Human Gene MAGE-3 Codes for an Antigen Recognized on a Melanoma by Autologous Cytolytic T Lymphocytes

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Summary

Human melanoma cell line MZ2-MEL expresses several antigens recognized by autologous cytolytic T lymphocyte (CTL) clones. We reported previously the identification of a gene, named MAGE-1, that codes for one of these antigens named MZ2-E. We show here that antigen MZ2-D, which is present on the same tumor, is encoded by another member of the MAGE gene family named MAGE-3. Like MAGE-1, MAGE-3 is composed of three exons and the large open reading frame is entirely located in the third exon. Its sequence shows 73% identity with MAGE-1. Like MZ2-E, antigen MZ2-D is presented by HLA-A1. The antigenic peptide of MZ2-D is a nonapeptide that is encoded by the sequence of MAGE-3 that is homologous to the MAGE-1 sequence coding for the MZ2-E peptide. Competition experiments using single Ala-substituted peptides indicated that amino acid residues Asp in position 3 and Tyr in position 9 were essential for binding of the MAGE-1 peptide to HLA-A1. Gene MAGE-3 is expressed in many tumors of several types, such as melanoma, head and neck squamous cell carcinoma, lung carcinoma and breast carcinoma, but not in normal tissues except for testes. It is expressed in a larger proportion of melanoma samples than MAGE-1. MAGE-3 encoded antigens may therefore have a wide applicability for specific immunotherapy of melanoma patients.

Mixed lymphocyte–tumor cell cultures carried out with human melanoma cells and lymphocytes from the same patient often generate cytolytic T lymphocytes (CTL)[1] that lyse the autologous tumor cells (1–4). Using blood lymphocytes of melanoma patient MZ2, a panel of CTL clones has been obtained that lyse autologous tumor cell line MZ2-MEL (3). These CTL clones were used to select antigen–loss variants and this led to the definition of several different antigens on the MZ2-MEL melanoma cells (5). Gene MAGE-1 that directs the expression of antigen MZ2-E was identified by transfecting a cosmid library prepared with the DNA of the MZ2-MEL cells into an E^- antigen–loss variant and by testing the ability of the transfected cells to stimulate anti-MZ2-E CTL (6). Gene MAGE-1 is composed of three exons. The third exon contains an open reading frame coding for a protein of 309 amino acids (7). A MAGE-1 encoded nonapeptide composed of amino acids 161–169 binds to MHC class I molecule HLA-A1 to form the complex recognized by the anti-MZ2-E CTL (8). Gene MAGE-1 is expressed in many melanoma tumors as well as in other types of tumors. No expression was detected on normal tissues with the exception of testes (7).

When the expression of gene MAGE-1 was analyzed in the MZ2-MEL cell line, two other cDNA species were found that crosshybridized with a MAGE-1 probe. The sequences of these cDNA proved to be closely similar to that of MAGE-1 and the corresponding genes were named MAGE-2 and MAGE-3 (6). We report here that gene MAGE-3 is responsible for the expression of another antigen present on the MZ2-MEL cell line, namely MZ2-D.

Materials and Methods

Cell Lines and Culture Conditions. Melanoma cell line MZ2-MEL was derived from patient MZ2, and various clonal sublines were obtained (3). MZ2-MEL.61, which does not express antigen MZ2-D, was obtained by in vitro immunoselection of MZ2-MEL with anti-MZ2-D autologous CTL clone 20/38 (5). The derivation of

[1] *Abbreviations used in this paper:* CHO, Chinese hamster ovary; CTL, cytolytic T lymphocyte; RT-PCR, reverse transcriptase–polymerase chain reaction.

anti-MZ2-D CTL clone 20/38 and its culture conditions have been previously described (5). EBV-transformed B cell line BM21 was derived from a HLA-A1 individual (9).

Screening of the Genomic Library and Sequencing. The genomic library was constructed in cosmid c2RB with DNA from PBL of patient MZ2 as previously described (10). Cosmid 4.12, which contained the MAGE-3 sequence, was identified by colony hybridization with ^{32}P-labeled oligonucleotide Chinese hamster ovary (CHO)-3 (6) as described by Lurquin et al. (11). Cosmid 4.12 was digested with EcoRI, size-fractionated in agarose gels, blotted on nitrocellulose filters, and hybridized with ^{32}P-labeled oligonucleotides CHO-3 or VDB19 (5'-CGGATGGTTGAATGAGC-3': MAGE-3 positions 1323–1339 sense). A 5- and 1.9-kb fragment hybridizing with CHO-3 and VDB19, respectively, were then subcloned in plasmid pTZ18R (Pharmacia Fine Chemicals, Piscataway, NJ) and single-stranded DNA was produced. Nucleotide sequence was determined using the T7 sequencing kit (Pharmacia Fine Chemicals) and synthetic primers. Sequence alignments were performed with the GeneWorks computer software (IntelliGenetics, Inc./Betagen, Mountain View, CA).

Transfection of COS-7 Cells. Transfection experiments were performed by the DEAE-dextran-chloroquine method (12). Briefly, 1.5×10^4 COS-7 cells were treated with 100 ng of plasmid pcDNAI/Amp (Invitrogen Corporation, San Diego, CA) containing the HLA-A1 gene and 100 ng of plasmid containing the cDNA of MAGE-1, MAGE-3 (cloned in pcDNAI/Amp), or MAGE-2 (cloned in pcDSRα). Plasmid pcDSRα was a gift of Kevin Moore (DNAX, Palo Alto). The COS-7 cells were incubated for 24 h at 37°C. The medium was then discarded and 1,500 CTL were added in 100 μl of Iscove medium (GIBCO BRL, Gaithersburg, MD) supplemented with 10% human serum and 25 U/ml rIL-2 (Cetus Corp., Berkeley, CA). After 24 h, the supernatant was collected and its TNF content was determined by testing its cytotoxicity for WEHI-164-13 (13) as previously described (14).

Antigenic Peptides and CTL Assay. Peptides were synthesized on solid phase using F-moc for transient NH_2-terminal protection as described by Atherton et al. (15), and characterized by mass spectrometry. All peptides were >90% pure as indicated by analytical HPLC. Lyophilized peptides were dissolved in 0.02 M PBS and stored at −20°C. Lysis of target cells by CTLs was tested by chromium release as previously described (16). In the peptide sensitization assay, target cells were ^{51}Cr-labeled for 1 h at 37°C and washed extensively. 1,000 target cells were then incubated in 96-well microplates in the presence of various concentrations of peptide for 30 min at 37°C. CTLs were then added in an equal volume. Chromium release was measured after 4 h at 37°C. In the peptide competition assay, 10^6 cells of the BM21 lymphoblastoid cell line (HLA-A1$^+$) were labeled with ^{51}Cr during 1 h at 37°C in the presence of a 1:40 dilution of anti-class I mAb W6/32 ascites in Tris Dulbecco buffer. Labeled targets (1,000 cells/well) were incubated for 15 min at room temperature with various concentrations of competitor peptides, before addition of the antigenic MAGE-3 peptide. Then, after 15 min, cells from CTL clone 20/38 were added at a lymphocyte to target cell ratio of 10:1. The assay was terminated after a 4-h incubation at 37°C.

mRNA Expression Analysis. Total RNA was extracted by the guanidine-isothiocyanate procedure as described (17). For cDNA synthesis, RNA (2 μg) was diluted with water, 4 μl of 5× reverse transcriptase buffer (GIBCO BRL), 1 μl each of 10 mM dNTP, 2 μl of a 20 μM solution of oligo(dT), 20 U of RNasin (Promega Biotec, Madison, WI), 2 μl of 0.1 M dithiothreitol, and 200 U of MoMLV reverse transcriptase (GIBCO BRL) in a 20-μl reaction volume, and incubated at 42°C for 60 min. One twentieth of the cDNA reaction was supplemented with 5 μl of PCR buffer (Perkin-Elmer Cetus Instruments, Norwalk, CT), 0.5 μl each of 10 mM dNTP, 1 μl each of 20 μM solutions of primers, 1.25 U of Taq polymerase (Perkin-Elmer Cetus Instruments) and water to a final volume of 50 μl. Primers were 5'-TGGAGGACCAGAGGCCCCC-3' (sense, exon 2) and 5'-GGACGATTATCAGGAGGCCTGC-3' (anti-sense, exon 3) for MAGE-3, and 5'-GGGACCAGGAGACAC-GGAATA-3' (sense, exon 2) and 5'-AGCCCGTCCACGCACCG-3' (anti-sense, exon 3) for HLA-A1. PCR was performed for 30 cycles (1 min at 94°C and 4 min at 72°C for MAGE-3; 1 min at 94°C, 2 min at 68°C and 2 min at 72°C for HLA-A1). The PCR product was size-fractionated on a 1% agarose gel. The conditions for PCR amplification of MAGE-1 and MAGE-2 were previously described (7, 18). The quality of RNA preparations was checked by PCR amplification of β-actin cDNA.

Results

CTL clone 20/38, which was derived by stimulating PBL of patient MZ2 with the autologous melanoma cell line MZ2-MEL, lyses MZ2-MEL cells but not autologous fibroblasts, autologous EBV-transformed B cells, or K562 (5). This CTL clone recognizes an antigen named MZ2-D, which is different from MZ2-E, the antigen encoded by gene MAGE-1. This follows from the observation that an MZ2-MEL.E$^-$ variant selected for resistance to an anti-MZ2-E CTL was still lysed by CTL 20/38 (Fig. 1). Conversely, a MZ2-MEL.D$^-$ antigen–loss variant, which was selected in vitro for resistance to CTL 20/38, was still lysed by the anti-MZ2-E CTL.

Anti-MZ2-D CTL Recognize HLA-A1 Melanomas That Express MAGE-3. CTL clone 20/38 secreted TNF when put in the presence of the MZ2-MEL cells that express antigen MZ2-D, but not in the presence of the D$^-$ antigen–loss variant (Table 1). To identify the HLA class I molecule presenting antigen MZ2-D to CTL 20/38, we performed the same test with a number of melanoma lines of patients sharing one HLA specificity with patient MZ2. This patient carries HLA-A1, A29, B37, B44, Cw6, and C.cl.10. But we focused on melanomas expressing either A1, B37, or Cw6, because variant MZ2-MEL.2.2.5, known to have lost HLA-A29, B44, and C.cl.10, still expressed antigen MZ2-D. 8 of 10 melanoma cell lines derived from HLA-A1 patients stimulated CTL 20/38 (Table 1) and several of these tumor cell lines were also lysed by this CTL clone (Fig. 2), suggesting that HLA-A1 was the class I molecule presenting antigen MZ2-D. The gene coding for MZ2-D did not seem to be MAGE-1 because several allogeneic melanomas that stimulated the CTL did not express this gene (Table 1). By looking at the pattern of expression of genes MAGE-1, -2, and -3, we noticed that gene MAGE-3 was expressed by the eight HLA-A1 melanomas that were recognized by CTL 20/38, whereas the two lines that were not recognized did not express this gene. This suggested that antigen MZ2-D might be a MAGE-3–encoded peptide presented by HLA-A1.

Expression of MZ2-D by COS Cells Transfected with HLA-A1 and MAGE-3. To find out whether gene MAGE-3 directed the expression of antigen MZ2-D, we transfected COS-7 cells with the HLA-A1 gene and either MAGE-1, MAGE-2, or

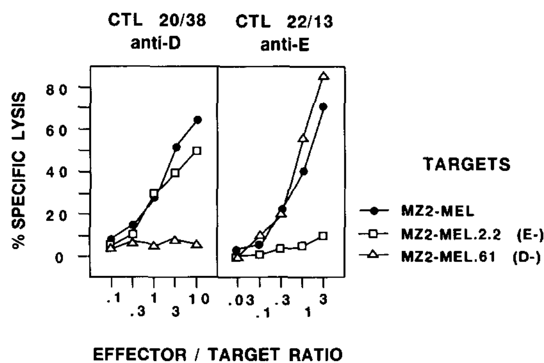

Figure 1. Cytolytic activity of CTL clones 20/38 and 22/13 of patient MZ2 on MZ2-MEL cells. Antigen–loss variants MZ2-MEL.2.2 E^- and MZ2-MEL.61 D^- were obtained by in vitro immunoselection with CTL 22/13 and 20/38, respectively. Lysis of chromium-labeled cells was measured after 4 h.

MAGE-3 cDNA cloned in an expression vector. After 1 d we added CTL 20/38 and 24 h later, the amount of TNF present in the supernatant was assayed by testing its cytotoxicity for WEHI-164-13 cells (Fig. 3). CTL 20/38 was strongly stimulated by COS-7 cells transfected with HLA-A1 and MAGE-3, but not by cells transfected with HLA-A1 alone or with HLA-A1 and MAGE-1 or MAGE-2. We concluded that antigen MZ2-D is a MAGE-3 product presented by HLA-A1.

We tested the expression of MAGE-3 in antigen–loss variant MZ2-MEL.61, which had lost the expression of antigen MZ2-D. RNA was reverse transcribed with an oligo(dT) primer, and the cDNA was amplified with a pair of primers specific for MAGE-3. The level of expression of MAGE-3 was considerably lower than that found in the D^+ MZ2-MEL cells. Quantitative PCR analysis revealed that D^- cells express about 6% of the level of MAGE-3 mRNA found in D^+ cells (data not shown). This low level is presumably insufficient to provide enough antigenic peptide to ensure recognition by CTL 20/38.

Sequence and Structure of Gene MAGE-3. The gene coding for the MAGE-3 mRNA was isolated by screening a cosmid library prepared with the DNA of PBL from patient MZ2. A cosmid containing the gene was identified by colony hybridization with an oligonucleotide probe corresponding to a region where the MAGE-3 sequence differs significantly from that of MAGE-1 and MAGE-2. The sequence of the whole gene was determined and aligned to that of the MAGE-3 cDNA. This allowed us to deduce the structure of gene MAGE-3, which proved very similar to that of gene MAGE-1 with two small exons followed by a large one. The nucleotide sequence of MAGE-3 is 73% identical to that of MAGE-1,

Table 1. *TNF Release by CTL 20/38 Incubated with Allogeneic Melanomas*

		‡Expression of			TNF release by CTL 20/38§	
Melanoma	Expression of HLA-A1*	MAGE-1	MAGE-2	MAGE-3	Exp. 1	Exp. 2
MZ2-MEL	+	+ + +	+ + +	+ + +	>120	>120
MZ2-MEL.61D⁻	+	+ + + +	+ + + +	±	1	4
LY1-MEL	+	+	–	+ + +	>120	>120
MI-10221-MEL	+	+	+ + +	+ + +	>120	
LY2-MEL	+	+ + +	+ + +	+ + +	57	
LY4-MEL	+	–	+ +	+ + +	>120	
SK23-MEL	+	–	+ + + +	+ + + +	112	
MI665/2-MEL	+	–	–	–	3	4
LB34-MEL	+	+	+ + + +	+ + + +	>120	
LB45-MEL	+	–	–	–	11	30
NA6-MEL	+	–	+ +	+ + +	77	98
MI-13443-MEL	+	+ + + +	+ + + + +	+ + + +	>120	
LB5-MEL	–	–	±	+	8	9
SK64-MEL	–	–	–	–	4	5
LB33-MEL	–	±	+ + +	+ + +		3.5
LB73-MEL	–	+	+ + +	+ + +	16	

* Expression of HLA-A1 was tested by RT-PCR.

‡ Expression of MAGE genes was measured by RT-PCR analysis and scored according to band intensity of PCR products.

§ 1,500 cells of CTL clone 20/38 and 25 U/ml IL-2 were mixed with 30,000 cells of the different allogeneic melanomas, except for the two MZ2-MEL lines, where 50,000 stimulator cells were used. After 24 h, the amount of TNF present in the supernatant was assayed by testing its cytotoxicity for WEHI-164-13. Results are expressed in pg/ml equivalent TNFβ. TNF release in the absence of CTL added was <5 pg/ml in the two experiments.

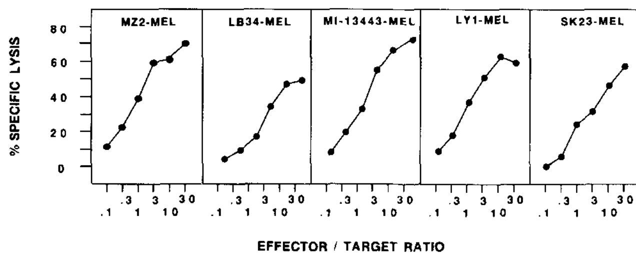

Figure 2. Lysis of melanoma target cells by CTL clone 20/38 of patient MZ2. Melanoma cell lines MI-13443-MEL, LB34-MEL, LY1-MEL, and SK23-MEL were derived from HLA-A1 patients. They all express MAGE-3. Lysis of chromium-labeled cells was measured after 4 h.

and in exon 3 the identity is 82%. The main structural difference between the two genes is the presence of two deletions in the first intron of MAGE-3, one of 700 bp and one of 400 bp (Fig. 4).

The cDNA sequence of MAGE-3 is shown in Fig. 5. Like MAGE-1, MAGE-3 contains a large open reading frame in the third exon. The MAGE-3 protein is 314 amino acids long and presents 66% identity with the MAGE-1 protein which is 309 amino acids long. The MAGE-3 protein is devoid of a signal sequence but contains a putative short transmembrane domain that is conserved in the MAGE-1 protein (De Plaen, E., K. Arden, C. Traversari, J. J. Gaforio, J.-P. Szikora, C. De Smet, F. Brasseur, P. van der Bruggen, B. Lethé, C. Lurquin, P. Chomez, R. Brasseur, W. Cavenee, and T. Boon, manuscript in preparation).

Identification of the Antigenic Peptide of Antigen MZ2-D. A 881-bp fragment of MAGE-3 cDNA (nucleotides 1–881 in Fig. 5) which did not contain the 3′ end of exon 3 proved capable of transferring the expression of antigen MZ2-D when transfected into COS-7 cells (data not shown). In our attempt to find out which part of this fragment coded for the MZ2-D antigenic peptide, we were helped by the existence of another

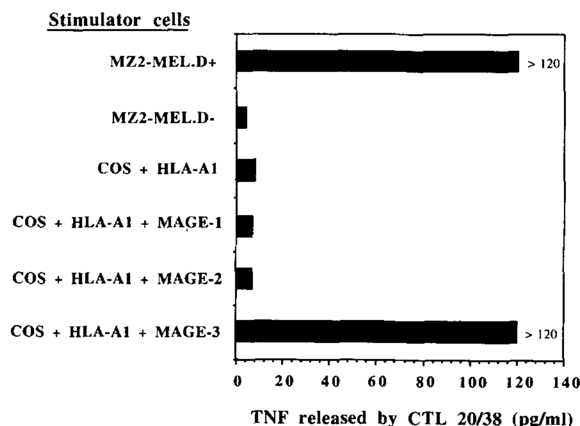

Figure 3. Stimulation of CTL 20/38 by COS-7 cells transfected with expression vectors containing the cDNA of MAGE-3 and the HLA-A1 gene as described in Materials and Methods. As controls, COS-7 cells were transfected with HLA-A1 gene alone or mixed with the cDNA of MAGE-1 or of MAGE-2. CTL 20/38 was added and the TNF content of the supernatant was tested for its cytotoxicity on WEHI-164-13 cells.

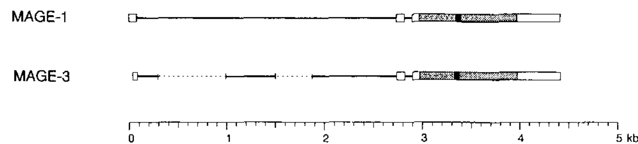

Figure 4. Gene structures of genes MAGE-1 and MAGE-3. Exons are indicated as boxes, with the sequences encoding the proteins and the antigenic peptides in grey and black, respectively. MAGE-1 and MAGE-3 sequences were aligned and the stippled lines indicate regions that are deleted in MAGE-3 relative to MAGE-1.

member of the MAGE gene family named MAGE-6, which presented 99% identity with MAGE-3 (De Plaen, E. et al., manuscript in preparation). Despite this nearly complete identity, MAGE-6 did not seem to code for antigen MZ2-D because it was expressed at a high level in the D$^-$ antigen–loss variant (data not shown). This was confirmed by transfecting into COS-7 cells a fragment of MAGE-6 corresponding to the 881-bp fragment of MAGE-3 cDNA; no expression of antigen MZ2-D was observed (data not shown). We examined the few amino acid differences between MAGE-3 and MAGE-6 that were localized in the 881-bp fragment. Six of seven substitutions could not be included in a peptide sequence carrying a tyrosine. This amino acid residue has been suggested to serve as anchoring residue for several class I molecules (19–21) and it is present at position 9 in the MAGE-1 peptide that binds to HLA-A1 (8). It is interesting to note that the last substitution was located in the region homologous to the region of MAGE-1 that codes for the MZ2-E peptide (8). On this basis, nonapeptide EVDPIGHLY was synthesized and corresponds to codons 168–176 of the long open reading frame of MAGE-3. This peptide sensitized D$^-$ cells to lysis by the anti-D CTL clone (Fig. 6).

Two Residues Involved in the Binding of the MAGE-1 Peptide to HLA-A1. The availability of the MAGE-1 and MAGE-3 peptides, which both bind to HLA-A1 but are recognized by different CTL, enabled us to perform competition experiments in order to identify the residues involved in the binding to the HLA-A1 molecule. HLA-A1 positive cells were incubated with competitor MAGE-1 peptide at various concentrations. Then, the MAGE-3 peptide was added and the cells were tested for recognition by anti-D CTL 20/38. As shown in Fig. 7, the MAGE-1 peptide was able to inhibit the lysis of cells pulsed with the MAGE-3 peptide. We then tested a panel of MAGE-1 peptides substituted with alanine in single positions. Substitutions of P, T, G, H, and S (residues 4, 5, 6, 7, and 8) by A did not prevent the peptide from competing. In contrast, competition was reduced by the substitutions of D by A in position 3 and it was abolished by the substitution of Y by A in position 9, indicating that these two residues are involved in the binding to HLA-A1 (Fig. 7 *A*).

We also tested peptides encoded by the homologous sequence of gene MAGE-2 and of additional genes that belong to the MAGE family (Fig. 7 *B*). The MAGE-2 peptide, which does not carry D in position 3, did not compete with the MAGE-3 peptide. Replacement of V by D in position 3 of the MAGE-2 nonapeptide significantly improved its ability

to bind to HLA-A1 (data not shown), confirming the essential role of this residue for binding to HLA-A1. In contrast, the peptides encoded by MAGE-4a, 4b, 5, and 6, which do carry D in position 3 and Y in position 9, were able to compete. These results suggest that these MAGE genes are potential sources of antigens presented by HLA-A1.

MAGE-3 Expression in Tumors and Normal Tissues. The expression of gene MAGE-3 was evaluated in various tumors and normal tissues by reverse transcription and PCR amplification (RT-PCR) with primers that are specific for this gene. Primers located in different exons were chosen so as to prevent occasional false positives due to DNA contamination of the RNA. A panel of tumor cell lines and fresh-frozen samples from tumors of various histological types were tested. Gene MAGE-3 is expressed in a higher proportion of melanomas (69%) than gene MAGE-1 (40%). Like MAGE-1, gene MAGE-3 is expressed in several tumor types other than melanoma, such as small cell and nonsmall cell lung cancer and head and neck squamous cell carcinoma (Table 2). Lower percentages of positive tumors were found in mammary carcinomas and colorectal carcinomas. No renal carcinoma expressed MAGE-3. The expression of MAGE-3 was tested in a variety of normal adult tissues and in some tissues from fetuses of more than 20 wk. All were negative except testes.

Discussion

The MAGE gene family is composed of at least 12 different closely related genes whose sequences show 64 to 85% identity with MAGE-1 (De Plaen, E., et al., manuscript in preparation). All these genes appear to be silent in normal adult tissues other than testis. Six of them, namely MAGE-1, -2, -3, -4, -6, and -12, are expressed in a significant proportion of human tumors of various histological types. Because these six genes code for proteins of more than 300 amino acids, it was surmised that they should produce many peptides combining with various HLA molecules to form tumor antigens recognized by T lymphocytes. This would be in line with the observations made with influenza proteins such as nucleoprotein which is known to produce several peptides recognized by CTL on different HLA alleles (22–26). On the other hand, it was impossible to exclude a priori that, because MAGE proteins are self proteins, the diversity of T lymphocytes recognizing MAGE-encoded antigens could be severely reduced by tolerance.

Our observation that MAGE-3 codes for an antigen recognized on a melanoma by autologous CTL fully confirms the notion that multiple antigens are coded by the MAGE gene family. Moreover, another antigen encoded by MAGE-1 and presented by the HLA-C cl.10 molecule has recently been identified (van der Bruggen, P., P. Boël, and T. Boon, manuscript in preparation). Accordingly, we will continue to test known antitumor CTL clones for their ability to crossreact with tumor cells sharing some HLA alleles with the syngeneic tumor target. By examining the pattern of expression of MAGE genes in the crossreacting tumors, we will try to identify new antigens encoded by MAGE genes.

An alternative approach should also prove useful. It is based on the observation that a given class I molecule combines only with a restricted set of peptides that carry certain anchor residues at a few crucial positions. These consensus motives have been identified for a number of HLA alleles (20, 27–30). It is possible to identify in the MAGE protein sequences several peptides that should be capable of binding to certain HLA molecules. These peptides could then be synthesized and tested for their binding to the relevant HLA molecule, which results in stabilization of these molecules (31–33). The peptides that show good binding could then be used to stimulate T cells in order to generate CTL reactive with the peptide/HLA complex. This has been achieved for the identification of malaria epitopes recognized by CTL (21). However, the lymphocytes restimulated in vitro with these peptides came from individuals already immunized against malaria. With MAGE peptides, one would have to generate primary T cell responses in vitro. This should be more difficult, but it has been achieved using peptide-pulsed dendritic cells or mutants that are defective for antigen processing like RMA-S or T2 (34–36).

The antigenic peptide that is encoded by MAGE-3 and that binds to HLA-A1 is located at a position homologous to that of the MZ2-E peptide in the MAGE-1 protein. Two residues, which are shared by both peptides, appear to be essential for binding to HLA-A1, namely aspartic acid in position 3, and tyrosine in position 9. These residues may constitute a general motive for peptide binding to HLA-A1. This would be in line with mounting evidence that the COOH-terminal residue is always an anchor residue for peptide binding to class I molecules (20, 27–29). Homologous peptides derived from genes MAGE-4 and 6 carry the same motive and were shown to bind to HLA-A1. It may therefore be possible to obtain CTL that recognize antigens formed by these peptides on HLA-A1. The MAGE-6 derived peptide was not recognized by the anti-MZ2-D CTL clone, even though it differs from the MAGE-3 peptide only at position 8 (L→V). This leucine residue in the MAGE-3 peptide is therefore involved in the interaction of the peptide with the T cell receptor.

Antigen MZ2-D encoded by MAGE-3 may prove to be a useful target for specific antitumor immunization of melanoma patients. Patients expressing this antigen on their tumor cells will be identified by HLA typing and by performing reverse transcription and PCR amplification with MAGE-3 specific primers on small tumor samples frozen immediately after surgical removal. The proportion of melanoma patients expressing this antigen should be ~18% in Caucasian populations, since 26% of individuals are HLA-A1 positive and 69% of melanomas express MAGE-3. This compares with ~10% of melanoma patients whose tumor expresses MAGE-1 encoded antigen MZ2-E. It is noteworthy that all melanomas that express MAGE-1 also express MAGE-3. Thus, the availability of MAGE-3 in addition to MAGE-1, should only increase from 10 to 18% the proportion of patients eligible for vaccination. On the other hand, it will be possible to attempt to immunize 10% of melanoma patients against both the MAGE-1 and the MAGE-3 encoded antigens. This should reduce the risk of tumor escape due to the emergence of antigen–loss variants.

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                                                                                    exon2
         exon1                                                                   ↓
MAGE-1   CCATTCTGAGGGACGGCGTA  GAGTTCGGCCGAAGGAACCT  GACCCAGGCTCTGTGAGGAG  GCAAGGTTTTCAGGGGACAG   80
MAGE-3   --------------------  ----------GAGGGAAGCC  GGCCCAGGCTCGGTGAGGAG  GCAAGGTTCTGAGGGGACAG   50
         exon1                                                                   ↑
                                                                                    exon2

                                                                   exon3
                                                                  ↓
MAGE-1   GCCAACCCAGAGGACAGGAT  TCCCTGGAGGCCACAGAGGA  GCACCAAGGAGAAGATCTGC  CTGTGGGTCTTCATTGCCCA  160
MAGE-3   GCTGACCTGGAGGACCAGAG  GCCCCCGGAGGAGCACTG--  -----AAGGAGAAGATCTGC  CAGTGGGTCTCCATTGCCCA  123
                                                                  ↑
                                                                   exon3

                                                       M  S  L  E  Q  R     S  L  H  C  K  P     12
MAGE-1   GCTCCTGCCCACACTCCTGC  CTGCTGCCCTGACGAGAGTC  ATCATGTCTCTTGAGCAGAG  GAGTCTGCACTGCAAGCCTG  240
MAGE-3   GCTCCTGCCCACACTCCCGC  CTGTTGCCCTGACCAGAGTC  ATCATGCCTCTTGAGCAGAG  GAGTCAGCACTGCAAGCCTG  193
                                                       M  P  L  E  Q  R     S  Q  H  C  K  P     12

          E  E  A  L  E  A  Q    Q  E  A  L  G  L  V    C  V  Q  A                       A  T    32
MAGE-1   AGGAAGCCCTTGAGGCCCAA  CAAGAGGCCCTGGGCCTGGT  GTGTGTGCAGGCT-------  --------------GCCACC  299
MAGE-3   AAGAAGGCCTTGAGGCCCGA  GGAGAGGCCCTGGGCCTGGT  GGGTGCGCAGGCTCCTGCTA  CTGAGGAGCAGGAGGCTGCC  273
          E  E  G  L  E  A  R    G  E  A  L  G  L  V    G  A  Q  A  P  A    T  E  E  Q  E  A  A    39

          S  S  S  S  P  L  V    L  G  T  L  E  E     V  P  T  A  G  S  T    D  P  P  Q  S  P  Q   59
MAGE-1   TCCTCCTCCTCTCCTCTGGT  CCTGGGCACCCTGGAGGAGG  TGCCCACTGCTGGGTCAACA  GATCCTCCCCAGAGTCCTCA  379
MAGE-3   TCCTCCTCTTCTACTCTAGT  TGAAGTCACCCTGGGGGAGG  TGCCTGCTGCCGAGTCACCA  GATCCTCCCCAGAGTCCTCA  353
          S  S  S  S  T  L  V    E  V  T  L  G  E     V  P  A  A  E  S  P    D  P  P  Q  S  P  Q   66

          G  A  S  A  F  P     T  T  I  N  F  T  R    Q  R  Q  P  S  E  G    S  S  S  R  E  E     85
MAGE-1   GGGAGCCTCCGCCTTTCCCA  CTACCATCAACTTCACTCGA  CAGAGGCAACCCAGTGAGGG  TTCCAGCAGCCGTGAAGAGG  459
MAGE-3   GGGAGCCTCCAGCCTCCCCA  CTACCATGAACTACCCTCTC  TGGAGCCAATCCTATGAGGA  CTCCAGCAACCAAGAAGAGG  433
          G  A  S  S  L  P     T  T  M  N  Y  P  L    W  S  Q  S  Y  E  D    S  S  N  Q  E  E     92

          E  G  P  S  T  S  C    I  L  E  S  L  F  R    A  V  I  T  K  K     V  A  D  L  V  G  F  112
MAGE-1   AGGGGCCAAGCACCTCTTGT  ATCCTGGAGTCCTTGTTCCG  AGCAGTAATCACTAAGAAGG  TGGCTGATTTGGTTGGTTTT  539
MAGE-3   AGGGGCCAAGCACCTTCCCT  GACCTGGAGTCCGAGTTCCA  AGCAGCACTCAGTAGGAAGG  TGGCCGAGTTGGTTCATTTT  513
          E  G  P  S  T  F  P    D  L  E  S  E  F  Q    A  A  L  S  R  K     V  A  E  L  V  H  F  119

          L  L  L  K  Y  R  A    R  E  P  V  T  K     A  E  M  L  E  S  V    I  K  N  Y  K  H  C  139
MAGE-1   CTGCTCCTCAAATATCGAGC  CAGGGAGCCAGTCACAAAGG  CAGAAATGCTGGAGAGTGTC  ATCAAAAATTACAAGCACTG  619
MAGE-3   CTGCTCCTCAAGTATCGAGC  CAGGGAGCCGGTCACAAAGG  CAGAAATGCTGGGGAGTGTC  GTCGGAAATTGGCAGTATTT  593
          L  L  L  K  Y  R  A    R  E  P  V  T  K     A  E  M  L  G  S  V    V  G  N  W  Q  Y  F  146

          F  P  E  I  F  G     K  A  S  E  S  L  Q    L  V  F  G  I  D  V    K  E  A  D  P  T     165
MAGE-1   TTTTCCTGAGATCTTCGGCA  AAGCCTCTGAGTCCTTGCAG  CTGGTCTTTGGCATTGACGT  GAAGGAAGCAGACCCCACCG  699
MAGE-3   CTTTCCTGTGATCTTCAGCA  AAGCTTCCAGTTCCTTGCAG  CTGGTCTTTGGCATCGAGCT  GATGGAAGTGGACCCCATCG  673
          F  P  V  I  F  S     K  A  S  S  S  L  Q    L  V  F  G  I  E  L    M  E  V  D  P  I     172

          G  H  S  Y  V  L  V    T  C  L  G  L  S  Y    D  G  L  L  G  D     N  Q  I  M  P  K  T  192
MAGE-1   GCCACTCCTATGTCCTTGTC  ACCTGCCTAGGTCTCTCCTA  TGATGGCCTGCTGGGTGATA  ATCAGATCATGCCCAAGACA  779
MAGE-3   GCCACTTGTACATCTTTGCC  ACCTGCCTGGGCCTCTCCTA  CGATGGCCTGCTGGGTGACA  ATCAGATCATGCCCAAGGCA  753
          G  H  L  Y  I  F  A    T  C  L  G  L  S  Y    D  G  L  L  G  D     N  Q  I  M  P  K  A  199

          G  F  L  I  I  V  L    V  M  I  A  M  E     G  G  H  A  P  E  E    E  I  W  E  E  L  S  219
MAGE-1   GGCTTCCTGATAATTGTCCT  GGTCATGATTGCAATGGAGG  GCGGCCATGCTCCTGAGGAG  GAAATCTGGGAGGAGCTGAG  859
MAGE-3   GGCCTCCTGATAATCGTCCT  GGCCATAATCGCAAGAGAGG  GCGACTGTGCCCCTGAGGAG  AAAATCTGGGAGGAGCTGAG  833
          G  L  L  I  I  V  L    A  I  I  A  R  E     G  D  C  A  P  E  E    K  I  W  E  E  L  S  226

          V  M  E  V  Y  D     G  R  E  H  S  A  Y    G  E  P  R  K  L  L    T  Q  D  L  V  Q     245
MAGE-1   TGTGATGGAGGTGTATGATG  GGAGGGAGCACAGTGCCTAT  GGGGAGCCCAGGAAGCTGCT  CACCCAAGATTTGGTGCAGG  939
MAGE-3   TGTGTTAGAGGTGTTTGAGG  GGAGGGAAGACAGTATCTTG  GGGGATCCCAAGAAGCTGCT  CACCCAACATTTCGTGCAGG  913
          V  L  E  V  F  E     G  R  E  D  S  I  L    G  D  P  K  K  L  L    T  Q  H  F  V  Q     252
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         E  K  Y  L  E  Y  R    Q  V  P  D  S  D  P    A  R  Y  E  F  L      W  G  P  R  A  L  A    272
MAGE-1   AAAAGTACCTGGAGTACCGG   CAGGTGCCGGACAGTGATCC   CGCACGCTATGAGTTCCTGT   GGGGTCCAAGGGCCCTCGCT   1019
MAGE-3   AAAACTACCTGGAGTACCGG   CAGGTCCCCGGCAGTGATCC   TGCATGTTATGAATTCCTGT   GGGGTCCAAGGGCCCTCGTT   993
         E  N  Y  L  E  Y  R    Q  V  P  G  S  D  P    A  C  Y  E  F  L      W  G  P  R  A  L  V    279

          E  T  S  Y  V  K  V    L  E  Y  V  I  K     V  S  A  R  V  R  F    F  F  P  S  L  R  E   299
MAGE-1   GAAACCAGCTATGTGAAAGT   CCTTGAGTATGTGATCAAGG   TCAGTGCAAGAGTTCGCTTT   TTCTTCCCATCCCTGCGTGA   1099
MAGE-3   GAAACCAGCTATGTGAAAGT   CCTGCACCATATGGTAAAGA   TCAGTGGAGGACCTCACATT   TCCTACCCACCCCTGCATGA   1073
          E  T  S  Y  V  K  V    L  H  H  M  V  K     I  S  G  G  P  H  I    S  Y  P  P  L  H  E   306

           A  A  L  R  E  E      E  E  G  V                                                         309
MAGE-1   AGCAGCTTTGAGAGAGGAGG   AAGAGGGAGTCTGAGCATGA   GTTGCAGCCAAGGCCAGTGG   GAGGGGGACTGGGCCAGTGC   1179
MAGE-3   GTGGGTTTTGAGAGAGGGGG   AAGAGTGAGTCTGAGCACGA   GTTGCAGCCAGGGCCAGTGG   GAGGGGGTCTGGGCCAGTGC   1153
           W  V  L  R  E  G      E  E                                                               314

MAGE-1   ACCTTCCAGGGCCGCGTCCA   GCAGCTTCCCCTGCCTCGTG   TGACATGAGGCCCATTCTTC   ACTC--TGAAGAGAGCGGTC   1257
MAGE-3   ACCTTCCGGGGCCGCATCCC   TTAGTTTCCACTGCCTCCTG   TGACGTGAGGCCCATTCTTC   ACTCTTTGAAGCGAGCAGTC   1233

MAGE-1   AGTGTTCTCAGTAGTAGGTT   TCTGTTCTATTGGGTGACTT   GGAGATTTATCTTTGTTCTC   TTTTGGAATTGTTCAAATGT   1337
MAGE-3   AGCATTCTTAGTAGTGGGTT   TCTGTTCTGTTGGATGACTT   TGAGATTATTCTTTGTTTCC   TGTTGGAGTTGTTCAAATGT   1313

MAGE-1   TTTTTTTTAAGGGATGGTTG   AATGAACTTCAGCATCCAAG   TTTATGAATGACAGCAGTCA   CACA--GTTCTGTGTATATA   1415
MAGE-3   TCC-TTTTAACGGATGGTTG   AATGAGCGTCAGCATCCAGG   TTTATGAATGACAGTAGTCA   CACATAGTGCTGTTTATATA   1392

MAGE-1   GTTTAAGGGTAAGAGTCTTG   TGTTTTATTCAGATTGGGAA   ATCCATTCTATTTTGTGAAT   TGGG--ATAATAACAGCAGT   1493
MAGE-3   GTTTAGGAGTAAGAGTCTTG   TTTTTTACTCAAATTGGGAA   ATCCATTCCATTTTGTGAAT   TGTGACATAATAATAGCAGT   1472

MAGE-1   GGAATAAGTACTT-----AG   AAATGTGAAAAATGAGCAGT   AAAATAGATGAGATAAAGAA   CTAAAGAAATTAAGAGATAG   1568
MAGE-3   GGTAAAAGTATTTGCTTAAA   ATTGTGAGCGAATTAGCAAT   AACATACATGAGAT----AA   CTCAAGAAATCAAAAGATAG   1548

MAGE-1   TCAATTCTTGCCTTATACCT   CAGTCTATTCTGTAAAATTT   TTAAAGATATATGCATACCT   GGATTTCCTTGGCTTCTTTG   1648
MAGE-3   TTGATTCTTGCCTTGTACCT   CAATCTATTCTGTAAAATT-   --AAACAAATATGCAAACCA   GGATTTCCTTGACTTCTTTG   1625

MAGE-1   AGAATGTAAGAGAAATTAAA   TCTGAATAAAGAATTCTTCC   TGT                                          1691
MAGE-3   AGAATGCAAGCGAAATTAAA   TCTGAATAAATAATTCTTCC   TCTTC                                        1670
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Figure 5. Comparison of the nucleotide sequence of the MAGE-3 cDNA with that of MAGE-1. Gaps indicated by dashes (–) were introduced for optimal alignment. The amino acid sequences of the proteins encoded by the large open reading frames are represented. The sequences corresponding to the MZ2-E and MZ2-D peptides are underlined. Exons boundaries are indicated by arrows. The MAGE-3 sequence is available from EMBL/GenBank/DDBJ under accession number V03735.

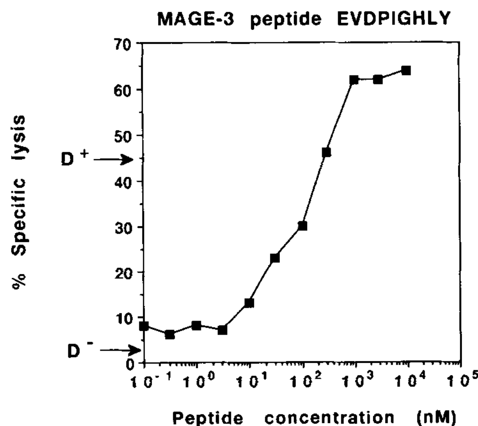

Figure 6. Lysis by anti-MZ2-D CTL of cells expressing HLA-A1 incubated with the MAGE-3-encoded peptide. MZ2-MEL.61 cells (D^-) were ^{51}Cr-labeled and incubated with CTL 20/38 at an E/T ratio of 10:1 in the presence of the synthetic MAGE-3 peptide at the concentrations indicated. Chromium release was measured after 4 h. The arrows indicate the level of lysis of D^+ and D^- MZ2-MEL cells incubated without peptide.

Other types of tumor could also be targets for immunization with antigen MZ2-D: MAGE-3 is expressed in 56% of head and neck squamous cell carcinomas, 30% of nonsmall cell lung carcinomas, 16% of colorectal carcinomas, and 12% of breast tumors. The proportions of these tumors that express MAGE-1 are 25, 35, 0, and 17%, respectively (18, 37). By contrast with melanomas, some of these tumors express only MAGE-1 or only MAGE-3, so that considering the antigens encoded by both genes increases the proportion of patients eligible for immunization. Like MAGE-1, MAGE-3 is never expressed in kidney tumors, leukemias, and lymphomas.

The optimal method of immunization to generate efficient

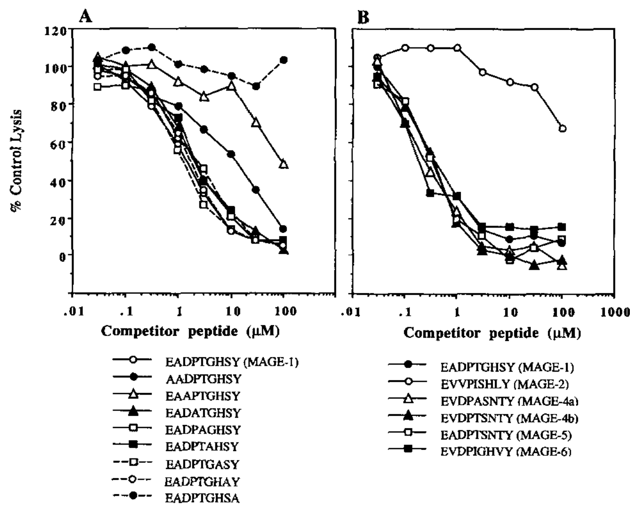

Figure 7. Competition of the MAGE-3 peptide with single Ala-substituted MAGE-1 peptides (*A*) or with homologous nonapeptides from other MAGE genes (*B*). Chromium-labeled cells of HLA-A1 positive B lymphoblastoid cell line BM21 were incubated with the indicated concentrations of competitor peptides (0.03–100 µM) for 15 min before addition of the antigenic MAGE-3 peptide at a concentration of 0.25 µM. 15 min later, cells from anti-MZ2-D CTL clone 20/38 were added at a lymphocyte to target ratio of 10:1. Lysis was measured 4 h later. Results are presented as percentages of the control lysis obtained with the MAGE-3 peptide alone, which was 67% (*A*) and 42% (*B*). In the absence of the MAGE-3 peptide, lysis of BM21 cells was 2% (*A*) and 1% (*B*).

CTL responses remains to be determined. Patients could be injected with irradiated tumor cells expressing antigen MZ2-D, or with the recombinant MAGE-3 protein combined with appropriate adjuvants. Effective priming of CTL has been reported in mouse systems after immunization with peptides either alone, associated with a lipid moiety, or mixed with β_2-microglobulin (38–41). A precise knowledge of the residues involved in the binding to HLA-A1 may help in designing peptides with improved capabilities to bind to HLA-A1 resulting in better immunogenicity.

Table 2. *Expression of Gene MAGE-3 by Tumoral, Normal, and Fetal Tissues*

Tumors			Normal tissues	
	Number of MAGE-3 positive tumors*			
Histological type	Cell lines	Tumor samples	Histological type	MAGE-3 expression*
			Adult tissues	
			Brain	–
Melanomas	50/62 (81%)	72/105 (69%)	Colon	–
			Stomach	–
Head and neck squamous cell carcinomas	–	20/36 (56%)	Liver	–
			Ovary	
Lung carcinomas			Skin	–
NSCLC‡	1/2	14/46 (30%)	Lung	–
SCLC	18/22 (82%)	2/3	Kidney	–
			Breast	–
Colorectal carcinomas	5/16	5/31 (16%)	Testis	+ +
Mammary carcinomas	2/6	16/132 (12%)		
			Fetal tissues	
Bladder tumors	–	2/6	Brain	–
			Liver	–
Sarcomas	1/4	3/10	Spleen	–
Prostatic carcinomas	–	3/20		
Renal carcinomas	0/5	0/38		
Leukemias	2/6	0/20		
Lymphomas	0/6	0/5		

* Expression of gene MAGE-3 was tested by RT-PCR amplification on total RNA, with the primers described in Materials and Methods. These primers distinguish MAGE-3 from the 11 other MAGE genes that have been identified.
‡ NSCLC, nonsmall cell lung carcinomas; SCLC, small cell lung carcinomas.

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References

1. Mukherji, B., and T. J. MacAlister. 1983. Clonal analysis of cytotoxic T cell response against human melanoma. *J. Exp. Med.* 158:240.
2. Knuth, A., B. Danowski, H.F. Oettgen, and L. Old. 1984. T-cell mediated cytotoxicity against autologous malignant melanoma: analysis with interleukin-2-dependent T-cell cultures. *Proc. Natl. Acad. Sci. USA.* 81:3511.
3. Hérin, M., C. Lemoine, P. Weynants, F. Vessière, A. Van Pel, A. Knuth, R. Devos, and T. Boon. 1987. Production of stable cytolytic T-cell clones directed against autologous human melanoma. *Int. J. Cancer.* 39:390.
4. Topalian, S.L., D. Solomon, and S.A. Rosenberg. 1989. Tumor-specific cytolysis by lymphocytes infiltrating human melanomas. *J. Immunol.* 142:3714.
5. Van den Eynde, B., P. Hainaut, M. Hérin, A. Knuth, C. Lemoine, P. Weynants, P. van der Bruggen, R. Fauchet, and T. Boon. 1989. Presence on a human melanoma of multiple antigens recognized by autologous CTL. *Int. J. Cancer.* 44:634.
6. van der Bruggen, P., C. Traversari, P. Chomez, C. Lurquin, E. De Plaen, B. Van den Eynde, A. Knuth, and T. Boon. 1991. A gene encoding an antigen recognized by cytolytic T lymphocytes on a human melanoma. *Science (Wash. DC).* 254:1643.
7. De Smet, C., C. Lurquin, P. van der Bruggen, E. De Plaen, F. Brasseur, and T. Boon. 1994. Sequence and pattern of expression of human gene MAGE-2. *Immunogenetics.* 39:121.
8. Traversari, C., P. van der Bruggen, I.F. Luescher, C. Lurquin, P. Chomez, A. Van Pel, E. De Plaen, A. Amar-Costesec, and T. Boon. 1992. A nonapeptide encoded by human gene MAGE-1 is recognized on HLA-A1 by cytolytic T lymphocytes directed against tumor antigen MZ2-E. *J. Exp. Med.* 176:1453.
9. Yang, S.Y., E. Milford, U. Hämmerling, and B. Dupont. 1989. Description of the reference panel of B-lymphoblastoid cell lines for factors of the HLA system: the B-cell line panel designed for the Tenth International Histocompatibility workshop. *In* Immunobiology of HLA. B. Dupont, editor. Springer-Verlag, New York. 11.
10. De Plaen, E., C. Lurquin, A. Van Pel, B. Mariamé, J.-P. Szikora, T. Wölfel, C. Sibille, P. Chomez, and T. Boon. 1988. Immunogenic (tum$^-$) variants of mouse tumor P815: cloning of the gene of tum$^-$ antigen P91A and identification of the tum$^-$ mutation. *Proc. Natl. Acad. Sci. USA.* 85:2274.
11. Lurquin, C., A. Van Pel, B. Mariamé, E. De Plaen, J.-P. Szikora, C. Janssens, M. Reddehase, J. Lejeune, and T. Boon. 1989. Structure of the gene coding for tum$^-$ transplantation antigen P91A. A peptide encoded by the mutated exon is recognized with Ld by cytolytic T cells. *Cell.* 58:293.
12. Seed, B., and A. Aruffo. 1987. Molecular cloning of the CD2 antigen, the T-cell erythrocyte receptor, by a rapid immunoselection procedure. *Proc. Natl. Acad. Sci. USA.* 84:3365.
13. Espevik, T., and J. Nissen-Meyer. 1986. A highly sensitive cell line, WEHI 164 clone 13, for measuring cytotoxic factor/tumor necrosis factor from human monocytes. *J. Immunol. Methods.* 95:99.
14. Traversari, C., P. van der Bruggen, B. Van den Eynde, P. Hainaut, C. Lemoine, N. Ohta, L. Old, and T. Boon. 1992. Transfection and expression of a gene coding for a human melanoma antigen recognized by autologous cytolytic T lymphocytes. *Immunogenetics.* 35:145.
15. Atherton, E., C.J. Logan, and R.C. Sheppard. 1981. Peptide synthesis. Part 2. Procedures for solid phase synthesis using Nα-fluorenylmethysoxycarbamylamino-acid on polymide supports. Synthesis of substance P and of acyl carrier protein 65-74 decapeptide. *J. Chem. Soc. Lond. Perkin Trans.* 1:538.
16. Boon, T., J. Van Snick, A. Van Pel, C. Uyttenhove, and M. Marchand. 1980. Immunogenic variants obtained by mutagenesis of mouse mastocytoma P815. II. T lymphocyte–mediated cytolysis. *J. Exp. Med.* 152:1184.
17. Davis, L.G., M.D. Dibner, and J.F. Battey. 1986. Basic Methods in Molecular Biology. Elsevier, New York., pp. 130–135.
18. Brasseur, F., M. Marchand, R. Vanwijck, M. Hérin, B. Lethé, P. Chomez, and T. Boon. 1992. Human gene MAGE-1, which codes for a tumor rejection antigen, is expressed by some breast tumors. *Int. J. Cancer.* 52:839.
19. Maryanski, J.L., P. Romero, A. Van Pel, T. Boon, F.R. Salemme, J.-C. Cerottini, and G. Corradin. 1991. The identification of tyrosine as a common key residue in unrelated H-2Kd restricted antigenic peptides. *Int. Immunol.* 3:1035.
20. Falk, K., O. Rötzschke, S. Stevanovic, G. Jung, and H.-G. Rammensee. 1991. Allele-specific motifs revealed by sequencing of self-peptides eluted from MHC molecules. *Nature (Lond.).* 351:290.
21. Hill, A.V.S., J. Elvin, A.C. Willis, M. Aidoo, C.E.M. Allsopp, F.M. Gotch, X.M. Gao, M. Takiguchi, B.M. Greenwood, A.R.M. Townsend, and A.J. McMichael. 1992. Molecular analysis of the association of HLA-B53 and resistance to severe malaria. *Nature (Lond.).* 360:434.
22. Townsend, A., J. Rothbard, F. Gotch, G. Bahadur, D. Wraith, and A. McMichael. 1986. The epitopes of influenza nucleoprotein recognized by cytotoxic T lymphocytes can be defined with short synthetic peptides. *Cell.* 44:959.
23. McMichael, A.J., F.M. Gotch, and J. Rothbard. 1986. HLA

B37 determines an influenza A virus nucleoprotein epitope recognized by cytotoxic T lymphocytes. *J. Exp. Med.* 164:1397.
24. Robbins, P.A., L.A. Lettice, P. Rota, J. Santos-Aguado, J. Rothbard, A.J. McMichael, and J.L. Strominger. 1989. Comparison between two peptide epitopes presented to cytotoxic T lymphocytes by HLA-A2. *J. Immunol.* 143:4098.
25. Pazmani, L., S. Rowland-Jones, S. Huet, A. Hill, J. Sutton, R. Murray, J. Brooks, and A. McMichael. 1992. Genetic modulation of antigen presentation by HLA-B27 molecules. *J. Exp. Med.* 175:361.
26. Silver, M.L., H.-C. Guo, J.L. Strominger, and D.C. Wiley. 1992. Atomic structure of a human MHC molecule presenting an influenza virus peptide. *Nature (Lond.).* 360:367.
27. Jardetzky, T.S., W.S. Lane, R.A. Robinson, D.R. Madden, and D.C. Wiley. 1991. Identification of self peptides bound to purified HLA-B27. *Nature (Lond.).* 353:326.
28. DiBrino, M., K.C. Parker, J. Shiloach, M. Knierman, J. Lukszo, R.V. Turner, W.E. Biddison, and J.E. Coligan. 1993. Endogenous peptides bound to HLA-A3 possess a specific combination of anchor residues that permit identification of potential antigenic peptides. *Proc. Natl. Acad. Sci. USA.* 90:1508.
29. Falk, K., O. Rötzschke, B. Grahovac, D. Schendel, S. Stevanovic, G. Jung, and H.-G. Rammensee. 1993. Peptide motifs of HLA-B35 and -B37 molecules. *Immunogenetics.* 38:161.
30. Zhang, Q.-J., R. Gavioli, G. Klein, and M.G. Masucci. 1993. An HLA-A11-specific motif in nonamer peptides derived from viral and cellular proteins. *Proc. Natl. Acad. Sci. USA.* 90:2217.
31. Townsend, A., T. Elliott, V. Cerundolo, L. Foster, B. Barber, and A. Tse. 1990. Assembly of MHC class I molecules analyzed in vitro. *Cell.* 62:285.
32. Elvin, J., V. Cerundolo, T. Elliott, and A. Townsend. 1991. A quantitative assay of peptide-dependent class I assembly. *Eur. J. Immunol.* 21:2025.
33. Parker, K.C., M.A. Bednarek, L.K. Hull, U. Utz, B. Cunningham, H.J. Zweerink, W.E. Biddison, and J.E. Coligan. 1992. Sequence motifs important for peptide binding to the human MHC class I molecule, HLA-A2. *J. Immunol.* 149:3580.
34. Macatonia, S.E., P.M. Taylor, S.C. Knight, and B.A. Askonas. 1989. Primary stimulation by dendritic cells induces antiviral proliferative and cytotoxic T cell responses in vitro. *J. Exp. Med.* 169:1255.
35. De Bruijn, M.L.H., J.D. Nieland, T.N.M. Schumacher, H.L. Ploegh, W.M. Kast, and C.J.M. Melief. 1992. Mechanisms of induction of primary virus-specific cytotoxic T lymphocyte responses. *Eur. J. Immunol.* 22:3013.
36. Houbiers, J.G.A., H.W. Nijman, S.H. van der Burg, J.W. Drijfhout, P. Kenemans, C.J.H. van de Velde, A. Brand, F. Momburg, M.W. Kast, and C.J.M. Melief. 1993. In vitro induction of human cytotoxic T lymphocyte responses against peptides of mutant and wild-type p53. *Eur. J. Immunol.* 23:2072.
37. Weynants, P., B. Lethé, F. Brasseur, M. Marchand, and T. Boon. 1994. Expression of MAGE genes by non-small cell lung carcinomas. *Int. J. Cancer.* In press.
38. Schild, H., K. Deres, K.H. Wiesmuller, G. Jung, and H.G. Rammensee. 1991. Efficiency of peptides and lipopeptides for in vivo priming of virus-specific cytotoxic T cells. *Eur. J. Immunol.* 21:2649.
39. Romero, P., G. Eberl, J.L. Casanova, A.S. Cordey, C. Widmann, I.F. Luescher, G. Corradin, and J.L. Maryanski. 1992. Immunization with synthetic peptides containing a defined malaria epitope induces a highly diverse cytotoxic T lymphocyte response. Evidence that two peptide residues are buried in the MHC molecule. *J. Immunol.* 148:1871.
40. Feltkamp, M.C.W., H.L. Smits, M.P.M. Vierboom, R.P. Minnaar, B.M. de Jongh, J.W. Drijfhout, J. ter Schegget, C.J.M. Melief, and W.M. Kast. 1993. Vaccination with cytotoxic T lymphocyte epitope-containing peptide protects against a tumor induced by Human Papillomavirus type 16-transformed cells. *Eur. J. Immunol.* 23:2242.
41. Rock, K.L., C. Fleischacker, and S. Gamble. 1993. Peptide-priming of cytolytic T cell immunity in vivo using β_2-microglobulin as an adjuvant. *J. Immunol.* 150:1244.