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**Author Manuscript** 

J Immunother. Author manuscript; available in PMC 2008 September 17.

Published in final edited form as: *J Immunother*. 1997 January ; 20(1): 15–25.

## Cloning and Characterization of the Genes Encoding the Murine Homologues of the Human Melanoma Antigens MART1 and gp100

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### Abstract

The recent identification of genes encoding melanoma-associated antigens has opened new possibilities for the development of cancer vaccines designed to cause the rejection of established tumors. To develop a syngeneic animal model for evaluating antigen-specific vaccines in cancer therapy, the murine homologues of the human melanoma antigens MART1 and gp 100, which were specifically recognized by tumor-infiltrating lymphocytes from patients with melanoma, were cloned and sequenced from a murine B16 melanoma cDNA library. The open reading frames of murine MART1 and gp 100 encode proteins of 113- and 626-amino acids with 68.8 and 77% identity to the respective human proteins. Comparison of the DNA sequences of the murine MART1 genes, derived from normal melanocytes, the immortalized nontumorgenic melanocyte line Melan-a and the B16 melanoma, showed all to be identical. Northern and Western blot analyses confirmed that both genes encoded products that were melanocyte lineage proteins. Mice immunized with murine MART1 or gp 100 using recombinant vaccinia virus failed to produce any detectable T-cell responses or protective immunity against B16 melanoma. In contrast, immunization of mice with human gp 100 using recombinant adenoviruses elicited T cells specific for hgp100, but these T cells also cross reacted with B16 tumor in vitro and induced significant but weak protection against B16 challenge. Immunization with human and mouse gp100 together [adenovirus type 2 (Ad2)-hep100 plus recombinant vaccinia virus (rVV)-mgp100], or immunization with human gp100 (Ad2-hgp100) and boosting with heterologous vector (rVV-hgp100 or rVV-mgp100) or homologous vector (Ad2hgp100), did not significantly enhance the protective response against B16 melanoma. These results may suggest that immunization with heterologous tumor antigen, rather than self, may be more effective as an immunotherapeutic reagent in designing antigen-specific cancer vaccines.

### Keywords

Cancer vaccine; In vivo model; B16 melanoma; Adenovirus; Vaccinia virus

Active immunotherapy using antigen-specific cancer vaccines is being developed as an experimental method for the treatment of patients with metastatic melanoma (1-5). Recently, a variety of melanoma-associated antigens (MAAs) have been identified using lymphocytes from patients with melanoma (6-12). MART1 and gp100 are melanocyte differentiation antigens specifically recognized by HLA-A2 restricted tumor-infiltrating lymphocytes (TILs) derived from patients with melanoma, and seem to be involved in tumor regression (6,7). Phase

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I clinical trials using immunodominant peptides from thes antigens and recombinant adenoviruses encoding human MART1 or gp100 for the treatment of patients with melanoma have begun in the Surgery Branch, National Cancer Institute (1,13,14). However, a major obstacle to the development of effective cancer vaccines with these melanocyte differentiation antigens is the paucity of animal models, in which the target tumor antigens are normal, nonmutated differentiation antigens. In this communication, we describe our attempts to determine whether melanocyte differentiation antigens can serve as immunotherapy targets in the B16 murine melanoma in syngeneic C57BL/6 mice. Therefore, we have cloned and characterized the genes encoding the murine homologues of the human melanoma antigens, MART1 and gp100, and evaluated whether these self-antigens can serve as immunotherapy targets for the development of experimental antigen-specific vaccine strategies for cancer therapy.

### MATERIALS AND METHODS

### **Cell Cultures and Animals**

The Murine B16 melanoma has been maintained in our laboratory for >15 years. After transduction with a retrovirus encoding the murine B7.1 gene, B7.1-expressing B16 cells were selected with the neomycin analogue G418 and were designated B16.B7. Hepa-1 and its subclone, K78-1.16, are murine hepatoma lines; MC-38 is a 1,2-dimethylhydrazine-induced murine colon adenocarcinoma; MCA-205 is a murine fibrosarcoma; EL4 is a T-cell lymphoma; 3LL is a lung carcinoma. All tumor lines already described are of H-2<sup>b</sup> origin. CT26 is a murine colon carcinoma derived from BALB/c mice; K1735 is a nonpigmented melanoma line derived by ultraviolet irradiation of C3H mice, whereas, M3 is a murine melanoma syngeneic with DBA/2 (H-2<sup>d</sup>) mice. Both K1735 and M3 were obtained from the American Type Culture Collection (ATCC, Rockville, MD.U.S.A.). Another C57B/J (H-2<sup>b</sup>) derived melanoma JB/MS and an immortalized melanocyte line Melan-a were provided by Dr. Vincent Hearing (National Cancer Institute, Bethesda, MD, U.S.A.).

Human melanoma cell line SK-23, human embryonic kidney line 293, monkey embryonic kidney line Cos7, and breast carcinoma line MDA-231 were purchased from ATTC. All tumor lines were grown and maintained in RPMI 1640 medium containing 10% fetal calf scrum, except MDA-231 and 293 cells, which used Dulbecco's Modified Eagle Medium as basal medium. HLA-A2-restricted TIL 1200, TIL 771, and TIL 1520 specifically recognized gp100, and TIL 1235 recognized MART1, whereas TIL 620 recognized both gp100 and MART1. These TILs were generated by culturing fresh tumor cell suspensions with 6,000 IU/ml interleukin-2 (IL-2) for 30-70 days as previously described (6,7,14,15). Female C57BL/6 mice, 6-12 weeks old, were obtained from the Frederick Cancer Research and Development Center, National Institutes of Health (Frederick, MD,U.S.A.) and Charles River Laboratories (Raleigh,NC, U.S.A.).

### cDNA Library Screening and Sequence Analysis

A cDNA library was constructed from poly (A)RNA from the B16 murine melanoma cell line using the Lambda ZAP expressing vector cloning system (Stratagene, La Jolla, CA, U.S.A.). Briefly, cDNA was synthesized and the fractionated cDNA was ligated in to the EcoR1 predigested ZAP Express vector arms, then followed by in vitro packaging with Gigapack II gold packaging extract. The cDNA libraries (a total of  $6 \times 10^6$  palques) were screened with [ $\alpha$ 32P]ATP-labeled human MART1 or human gp100 cDNA probes. MART1 or gp100-positive pBK-cytomegalovirus phagemids were purified, excised, and further characterized by DNA sequencing.

To test whether the cloned cDNAs encoding murine MART1 or gp100 were nonmutated, total RNA was isolated from the Melan-a melanocyte line and from melancoytes that were obtained from the skin of normal C57BL/6 mice. Reverse transcriptase polymerase chain reaction (RT-PCR) was performed using murine MART1 or gp100 specific primers. The amplified products were cloned into the pCRIII expression vector (Invitrogen, San Diego, CA, U.S.A.). DAN sequencing of the cloned genes was performedusing the Sequenase quick-denature plasmid sequencing kit (United States Biochemical Corp., Cleveland, OH, U.S.A.).

### **Northern Blot Analysis**

Total RNA from tumor cell lines was isolated using RNAzol (Tel-Test, Friendswood, TX, U.S.A.). Total RNA from mouse normal tissues was purchased from Clontech (Palo Alto, CA, U.S.A.). Fifteen micro-grams of RNA was subjected to electrophoresis in a 0.6% formaldehyde-agarose gel. After transfer to anylon membranc, the membranes were hybridized with cither a mouse MART1, or mouse gp100-specific probe, then wahsed twice according to the QuikHyb procedure (Stratagene) before autoradiography.

### Western Blot Analysis

Immunoblotting procedures were carried out using standard protocols. Briefly, all tumor cell lines were washed twice with ice-cold phosphate-buffered salineand then lysed with NP-40 lysis buffer (20m*M* Tris HCl, pH 8.0; 1% NP-40; 0.9% NaCl; 5 m*M* EDTA; 0.23 U/ml aprotinin; 2 m*M* phenylmethylsulfonyl fluoride; 1  $\mu$ *M* pepstatin A; 1  $\mu$ *M* leupeptin; 50  $\mu$ g/ml RNAse and 50  $\mu$ g/ml DNAase I). The protein concentration was determined by the BCA protein assay (Pierce Chemical Co., Rockville, MD, U.S.A.). Equivalent amounts of protein (15  $\mu$ g) from eachtumor line were separated by sodium dodecyl sulfate—polyacrylamide gel electrophoresis (4–15% gradient) and then were transferred onto a nylon membrane. The membranes were probed either with  $\alpha$ PEP13, a rabbit polyclonal antibody that recognized a 15-amino-acid peptide from the carboxyl terminus of mouse Pme117 (a gift from Dr. Vincent Hearing), or with M2-9E3, a mouse mAb that recognized human MART1 but also cross reacted with its murine homologue. Subsequent washing and visualization of antibody binding was carried out with Enhanced Chemiluminescence (Amersham Corp., Arlington Heights, IL, U.S.A.) according to the manufacturer's instructions.

### Construction of Recombinant Vaccinia Viruses Encoding Murine MART1 and gp100

To construct plasmids containing the murine MART1 (mMART1) or gp100 (mgp100), cDNAs (Sal I/Xho I predigested fragments) were inserted into the Sal I digested parental plasmid pSC65, in which the transgene was under the transcriptional control of the strong synthetic early/late promoter S<sub>F/L</sub>. After homologous recombination in BSC-1 cells, three rounds of plaque purification under BrdU selection were carried out in huTK<sup>-</sup> cells, and the recombinant vaccinia viral vectors (rVV-mMART1 and rVV-mgp100) were amplified and purified on sucrose cushions. Expression of mMART1 and mgp100 in infected cells was confirmed by immunostaining and RT-PCR analyses. The recombinant vaccinia and fowlpox viruses encoding human MART1 or gp100 (named as rVV-hMART1, rVV-hgp100, rFPV-hMART1, and rFPV-hgp100, respectively)were generated in a similar fashion and provided by Therion Biologics (Cambridge, MA, U.S.A.).The control vaccinia and fowlpox viruses containing LacZ (rVV-LacZ and rFPV-LacZ, respectively) were described previously (16).

### In Vivo Protection Studies

C57BL/6 mice were immunized intravenously with  $10^9$  plaque-forming units (PFU) of recombinant adenoviruses encoding either human MART1, or human gp100 or LacZ gene. Fourteen days later, immunized mice were boosted with various recombinant adenoviruses ( $10^9$  PFU) or vaccinia viruses ( $2 \times 10^7$  PFU) encoding human MART1/gp100 or the mouse

homologues. Twenty-one days later, mice were challenged intravenously with  $2 \times 10^5$  B16 cells. Mice were tagged, randomized, and killed on day 14. Lung metastatic nodules were enumerated in a blinded, coded fashion. When metastases exceeded 250, they were deemed too numerous to count and were arbitrarily assigned a value of 250. Statistical evaluation of the data was performed using the nonparametric two-tailed Kruskal-Wallis test.

### Generation of gp100-Reactive T Cells

Splenocytes from two mice from each of the vaccinated groups already described were harvested before the remaining mice were challenged with B16 tumor cells. These splenocytes were stimulated in vitro with either irradiated ( $3 \times 10^4$  cGy B16.B16.B7, or with irradiated K78-1.16 cells infected for 24–48 h at a multiplicity of infection of 100 with adenoviruses encoding human MART1/gp100 or control LacZ. K78-1.16 was selected as the H-2<sup>b</sup> tumor line for which adenovirus type 2 (Ad2) has the greatest trapism. The  $3 \times 10^6$  splecnocytes were added to  $2 \times 10^5$  tumor cells (stimulators) in 2 ml of complete medium/well in 24-wellplates plus a final concentration of 30 IU IL-2/ml. The T-cell lines were tested for reactivity by measuring the secretion of murine interferon- $\gamma$ (IFN $\gamma$ ) after coculture with MC-38 cells infected with rVV encoding different genes including human MART1/gp100, their murine homologues, and control LacZ.

### **Cytokine Release Assay**

Lymphokine release assays were performed to detect T-cell reactivity with the MART1 and gp100 antigens. To test whether the murine MART1 and gp100 genes isolated from the B16 cDNA library were functional, the cloned mMART1 or mgp100 genes were transiently cotransfected into Cos-7 cells along with the HLA-A2 gene using lipofectamine(Life Technologies, Gaithersburg, MD, U.S.A.). After 24-h incubation, cells were washed, and the ability of the transfected Cos-7 cells to trigger IFN $\gamma$  release from TILs was assessed. An equal number(10<sup>5</sup>) of responder and stimulator cells were mixed, incubated for 20 h, and then supernatants were collected. Secretion of human IFN $\gamma$  was detected using enzyme-linked immunosorbent assay kits purchased from Endogen. Murine IFN $\gamma$  secretion was determined using biotinylated anti-mouse IFN $\gamma$  monoclonal antibody (mAb) (Endogen) as previously described (13).

### RESULTS

### Comparisons of Nucleotide and Amino AcidSequences of Mouse MART1 and gp100

MART1 and gp100 cDNA clones, isolated from the murine B16 melanoma, normal skin melanocytes, and the immortalized melanocyte line Melan-a, were sequenced and compared. The nucleotide sequence of mouse MART1 cDNA from B16 and its predicted amino acid (AA) sequence is shown in Fig. 1. The full-length open reading frame of mMART1 consists of 342 bp encoding a protein of 113 AA with a predicted molecular weight of ~13. The mMART1 sequence contains two small deletions resulting in a protein that is 5AA shorter than the human MART1 protein. Alignment of human and mouse MART1 AA sequences showed 68.6% identity. The mouse MART1 gene cloned from B16 did not show any variation from the MART1 genes colned from normal melanocytes and Melan-a.

The mouse gp100 gene cloned from the B16 cDNA library consists of 1,878 bp encoding a protein with 626 AA bearing 75.5% identity to human gp100. The mgp100 gene cloned from B16 melanoma was almost identical to the published sequences of the murine Pme117 gene cloned from melanocytes from normal C57BL/6 mice and silver mice (17,18). The nucleotide and amino acid differences among mgp100 from B16, Pme117, and the silver mouse are summarized in Table 1. The most striking difference between mgp100 and murine Pme117 is

deletion of codon 2 and an insertion of A, G, and C at codons 582, 603, and 610, respectively, which result in AA changes as shown in Table 1.

### Expression of Murine MART1 and gp100

Northern blot analyses of a variety of murine cell lines including pigmented and nonpigmented melanomas, melanocyte and nonmelanoma cancer cell lines, and normal tissues were performed to evaluate the expression pattern of mMART1 and magp100. As shown in Fig. 2, among normal tissues tested, only testis contained the gp100 mRNA transcript (Fig. 2B). Among cell lines tested to date, both murine MART1 and gp100 were expressed only in pigmented melanomas and theimmortalized melanocyte line Melan-a, but were not expressed in the K1735 amelanotic melanoma and in nonmelanoma tumor lines examined. This result was confirmed at the protein level by Western blot analyses (Fig. 3) and by fluorescence activated cell sorter analysis (data not shown). Thus, like human MART1 and gp100, the expression pattern of murine homologues appeared to be restricted to melanocyte lineage cells.

The observed molecular weight of murine MART1 is ~16, bigger than we predicted, probably because of glycosylation (Fig. 3A). The murine gp100 protein is about 85 kDa by immunoblotting analysis (Fig. 3B), and was larger than the predicted size from the AA sequence as previously reported by other laboratories (19). It has been demonstrated that the silver mutation is the result of a single base insertion that alters the predicted carboxyl terminus sequence normally recognized by  $\alpha$ PEP13 mAb, and consequently would not be recognized in immunoblotting. As shown in Fig. 3B, the 85-kDa band was detected in both melanocytes (Melan-a) and all pigmented melanoma lines tested (B16, M3 and JB/MS) as well. These results, combined with our sequence data, suggest that the murine gp100 from tumor cell is anormal protein not identical to the silver.

### Cross-Reactivity Between Human Melanoma Antigens MART1 and gp100 and Their Murine Homologues Recognized by Human MART1/gp100 Specific TILSs

MART $1_{27-35}$  is the highly immunogenic dominant epitope of human MART1 (14), whereas five different epitopes have been identified in human gp100 (15). These epitopes were recognized by different MART1 or gp100-specific, HLA-A2-restricted TILs. Comparing the AA sequences of human and mouse MART1 and gp100, THE G9-209 epitope recognized by TIL 1520 was the only epitope among the six epitopes identified that was identical in mice and humans (Table 2). To determine whether the murine MART1 and gp100 cDNAs isolated from the B16 cDNA library encoded functional proteins, the cytokine release assays were performed using human TIL. Specific secretion of human IFNy was observed when the cloned mMART1 gene was transiently contrans-fected into Cos7 cells along with HLA-A2, and these cells were with human MART1-specific TIL 1235(Table 3), even though one amino acid substitution (Tto I at position 8) was found in the murine sequence compared with the human epitope. Similarly, specific recognition of murine gp100 by TIL 1520 (reactive with G9-209) occurred when Cos7 cells were contrans-fected with HLA-A2 and mgp100 (Table 4). Expression of the HLA-A2, human and mouse MART1/gp100 were confirmed by FACS analysis (data not shown). Thus, expression of murine MART1 and gp100 cDNA in nonpigmented Cos 7 cells results in immunoreactivity with selected human MART1 or gp100-specific TILs.

# Protective Anti-Melanoma Immune Response in Mice Immunized with Human gp100, but Not Murine gp100

In previous studies, we have demonstrated that immunization of mice with recombinant adenovirus encoding human gp100 (Ad2-hgp100) protected syngeneic mice from B16 challenge (13). In vivo protection assays were performed to investigate whether mouse MART1 or gp100, the "self-proteins," were able to generate protective immunity against B16 challenge. As shown in Table 5, no protection against B16 melanoma was observed in mice

immunized with recombinat vaccinia viruses encoding mgp100 or mMART1. In contrast, immunization with Ad2-hgp100 significantly reduced the number of lung metastases compared with control mice [65 versus 224 (p = 0.007) and 66 versus 163 (p = 0.001) in experiments 1 and 2, respectively]. Mice immunized with recombinant vaccinia virus encoding human gp100, however, did not elicit a protective effect against B16. Neither homologous boosting (with Ad2-hgp100) nor heterologous boosting (with rVV-hgp100 or rVV-mgp100) significantly reduced the number of lung metastases when compared with a single Ad2-hgp100 immunization (Tabel 5, experiment 2).

### In Vitro Generation of Human gp100 Specific TCells that Cross React with Murine B16 Melanoma

Studies were undertaken to determine which immunization strategy was most effective in eliciting T-cell responses to the murine homologues of the human melanoma antigens. As shown in Table 6, immunization of mice with Ad2-hgp 100 and stimulation in vitro with B16.B7 or K78-1.16 cells expressing hgp100 elicited T cells that recognized murine melanoma B16 as well as murine MC-38 cells infected with rVV-hgp100, little, if any release of murine IFN $\gamma$  was seen with MC-38 cells infected with rVV-mgp100, but not uninfected MC-38 cells, or cells infected with rVV expressing LacZ, or mouse or human MART1. These same T cells also recognized MC-38 cells infected with rFPV expressing hgp100 but not LacZ or hMART1. No other immunization stategies were able to elicit clear specific T-Cell response to murine gp100. Murine gp100 reactivity in mice immunized with rVV-mgp100 could not be evaluated against target cells infected with rVV-map100 because of confounding antivaccinia reactivity. All attempts to generate murine MART1 reactive T cells were also unsuccessful.

### DISCUSSION

Recent studies identifying MAAs or melanocyte differentiation antigens on melanomas have generated renewed enthusiasm for the development of cancer vaccines. Evidence has suggested that the melanocyte differentiation antigens MART1 and gp100 may be tumor rejection antigens in vivo (1,6,7). We have thus isolated genes encoding the murine homologues of the human MART1 and gp100 antigens and have studied their possible role as tumor antigens using the B16 melanoma in C57BL/6 mice.

This is the first report of the DNA sequence of the gene encoding murine MART1 and the tissue distribution of the encoded protein. Previous studies established that the murine Pme117 gene (similar to gp100) isolated from normal melanocytes mapped near the si (silver) locus on mouse chromosome 10 and encoded a melanosomal matrix protein with an unknown enzymatic function (19). The mouse silver mutation was caused by a single G insertion at codon 603 in the putative cytoplasmic tail of Pme117, which altered the last 24 AA sequence at the Cterminus(18). Thus, it was important to determine whether the gp100 expressed by B16 was a mutated or nonmutated self-antigen. Studies presented in this communication demonstrate that murine gp100 is indeed a melanocyte lineage protein and that the product encoded by mgp100 cDNA isolated from B16 tumor cells is not a protein with the silver mutation. Even though serveral nucleotide differences and insertions were observed when comparing the gp100 from B16 to the published DNA sequence of murine Pme117 derived from normal melanocytes, it is not not yet clear whether these differences result from alternative splicing of the same gene or from polymorphism. Nevertheless, the human MART127-35 and gp100 G9-209 epitopes, processed and presented from their murine homologues, could be recognized by selected human TILs. Thus, these epitopes may provide a useful in vivo model to study peptide-based vaccines against melanoma in HLA-A2 transgenic mice.

Because human MART1 and gp100 are human melanoma antigens recognized by human T cells, we next evaluated whether the murine homologues of these proteins might serve as T-

Cell antigens on the B16 melanoma. Murine MART1 was a melanocyte lineage protein as demonstrated by DNA sequence, Northern blot, and Western blot analyses. However ,all attempts to generate murine MART1 specific CTL in vitro, and to generate in vivo protective immunity against the B16 melanoma in mMART1 immunized mice under our experimental conditions were unsuccessful. As shown in Table 6, human gp100-reactive T cells generated from Ad2-hgp100 immunized mice did recognize B16 and B16.B7 melanoma, but only weak reactivity was seen to murine gp100. In addition, attempts to generate murine gp100 reactive T cells from mice immunized with rVV expressing murine gp100 (rVV-mgp100) were unsuccessful. Because the anti-B16 reactivity seen was disproportionately greater than any anti-mgp100 activity seen, it is possible that B16 reactivity exists to targets not related to mgp100. Moreover, normal mgp100 alone was clearly insufficient to elicit an autoreactive T-cell response using the immunizations described.

Our studies demonstrated that immunization with Ad2-hgp100, containing the human homologue of mgp100, significantly reduced the number of lung metastases compared with control mice as previously reported (13). However, mice immunized with rVV encoding human gp100 (rVV-hgp100), or murine gp100 (rVV-mgp100) did not elicit a protective effect against B16. Among recombinant adenoviruses examined, Ad2-hgp100, but not the Ad2-hMART1 nor Ad2-LacZ, reproducibly elicited anti-B16 tumor effects (13). We cannot rule out the possibility that the adenoviral vector itself presents unknown or nonspecific T-helper epitopes in vivo that augment the anti-tumor effects of gp100 vaccination as an explanation for the efficacy of Ad2-hgp100 but not rVV-hgp100. The generation of potent protective immunity against melanoma may require additional interactions of tumor-associated antigens and other "helper epiopes" presented by adenoviral vectors, but not the rVV vectors. Vaccinia viruses are replicating viruses, and the timing of transgene expression, the expression of multiple viral proteins, and the replication processes of rVV may explain the different results obtained, compared with nonreplicating rAd2 vectors. All of these factors could affect antigen presentation, and lead to the inability of rVV to generate protective immunity in vivo in this model.

The mechanisms by which Ad2-hgp100 immunization mediated protective immunity against B16 challenge in mice are not yet understood. The concept of molecular "mimicry," in which heterologous proteins can induce strong T-cell responses against cryptic self-determinants, is similar to the concept of molecular mimicry of viral peptides in the initiation of autoimmune disorders (20-23). Previous studies using cytochrome c (cyt c) as a model autoantigen (24,25) have demonstrated that mice failed to elicit cyt-c-specific T cells in response to immunization with either human or mouse cyt c alone; howerver, sequential immunization with foregin cyt c followed by self (mouse) cyt c, or immunization with human and mouse cyt c together, was able to break T-cell tolerance and generated T cells that could be stimulated by either human or mouse cyt c. Similarly, in a murine systemic lupus erythematosus model, neither T- nor Bcell responses could be detected after immunization with native self-snRNPs (small nuclear ribonucleoprotein). T cells elicited by self-peptides did not respond to stimulation with native snRNPs, suggesting that the peptides were cryptic and were not processed from the native protein for presentation by antigen-presenting cells (26,27). Influenced by the cross-priming theory from autoimmune diseases, we tested vaccine strategies immunizing mice with self (mgp100) or human "mimic" (hgp100) alone, or human and mouse gp100 together, or sequentially. No immunization approach using these strategies generated a better antitumor response than using single vaccination with recombinant adenovirus encoding hgp100, the homologue of mouse gp100. It seems that foregin molecule mimicry (hgp100) probably provided the stimulus required for breaking T-cell tolerance to self-mgp100 in syngeneic mice, although further studies with recombinant adenovirus expressing mgp100 (which is not currently available) would be necessary to support this conclusion.

In summary, the present study provides an animal model of molecular minicry of the melanoma antigen gp100 for the induction of antigen-specific T-cell response in vitro and a protective immune response against B16 tumor in vivo. This phenomenon deserves further study in other murine and human tumor models for clinical design of more potent cancer vaccines.

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mMART	ATGCCCCAA	LO GAAGACAT	20 TCACTT	TGGTT	30 ATCCCAGGA	40 AGGGGCACAGA	50 CGCTCC
hMART	 ATGCCAAGA	 GAAGATGC	 TCACTTCA	 TCTATGGTI			 CACTCT
	:	10	20	30	40	50	60
mMART	60 TATGTCACI	70 GCTGAAGA	GGCCGCAG	80 GGATCGGCA	90 TCCTGATCG	100 IGGTCCTGGGG	110 SATTGCT
hMART	TACACCACO	GCTGAAGA		GGATCGGCA	TCCTGACAG		GTCTTA
		70	80	90	100	110	120
mMART	120 CTGCTTATC		1 GTACTGTA	40 GAAGACGAA	150 GTGGATACAG	160 SAACCTTGATO	170 GACAAA
hMART							
	1	30	140	150	160	170	180
mMART	180 AGGCGTCAT	190 אדדככדאד	2	00	210	220	230
hMADT							
Indext	19	90	200	210	220	230	240
	240	250	2	60	270	280	290
mMART	CACCAGGAC	AGCCGACT	GTCTTCTC	AAGAGAAA	CCCATCAGC	CGTGGTTCC	CAACGCT
hMART	CATCGGGAC	AGCAAAGI	GTCTCTTC	AAGAGAAAA	ACTGTGAAC	CTGTGGTTCC	CAATGCT
	23	50	260	270	280	290	300
mMART	CCCCCTCC	TATGAGA	AGCTCTCT		TCACCGCCA	CCTTATTCAC	CCTGA
hMART	CCACCTGC	 TTATGAGA	 AACTCTCT	GCAGAACAG	TCACCACCA	CCTTATTCAC	CTTAA
	3	10	320	330	340	350	
В		10	20	3.0	4.0	50	h
mMART	MPQEDIHF-	-GYPRKGH	IRRSYVTAE	EAAGIGILI	VVLGIALLI	GCWYCRRRSG	, (RTLMDK
hMART	MPREDAHFI	YGYPKKGH	IGHSYTTAE	EAAGIGILI	VILGVLLLI	GCWYCRRRNG	RALMOK
	60	70	20	30	40	50	30
mMART	RRHIGIQKT	FRERCSCE	SPDHQDSR	LSSQEKSH	2PVVPNAPPA	YEKLSSP	PPYSPX
hMART	SLHVGTQCA	LTRRCPQE	GFDHRDSK	VSLQEKNCI	EPVVPNAPPA	YEKLSAEQSE	PPYSPX
		70	80	90	100	110	

### FIG. 1.

Comparison nucleotide sequences between mouse and human MART1 cDNA (A) and their predicted amino acid sequences (B).



### FIG. 2.

Northern blot analyses of the expression of mouse MART1 and gp100 mRNA. Fifteen micrograms of total RNAs from different murine melanoma tumor lines, nonmelanoma lumor lines, and normal tissues were loaded in each lane. Mouse MART1 mRNA (**A**) and gp100 mRNA (**B**) were detected using the full-length murine MART1 and gp100 cDNA as the probes, respectively. Ethidium bromide staining of RNA as shown in (**C**) was used as a control. The positions of mMART1 RNA, mgp100 RNA, AND 28S and 18S RNA were marked.



### FIG. 3.

Western blot analyses of mouse MART1 and gp100 proteins. Equal quantities of protein (10  $\mu$ g) from each cell line were subjected to sodium dodecyl sulfate/polyacrylamide gel electrophoresis and immunoblotting with MART1-specific monoclonal anibody (mAb)2D12 (**A**) or gp100-specific mAb  $\alpha$  PEP13 (**B**). The 16-kDa mouse MART1 and the 85-kDa mouse gp100 proteins are marked. The position and size of molecular weight markers are indicated.

531

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ACA ACA ACT T T

J Immunother. Author manuscript; available in PMC 2008 September 17.

KAPWISWGX

LL S GQQVX LL S GQQVX PQWTAGLI IL

RARGLGENSP RARGLGENSP SRPRPWKQPA

THWLRLPPVF ALTAAPASGL ALTSCACLRS

GSVSOMPHGS AQFPKC\*-MV AQFPKC\*-MV

1 I HRHR L KKQ - - LGID-RSR --MGID-RSR

B16 mPmel17 Silver

582

Result in the following amino acid changes: 603 610

### TABLE 2

Comparison of amino acid sequences of HLA-A2 restricted epitopes between human (h) and mouse (m) MART1 or gpIO0 (identical amino acids are indicated by dashes)

Gene	Epitope		Sequence	Recognition by
MART1	MART <sub>27-35</sub>	(h)	AAGIGILTV	TIL1235
p100	G9-154	(m) (h) (m)	I- KTWGQYWQV	TIL1200
	G9-209	(h)	ITDQVPFSV	TIL1520
	G9-280	(h) (m)	LEPGPVTA S-S	TIL771
	G10-457	(h) (m)	LLDGTATLRL D-D-IM-	TIL1200
	G10-476	(h) (m)	VLYRYGSFSV L	TIL660

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Zhai et al.

# Recognition of mouse MART1 by human MART1-reactive tumor-infiltrating lymphocytes (TILs) **TABLE 3**

			IFN	$\gamma$ secretion (pg/ml/10 <sup>5</sup> cells) <sup>a</sup>	
Stimulator	Transfccted gene(s)	HLA-A2	$TIL620^b$	TIL1200	TIL1235
Cos7	none		0	0	0
Cos7	HLA-A2	+	12	73	46
Cos7	hMART1		0	66	28
Cos7	mMART1		0	62	43
Cos7	hMART1 + HLA-A2	+	112	06	460
Cos7	mMART1 + HLA-A2	+	168	83	552
$SK-23^{C}$		+	1,702	1,712	1,663
B16		ı	0	10	54
a Uuman interferon 27 (1	ENd) concentration was determined by an	arima linbad imminocorhant ac	sou ofter TII s ware coincidented for 34	a with stimulators with a without	tranciantly transfacted range
indiant must with the start of the			and and the way companying the 24		u anotonu y u anotocicu geneo
indicated.					

<sup>b</sup> TIL620 and TIL235 are HLA-A2-restricted cytotoxic T-lymphocytes that recognize the MART1 antigen, whereas TIL1200 recognizes human gp100 specifically.

 $^{c}$ SK-23 and B16 are melanoma turnor lines used as positive and negative controls, respectively.

### TABLE 4

### Recognition of mouse gp100 by human gp100-reactuve tumor-infiltrating lymphocytes (TILs)

Cells transfected		Human IFNy secretion	$(U/ml/10^5 \text{ cells})^a$	
genes	HLA-A2	TIL771	TIL1200	TIL1520
Cos7 Nonc	-	0	0	0
$\cos 7 \text{ HLA-A2}^{b}$	+	0	0	1
Cos7 hgp100	-	0	0	0
Cos7 mgp100	-	0	0	0
Cos7 hgp100 +	+	4	179	146
HLA-A2				
Cos7 mgp100 +	+	0	0	236
HLA-A2				
SK-23 <sup>c</sup>	+	37	274	314
397mcl	-	0	1	0
B16	-	0	0	0

 $^{a}$ Human interferon- $\gamma$  (IFN $\gamma$ ) concentration was measured after TILS were coincubated for 24 h with Cos7 cells that were transiently transfected with or without gene(s) indicated.

<sup>b</sup>TIL771 recognizes G9-280, TIL1200 recognizes G9-154 and G10-457, and TIL1520 recognizes G9-209 epitope specifically.

 $^{c}$ SK-23, 397mel and B16 are melanoma tumor lines used as positive and negative controls, respectively.

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TABLE 5

Protection of C57BL/6 mice against challenge with B16 melanoma using different immunization strategies

				No. of lung metastases	p value compared with group 1
Group	Immunization <sup>a</sup>	Boost	Avg.	Metastases/mouse	(no. 6)
Exp. 1					
	None	None	224	250  imes 4, 173, 168	
2	rVV-hgp100	None	162	220, 228, 205, 104, 53	0.13
33	rVV-mgp100	None	250	250  imes 6	0.98
4	rVV-mMART1	None	199	248,205,199,195,181,160	0.25
5	rVV-LavZ	None	193	250, 243, 223, 144, 103	0.36
9 0 9	Ad2-hgp100	None	65	78,74,66,65,44	0.001
EXP. 2	Marra	Morre	5	00 311 101 311 201 200 300 010	
	None	None	103	240,225,207,155,148,121,116,90	
2	rVV-hpg100	None	164	219,214,211,207,198,168,168,135,120	0.5
3	rVV-mgp100	None	212	250  imes 3,200,182,180,169	0.07
4	rVV-mMART1	None	ND		
5	rVV-LacZ	None	186	250  imes 3, 230, 190, 183, 156, 130, 37	0.23
9	Ad2-hgp100	None	99	102,77,61,49,41	0.007
7	Ad2-hgp100	Ad2-hgp100	133	250,203,195,158,136,104,78,51,16	0.41(0.08)
8	Ad2-hgp100	rVV-hgp100	52	172,98,49,39,34,10,8,3	0.007 (0.19)
6	Ad2-hgp100	rVV-mgp100	92	132, 123, 105, 97, 91, 79, 64, 41	0.002(0.14)
10	Ad2-hgp100 +	None	79	120,105,100,96,96,71,25,22	0.007(0.51)
	rVV-mgp100				
11	Ad2-hMART1	Ad2-hMART1	169	218,201,194,188,173,160,153,149,146,104	0.79
12	Ad2-hMART1	rVV-mMART1	215	250  imes 3,222,214,203,190,139	0.08
13	Ad2-LacZ	None	143	180, 172, 156, 152, 147, 145, 137, 133, 112, 97	0.56
14	Ad2-LacZ	Ad2-LacZ	179	250  imes	0.50
				2, 198, 198, 183, 170, 168, 164, 106, 105	
15	Ad2-LacZ	rVV-LacZ	157	208, 174, 165, 157, 149, 139, 131, 129	0.87
<sup>a</sup> C57B1/6 mice we	sre immunized intravenously wit	th either $10^9$ or $2 \times 10^7$ plaque-for	ming units of either rec	mhinant adenovirus type 2 (Ad2) or recomhinanat vac	cinia virus (rVV) encoding gene as

indicated. Eighteen days later, these mice were boosted with same amount of recombinant virus indicated. These mice were then injected intravenously with  $2 \times 10^5$  B16 cells 21 days after boosting. On day 14 after tumor challenge, lungs were harvested, and the number of pulmonary metastases were enumerated in a coded and blinded fashion.

								-							
						MC-36	8 cells infected v	with <sup>b</sup>							
					rVV	encoding				rFPV encoding					
Immunization	Boost	In vitro stimulation	None	LacZ	hMART1	mMART1	hgp100	mgp100	LacZ	hMART	hgp100	B16	B16.B7	E22 <sup>c</sup>	EL4
Ad2-hgp100	None	B16.B7 V70 Ad- L100					34	• و			21 75	22 LL	74	0 -	0,0
None	rVV-mgp100	R/8-Adz-ngp100 B16.B7	- 0	73	75	75	42	8 71	- 0	- 0	0 0	00 47	74	- 0	7 - 1
Ad2-hgp100	rVV-mgp100	K78-Ad2-hgp100 B16.B7		70 75	75 56	77 81	61 65	73 71	<del>ω</del> –	m 11	29 5	62 69	72 70	- 1	00
Ad2-hMART1	rVV-MART1	K78-Ad2-hgp100 Bl6.B7		72 67	75 41	75 45	59 56	73 66	4 –	<del>ω –</del>	77 1	38 70	61 76		- 0
None	None	K78-Ad2-hMART1 B16 B7	~ ~	74 0	74 0	78	65 1	72 0	ω ο	ω -	<del>.</del> - 3	67 15	73 19	n u	
Ad2-LacZ	rVV-LacZ	K78-Ad2-LacZ	0	80	67	72	83	78	2 77	0	- 0	ov <u>c</u>	9	80	

 $^{b}$ MC-38 cells were infected with 10 multiplicities of infection of different rVVs or rFPVs as stimulators right before being mixed with T cells.

 $^{c}$ E22 and EL4 are H-2<sup>b</sup> tumors transfected with or without  $\beta$ -gal, respectively.

Page 18

Zhai et al.

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