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pMel17 is recognised by monoclonal antibodies NKI-beteb, HMB-45 and HMB-50 and by anti-melanoma CTL

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Summary Recently, we cloned the cDNA encoding the melanocyte lineage-specific antigen gp100 and demonstrated that gp100 is recognised by three different monoclonal antibodies (MABs) used to diagnose malignant melanoma. In addition, we showed that tumour-infiltrating lymphocytes (TIL 1200) from a melanoma patient reacted specifically with cells transfected with the gp100 cDNA. Molecular characterisation of the gp100 cDNA revealed that the gp100 antigen is highly homologous, but not identical, to another melanocyte-specific protein, pMel17. Here, we report that cells transfected with pMel17 cDNA also react with all three MABs used to diagnose malignant melanoma, NKI-beteb, HMB-45 and HMB-50. Moreover, pMel17 transfectants are specifically lysed by TIL1200. These data demonstrate that antigenic processing of both gp100 and pMel17 give rise to peptides seen by anti-melanoma cytotoxic T lymphocytes (CTL) and are therefore potential targets for immunotherapy of malignant melanoma.

Keywords: melanoma; gp100/pMel17; cytotoxic T cell; NKI-beteb

Melanoma is a neoplasm that originates from melanocytes, pigment-producing cells in the skin. Melanoma is a relatively immunogenic tumour, as demonstrated by the presence of both cytotoxic T lymphocytes (CTLs) and antibodies (Mettes et al., 1983; Knuth et al., 1992) in melanoma patients that react with melanoma tumour cells. The availability of antibodies and CTLs with anti-melanoma reactivity allowed the identification of several tumour-associated antigens. These include tumour-specific antigens and melanocyte differentiation antigens that are expressed by melanoma tumour cells as well as by normal melanocytes and retina (van der Bruggen et al., 1991; Brichard et al., 1993; Vijayasaradhi et al., 1990; Bakker et al., 1994; Kawakami et al., 1994a,b; Coulie et al., 1994; Gaugler et al., 1994 and Wang et al., 1995). Identification of the antigens recognised by anti-tumour CTL is important for understanding the molecular basis of tumour recognition by T cells and may lead to the development of new immunotherapeutical strategies to treat cancer patients.

Recently, we cloned the cDNA encoding the melanocyte differentiation antigen gp100 and demonstrated that it is recognised by three different MABs used to diagnose malignant melanoma, NKI-beteb, HMB-50 and HMB-45 (Adema et al., 1993, 1994). In addition, we demonstrated that gp100 is recognised by a tumour-infiltrating T-cell line (TIL 1200), isolated from a melanoma patient (Bakker et al., 1994). Molecular characterisation of the cDNA encoding gp100 revealed that it is a type I transmembrane glycoprotein of 641 amino acids highly homologous to another melanocyte-specific protein, pMel17 (Adema et al., 1994; Kwon et al., 1991). Nucleotide sequence analysis of genomic DNA indicated that the transcripts corresponding to gp100 and pMel17 cDNAs originate from a single gene via alternative splicing. The difference between gp100 and pMel17 consists of a stretch of seven amino acids in the carboxy terminal part of pMel17 (position 567; Adema et al., 1994) that is absent in gp100. In all normal and malignant melanocytic cells expressing the gp100/pMel17 gene, gp100 and pMel17 mRNAs are expressed simultaneously.

Here, we demonstrate that pMel17, like gp100, is recognised by all three MABs used to diagnose malignant melanoma and is properly processed and presented to anti-melanoma tumour-infiltrating lymphocytes.

Materials and methods

Cells and monoclonal antibodies

Culturing of the melanoma cell lines MEWO, BLM and of COS-7 cells has been described previously (Adema et al., 1993, 1994). TIL 1200 was generated from a metastatic melanoma and cultured with 1000 U ml−1 interleukin-2 (IL-2) (Cetus Corp., Emeryville, CA, USA) as described previously (Kawakami et al., 1992). NKI-beteb and HMB-50 have been described previously (Vennegoor et al., 1988; Vogel and Esclamado, 1988). HMB-45 was purchased from Enzo Biochem.

Molecular cloning and nucleotide sequence analysis

Using a reverse transcriptase-polymerase chain reaction (PCR) (GeneAmp kit, Perkin elmer, the Netherlands) approach with 5'-ctgcatggagatcttcatcg-3' as the 5' primer and 5'-ttcttgagctcaggaaaatacagcat-3' as the 3' primer we isolated the 3' part of pMel17 cDNA from total RNA isolated from the melanoma cell line MEWO. The PCR product was used to replace the 3' part of the gp100 cDNA as present in pSVLgp100+ (Adema et al., 1994) using BglII and the newly created SacI site in the 3' primer (underlined). The resulting construct, pSVLpMel17, was sequenced by the dideoxy-nucleotide sequencing method using T7 DNA polymerase (Pharmacia, Woerden, The Netherlands). pCMVneoP Mel17 was constructed by cloning the complete pMel17 cDNA from pSVLpMel17 as a blunt-ended XbaI–SacI fragment in the blunt-ended BamHI site of pCMVneo (Bakker et al., 1994).

Transfections and immunostaining

Transient expression of DNA constructs in COS-7 cells was performed using 40 µg ml−1 lipofectin reagent (BRL, Gaithersburg, MD, USA) and 7.5 µg of DNA. BLM cells were transfected with 20 µg of pCMVneoP Mel17 DNA using calcium phosphate transfection systems (BRL, Gaithersburg, MD, USA) and stable clones were isolated by G418 selection (1 mg ml−1) as previously described (Bakker et al., 1994).
Transfected cells were prepared for immunofluorescence using FITC-conjugated GAM-IgG-F(ab’)$_2$ (Zymed, San Francisco, CA, USA) as described previously (Adema et al., 1993) and examined using confocal laser scanning microscope at 488 nm (Biorad MRC 600).

Metabolic labelling and immunoprecipitations

Immunoprecipitation experiments were performed on metabolically labelled (l-$^{35}$S)methionine/cysteine (Amer- sham) cells as described by Vennegoor et al. (1988) using either NKI-beteb or HMB-50 covalently linked to protein A-CL 4B sepharose beads (Pharmacia, Woerden, The Netherlands). Immunoprecipitates were analysed under reducing conditions by SDS-PAGE using 5-17.5% gradient gels. The relative molecular weight of the proteins was determined using co-electrophorised, prestained markers (BRL, Gaithersburg, MD, USA). Gels were treated with 1M sodium salicylate (pH 5.4) before autoradiography (Kodak XAR).

Chromium-release assay

Chromium release assays were performed as described previously (Bakker et al., 1994). Briefly, 10$^6$ target cells were incubated with 100 µCi $^{51}$Cr sodium chromate (Amer- sham, Bucks, UK) for 1 h. Various amounts of effector cells were then added to 2 x 10$^2$ target cells in triplicate wells of U-bottomed microtitre plates (Costar, Badhoevedorp, The Netherlands) in a final volume of 150 µl. After 5 h of incubation part of the supernatant was harvested and its radioactive content was measured.

Results

The gp100/pMel17 gene encodes both gp100 and pMel17 mRNA as a consequence of alternative RNA processing. The pMel17 mRNA encodes a stretch of seven amino acids not encoded by the gp100 mRNA (Figure 1). To investigate the immunological properties of pMel17 we constructed a pMel17 cDNA. Using an RT-PCR approach we first cloned the 3' part of the pMel17 cDNA encoding the carboxy terminal part of pMel17, including the additional seven amino acids absent in gp100. Nucleotide sequence analysis of the 3' part confirmed the presence of the nucleotide sequence

Figure 1 Peptides unique in pMel17 and gp100 that fit the HLA-A2.1 binding motifs [Falk et al. (1991), Drijfhout et al. (1995)]. The pMel17 specific amino acids are indicated in bold.
encoding the pMell7-specific amino acids. In addition, we found pMell7 cDNAs containing either a thymidine (as in the gp100 cDNA; Adema et al., 1994) or a cytosine at position 1998. This nucleotide change does not result in an amino acid substitution. The finding that the same nucleotide difference was found in a gp100 cDNA clone isolated from the same cell line, indicates that this particular cell line contains two different alleles of the gp100/pMell7 gene. Subsequently, we created a full length pMell7 cDNA by exchanging the 3’ part of the gp100 cDNA with the 3’ part of pMell7 cDNA.

To investigate whether the difference between gp100 and pMell7 affects recognition by the anti-gp100 MABs NKI-beteb, HMB-45 and HMB-50, we transfected the cDNA encoding pMell7 into the gp100/pMell7 negative melanoma cell line BLM. As shown in Figure 2, expression of the pMell7 cDNA resulted in immunoreactivity with all three MABs. The typical speckled staining pattern of the pMell7 transfectants was identical to that previously observed for gp100, suggesting that pMell7, like gp100, localises in melanosomes. Immunoreactivity with all three MABs was also observed when pMell7 cDNA was transiently expressed in non-melanocytic COS-7 cells (data not shown). We also analysed the pMell7 protein detected by MABs NKI-beteb or HMB-50 in COS-7 cells transfected with the pMell17 cDNA using immunoprecipitations reactions. As shown in Figure 3, NKI-beteb and HMB-50 both specifically detect proteins of approximately 100 kDa (95–110 kDa) in extracts of metabolically labelled COS-7 cells transfected with the pMell7 cDNA. The pMell7 protein co-migrates with the gp100 protein immunoprecipitated from COS-7 cells transfected with gp100 cDNA as well as with the proteins immunoprecipitated from MEWO melanoma cells. The slight difference in mobility between transfected COS-7 cells and MEWO melanoma cells, which express both gp100 and pMell7 endogenously, has previously been shown to be due to differential glycosylation (Adema et al., 1994). Collectively, these data demonstrate that the difference between gp100 and pMell7 does not affect recognition by either of the MABs used to diagnose malignant melanoma, NKI-beteb, HMB-50 and HMB-45. The data describing the specificity of these MABs for cells of the melanocytic lineage can therefore be extrapolated to the expression of pMell7.

Previously, we showed that gp100 is recognised by tumour-infiltrating lymphocytes, (TIL)1200, isolated from a melanoma patient in an HLA-A2.1 restricted manner (Bakker et al., 1994). To investigate whether the pMell7 antigen also gives rise to peptide epitopes that gain access to the MHC class I antigen presentation pathway, we determined the cytolytic activity of TIL 1200 against HLA-A2.1 + BLM cells transfected with the pMell7 cDNA. As demonstrated in Figure 4, the pMell7 transfectants were efficiently lysed by TIL 1200. No specific lysis was observed using the parental, untransfected BLM cells or BLM cells transfected with the expression vector without an insert (not shown). These data demonstrate that peptide epitope(s) recognised by TIL 1200 are properly processed from the pMell7 protein and presented in the context of HLA-A2.1. Two gp100-derived peptides (corresponding to the amino acids at positions 154–162 and 457–466) have been identified that are recognised by TIL 1200 (Bakker et al., 1995; Kawakami et al., 1995). These peptides are located in the common part between gp100 and pMell7. Since TIL 1200 is an oligoclonal, CD8+ T-cell line expressing a restricted number of T-cell receptors (Shilyanski et al., 1994), it is most likely that either one or both the aforementioned immunogenic peptides are responsible for the observed lysis of the pMell17 and gp100 transfectants.

Figure 3 The pMell17 protein is recognised by NKI-beteb and HMB-50 in extracts from pSVLpMell7 transfected COS-7 cells. MEWO cells (MEWO) and COS-7 cells transfected with either pSVLpMell7 (pMell7), pSVLgp100 (gp100) or with a construct encoding the gp100 cDNA in the non-coding orientation (Mock) were metabolically labelled and subjected to immunoprecipitations using NKI-beteb (NKI), HMB-50 (50) or normal mouse serum (NMS) as indicated above each lane. Immunoprecipitated proteins were analysed under reducing conditions by SDS–PAGE (linear gradient of 5–17% acrylamide) and visualised by autoradiography. The position and size (kDa) or pretransferred molecular weight markers are indicated.

Figure 4 Lysis of HLA-A2.1 + pMell17 transfectants by TIL1200. BLM cells transfected with pCMVneoMell17, pCMVneoGP100, the parental BLM cells and the gp100/pMell7 positive Mel624 cells were tested for sensitivity to lysis by TIL1200. One representative experiment with the stable pMell17 transfected clone AB1 is shown. - - -, BLM; - - -, Mel624; - - BLM gp100 H2.3; - - -, BLM pMell17 AB1.
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YVWKTWGQYWCQVLGLPVPGLSLSIGTRAMLGTHMETVTVHRRGR
201
AHSSSAFTTITDOFPFESVSQRLALGGNKHLRNPQTFLALQHDPST
251
LAEADLSYTDFGDSSGLTISRALVVTHTYLEPFPVTAQVVLQAAIPL
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301
CGSSPVPTTDGHRPTAAEPNTTAGQVPTTEVGTTPQA2PAPTEAPS
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401
TPAEVISIVVLSGTTAQQVTTEWVETTARELPFPEPEPGPDASSIM
451
TSGLPDLLSATNLRVKRQVPPLDVLYRGRGFSVTILDIOVGIESAB
501
AVPSGEGDFELTVSCQGLPKEACMEISSPGCQPPAPAQLQPVLPSAC
551
QLVLHQLKGSSTYGCLNVLSDTNSLVSTQLIMPVPGILLTQEGAG
600
LGQVPLTVGILLVLMAVLSIYRRLMKQDFSVPQLPHSSHWLRLPR
650
IFCSCPGIESPLSLQQV

Figure 5 Amino acid sequence of the pMell17 antigen (including signal peptide) and location of the peptide epitopes. The peptide epitopes as recognised in the gp100 antigen are underlined [Bakker et al., 1995], Kawakami et al., 1995, Cox et al., 1994]; the amino acids uniquely present in pMell17 are in italic capitals.

Discussion

The data described in this report demonstrate that pMell17, like gp100, is recognised by three MAb s frequently used to diagnose melanoma. In addition, we demonstrate that cells transfected with pMell17 cDNA are effectively lysed by anti-melanoma T cells.

Because of the exclusive reactivity of MAb s NKI-beteb, HMB-45 and HMB-50 with cells of the melanocytic lineage, they are frequently used to diagnose malignant melanoma (Ruiter, 1990). The finding that not only gp100 but also pMell17 reacts with these antibodies emphasizes the specific expression of both gp100 and pMell17 in cells of the melanocytic lineage. The identical staining pattern observed with the MAb s in gp100 and pMell17 transfecteds further indicates that, like gp100, pMell17 is also present in melanomas, which is in line with their proposed role in the process of pigmentation (Kwon et al., 1991). Whether there exists a functional difference between gp100 and pMell17 remains to be determined.

The relative immunogenicity of melanoma tumours has long been recognised. Both cytotoxic T cells and MAb s have been identified that specifically recognise melanoma tumour cells. So far, a number of the antigens recognised have been characterised in detail. They include the tumour-specific proteins, MAGE-1 (van der Bruggen et al., 1991) and MAGE-3 (Gaugler et al., 1994), which are expressed in different types of tumour cells and in tests. In addition, the melanocyte differentiation antigens tyrosinase, gp100, Melan-A/MART-1 and gp75 (Bri chard et al., 1993; Bakker et al., 1994; Kawakami et al., 1994a,b; Coule et al., 1994; Wang et al., 1995) that are expressed in normal and malignant melanocytes as well as in retina have been identified as targets for anti-melanoma CTLs. Potentially, these antigens are targets for specific immunotherapy.

TIL1200 was isolated from a melanoma metastasis and was shown to recognise the melanocytic differentiation antigen gp100. Interestingly, reinfusion of in vitro expanded TIL1200 together with IL-2 in the autologous patient resulted in objective tumour regression (Kawakami et al., 1994, 1995). Here we demonstrate that TIL1200 not only recognises the gp100 antigen, but also the pMell17 antigen that is encoded by an mRNA species derived from the same gene via alternative splicing. Since we have previously shown that melanoma cells express gp100 and pMell17 mRNA simultaneously, both proteins contribute to the total amount of immunogenic peptides presented in the context of HLA-A2.1 that are recognised by TIL1200. This finding is also consistent with the recent mapping of two peptide epitopes (corresponding to the amino acids at positions, 154-162 and 457-466) recognised by TIL1200 in the common part of gp100 and pMell17 (Bakker et al. 1995; Kawakami et al., 1995 and Figure 5). Although it has been observed that sequence context can affect processing and/or presentation of T-cell epitopes (Eisenlohr et al., 1992; Del Val et al., 1991), this does not seem to be the case for pMell17 and gp100. The fact that TIL1200 is an oligoclonal, CD8+ T-cell line expressing a restricted number of T-cell receptors (Shi yanski et al., 1994), implies that either one or both these epitopes are properly processed from the pMell17 antigen and presented by HLA-A2.1. Attempts to further investigate the recognition of the pMell17 epitopes using cloned TIL have not been successful.

Besides TIL1200, other CTL-recognising distinct epitopes encoded by the gp100/pMell17 have recently been characterised (Cox et al., 1994; Kawakami et al., 1995). A total of five distinct peptides have now been identified (Figure 5), all of which are present in both gp100 and pMell17, and are presented by the same restriction element, HLA-A2.1. Examination of the additional amino acid sequence present
in pMeli7 revealed that six peptides (including 9- and 10mers) bearing the HLA-A2.1 binding motif are uniquely present in pMeli7, whereas three peptides are specifically present in gp100 (Figure 1). HLA-A2.1 stabilisation experiments revealed that two of the pMeli7-specific peptides listed in Figure 1 bind to HLA-A2.1 (ABHIB and GJA unpublished observation). When analysing immunoreactivity against the products of the gp100/pMeli7 gene, one should therefore include both gp100 and pMeli7.

In conclusion, the data presented in this report demonstrate that pMeli7 is recognised by three different MAbs used to diagnose melanoma and functions as a target for anti-melanoma CTLs.

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