence of xenoantibodies, they also demonstrated that NK cells may mediate xenograft rejection via direct cytotoxicity. In addition to xenogeneic solid tissue transplantation, NK cells play a role in xenogeneic bone marrow transplantation. Transplantation of rat bone marrow into supralethally irradiated mice revealed that B6 and (B6 × A)F_1 hybrids are resistant, whereas A, BALB/c, CBA, DBA, and C3H mice are not (69). This phenomenon, termed xenogeneic resistance, is believed to be mediated by radioresistant NK cells and bears many physiologic and genetic similarities to allogeneic resistance, suggesting that the two types of incompatibility are similar, if not identical (70–72). Interestingly, the *Chok* distribution pattern among the mouse strains tested in this study is reminiscent of that for xenogeneic rat bone marrow rejection described above, suggesting that these may be different manifestations of a single mechanism. Importantly, therefore, allelic determinants of NK cell reactivity against xenogeneic cells, such as *Chok*, may affect xenotransplantation outcomes. Elucidation of the *Chok* gene product and its putative ligand on CHO target cells will provide insights into NK cell xenorecognition and facilitate potential clinical applications.

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