Advances in Brief

Immune Escape of Melanoma: First Evidence of Structural Alterations in Two Distinct Components of the MHC Class I Antigen Processing Pathway[1]

Barbara Seliger,[2] Ulrike Ritz, Rupert Abele, Michaela Bock, Robert Tampé, Gert Sutter, Ingo Drexler, Christoph Huber, and Soldano Ferrone

Johannes Gutenberg-University, Third Department of Internal Medicine, 55101 Mainz, Germany [B. S., U. R., M. B., C. H.]; Philipps-University Marburg, Institute of Physiological Chemistry, Medical School, Marburg, Germany [R. A., R. T.]; GSF Research Center, Institute for Molecular Virology, 81675 Munich, Germany [G. S.]; Technical University, Institute for Virology, 81675 Munich, Germany [G. S., I. D.]; and Roswell Park Cancer Institute, Department of Immunology, Buffalo, New York 14263 [S. F.]

Abstract

Sequence analyses of the transporter associated with antigen processing (TAP) in tumor cell lines with deficient MHC class I surface expression identified a bp deletion at position 1489 near the ATP-binding domain of *Tap1,* causing a frameshift in one melanoma cell line. The impaired TAP1 protein expression was associated with deficient TAP2 protein expression, peptide binding, translocation, and MHC class I surface expression. Stable *TAP1* gene transfer reconstitutes the described defects, whereas lysis by HLA-A2-restricted CTLs was still abrogated. This was attributable to a 2-bp insertion at position 890 in the *HLA-A2* gene and was corrected after HLA-A2 cotransfection. This study describes for the first time mutations in two distinct components of the MHC class I antigen processing pathway, suggesting an immune selection against CTLs recognizing both TAP-dependent and -independent T-cell epitopes.

Introduction

Antigen presentation in the context of the MHC class I molecules to $CD8^+$ CTLs requires the ATP-dependent TAP[3] consisting of the subunits TAP1 and TAP2 (1). TAP transports cytosolic peptides into the endoplasmic reticulum (2). The crucial role for TAP in antigen processing was underscored by the characterization of mutant cell lines with defects in the presentation of antigenic peptides (3), by the existence of viral proteins abrogating TAP function (4), and by the analysis of TAP1$-/-$ mice (5).

In human tumors of distinct histology, changes in the expression and/or function of the MHC class I antigens were frequently found and may provide malignant cells with mechanisms to escape from T-cell recognition and destruction (6–9). The deficient MHC class I surface expression can be caused by total, locus, and allele-specific loss or down-regulation of MHC class I antigens attributable to distinct molecular mechanisms (6, 7). Loss of MHC class I antigens is often attributable to structural alterations of components of the MHC class I APM. In addition, deficiencies in MHC class I surface expression could also be caused by defects in the expression and/or function of different components of the MHC class I antigen processing pathway.

Indeed, down-regulation of MHC class I antigen expression was frequently associated with impaired TAP expression in many tumors (10). Until now, limited information exists about the underlying molecular mechanisms of these TAP deficiencies. Thus far, only a single structural alteration in TAP has been described in a lung cancer cell line that is attributable to a functionally defective allele of *Tap1,* resulting in the loss of proper MHC class I antigen processing and presentation (11). To investigate the underlying mechanisms of MHC class I abnormalities, a series of melanoma and renal cell carcinoma cell lines with deficient MHC class I surface expression was analyzed for structural integrity, expression, and function of MHC class I antigens and the peptide transporter subunits.

Materials and Methods

Cell Lines and Culture. buf1280 cells were established from a metastatic lesion of a melanoma patient expressing the HLA phenotype HLA-A2, -B51, -CW16, -DR4, -DR9, and -DQ3.

Stable Transfection. Transfections of buf1280 cells were carried out by lipofection using Lipofectamine (Life Technologies, Inc., Gaithersburg, MD) according to the manufacturer's instructions. For transfection, wt TAP1 and HLA-A2 expression vectors were used (12, 13). Cells were selected in medium supplemented with 500 μg/ml G418 (Roche Molecular Biochemicals, Mannheim, Germany).

Genomic and RT-PCR. For genomic PCR, 1×10^4 cells were resuspended in 20 μl of H_2O, incubated for 10 min at 95°C, followed by an incubation with 10 μg of proteinase K for 1 h at 55°C. Then, PCR was directly performed using 50 pmol of each primer and the following conditions: 95°C for 1 min, annealing temperature for 1.5 h and 72°C for 1.5 h. One-step RT-PCR was performed using the Titan kit as described by the manufacturer (Roche, Mannheim, Germany).

Membrane Preparation and Peptide Binding Assays. Cells were thawed on ice in 10 mM Tris-buffer (pH 8.0) supplemented with protease inhibitors and 1 mM DTT and homogenized with a glass homogenizer. Lysed cells were centrifuged at $1000 \times g$ for 10 min. For collection of crude membranes, supernatant was centrifuged at $200,000 \times g$ for 30 min, and pellets were resuspended in PBS. For peptide binding, the peptide RRYQKSTEL was labeled by the chloramine-T method using 1.5 nmol of peptide and 100 μCi of ^{125}I. To determine the amount of functional TAP, the membranes were incubated with radiolabeled peptide (200 nM) in a total volume of 50 μl in PBS, 5 mM $MgCl_2$ 15 min on ice. Unbound peptide was removed by adding 500 μl of PBS, 5 mM $MgCl_2$ and centrifuged for 8 min at $20,000 \times g$. The supernatant was discarded, and the washing procedure was repeated once. The membrane-associated radioactivity was directly quantified by gamma counting.

Peptide Transport Assay. The peptide translocation experiments were performed as described earlier (14) using the ^{125}I-labeled peptides #63 (RY-WANATRI) and #600 (TNKTRIDGQY). Briefly, 2.5×10^6 cells were permeabilized with 2 IU streptolysin O (Welcome Reagent Ltd., Beckenham, United Kingdom) in 50 μl of incubation buffer for 5 min at 37°C, followed by the addition of 10 μl of ATP (10 mM; Roche Diagnostics, Mannheim, Germany) and 2.5 μl of radioiodinated peptides (0.5 μmM) in a final volume of 100 μl and incubated at 37°C for 20 min. Subsequent to cell lysis in 1% NP40 (Sigma Chemical Co., Deisenhofen, Germany), glycosylated peptides were recovered by Concanavalin A-Sepharose beads (Pharmacia, Uppsala, Sweden) overnight. The radioactivity associated with the beads was determined by gamma counting, and translocation efficiencies were calculated as described.
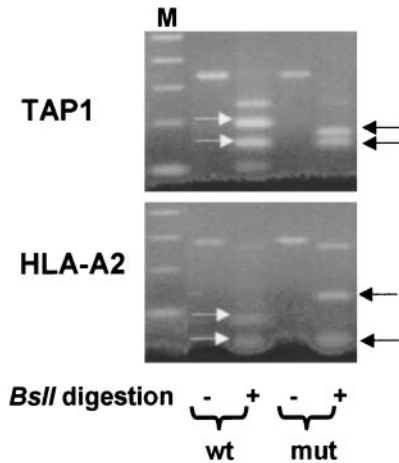
Fig. 1. Genomic PCR of mutant (*mut*) and wt TAP1. *a,* amplification products obtained by genomic PCR from the wt and mut *Tap1* gene were tested for the presence of the distinct *Bsl*I cleavage pattern generating in the mutated *Tap1* three fragments and two fragments in the wt *Tap1* gene. *Lane 1,* 100-bp molecular weight marker; *Lane 2,* uncut PCR product from wt *Tap1* (326 bp, cell line MZ1257); *Lane 3, Bsl*I-digested PCR products of wt *Tap1* (sizes 137 and 191 bp); *Lane 4,* uncut PCR product from mut *Tap1* (326 bp, cell line buf 1280); *Lane 5, Bsl*I-digested PCR products of mut *Tap1* [sizes 22 (not visible) 68 and 137 bp]. *b,* amplification products of the *HLA-A2* gene were tested for the presence of the different *Bsl*I digestion profile, resulting in six fragments of the mutated *HLA-A2* and eight of the wt *HLA-A2* gene. *Lane 1,* 100-bp molecular weight marker; *Lane 2,* uncut PCR product from wt *HLA-A2* (391 bp, cell line MZ1257); *Lane 3, Bsl*I-digested PCR products of wt *HLA-A2* [sizes 7, 22, 30, (not visible) 44, 48, 51, 89, and 90 bp]; *Lane 4,* uncut PCR product from mut *HLA-A2* (391 bp, cell line buf1280); *Lane 5, Bsl*I-digested PCR products of mut *HLA-A2* [sizes 7, 22, 30 (not visible), 48, 51 and 138 bp].

Western Blot Analysis. For Western blot analysis, 20 μg protein/lane obtained from crude membrane preparation were separated by a 10% SDS polyacrylamide gel. Proteins were blotted onto nitrocellulose membrane (Schleicher & Schuell, Dassel, Germany) and subsequently identified using specific mAbs directed against the human TAP1 (mAb 148.3 and TM6) and the human TAP2 (mAb 429.3) protein (15, 16). Western blots were developed by secondary antibodies and enhanced chemiluminescence (ECL; Amersham Pharmacia, Freiburg, Germany).

Flow Cytometry. For indirect immunofluorescence analysis, 5×10^5 cells were incubated for 30 min on ice using the anti-MHC class I antibody HLA-ABC-FITC- and the anti-HLA-A2-specific mAb mA2.1 and then washed twice with PBS. HLA-A2-stained cells were further incubated with a FITC-conjugated goat-antimouse immunoglobulin (Coulter/Beckman, Krefeld, Germany) as a secondary antibody for an additional 30 min at 4°C. Upon washing with PBS, 10,000 viable cells were analyzed after gating on forward and side scatter on a flow cytometer (Coulter Epics XL MCL software; Coulter Epics XL MCL System II 3.0; Beckman/Coulter).

Cytolytic Assay of Tumor Cells and TAP1 Transfectants. buf1280 cells and its TAP1- and/or HLA-A2-transfected derivatives were used as targets for HLA-A2-restricted tyrosinase-specific CTLs using the standard chromium release assay (17). Cells were infected with 10 units/cell of vaccinia-tyrosinase virus and incubated for 3 h at 37°C before cells were labeled with ^{51}Cr prior to an additional incubation period at 37°C (17). Twelve h after infection, a standard chromium release assay was performed. Briefly, ^{51}Cr-labeled targets were mixed with different concentrations of effectors in triplicates using E:T ratios ranging between 30:1 and 1:1 and then incubated for 4 h at 37°C. Supernatants were then harvested, and radioactivity was determined in a gamma counter. The percentage of specific lysis was calculated as $100 \times$ (Ex-
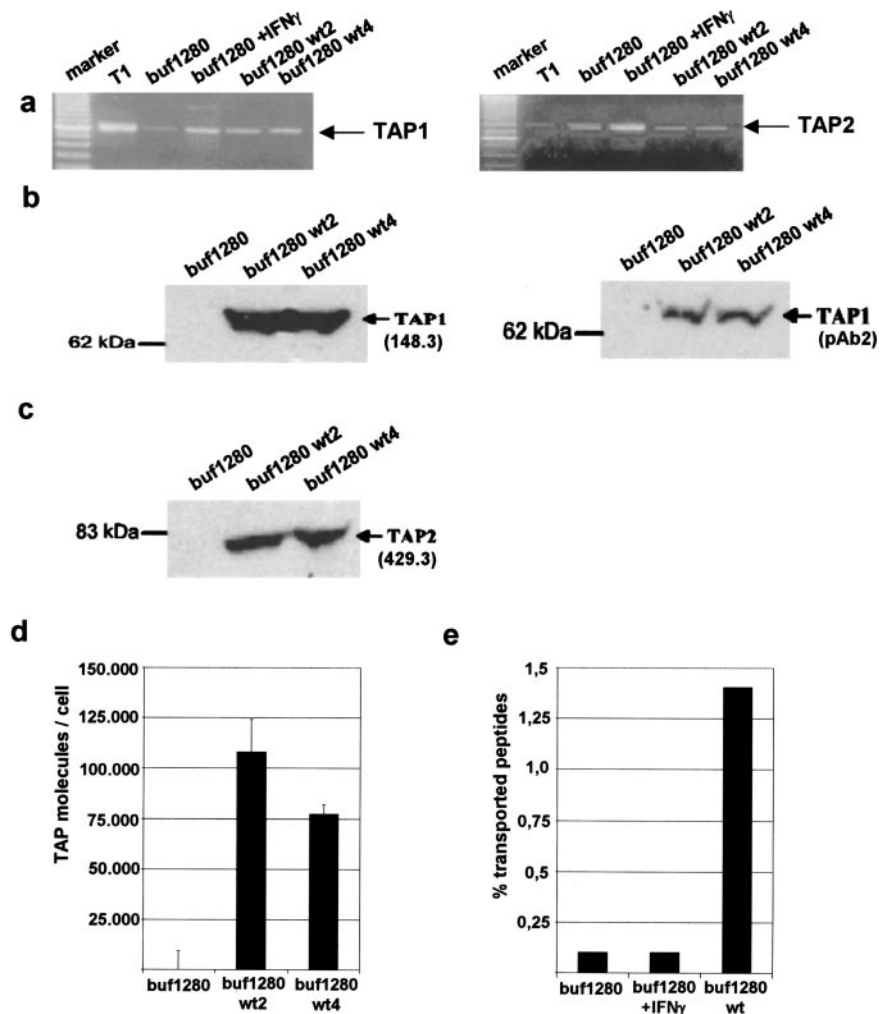

Fig. 2. Expression and function of TAP in TAP1- and TAP1- buf1280 cells. *a,* RNA expression of both TAP1 and TAP2 in the buf1280 cell line and control cell line is shown. Expression of both subunits is up-regulated by IFN-γ. *b,* using two different TAP1-specific antibodies, no TAP1 protein expression could be detected in parental buf1280 cells, whereas wt *Tap1* gene transfer results in wt TAP1 protein expression, as demonstrated in two TAP1 transfectants (*wt2* and *wt4*). *c,* the cell line buf1280 expressed TAP2 protein only after *Tap1* gene transfer. *d* and *e,* the restoration of TAP function was determined in untreated and IFN-γ treated TAP1$^-$ and TAP1$^+$ buf1280 cells using peptide binding (*d*) and translocation (*e*). *Bars,* SE. Lack of TAP function was found in TAP1$^-$ buf1280 cells, whereas *Tap1* gene transfer reconstitutes TAP function in the TAP1 wt transfectants.
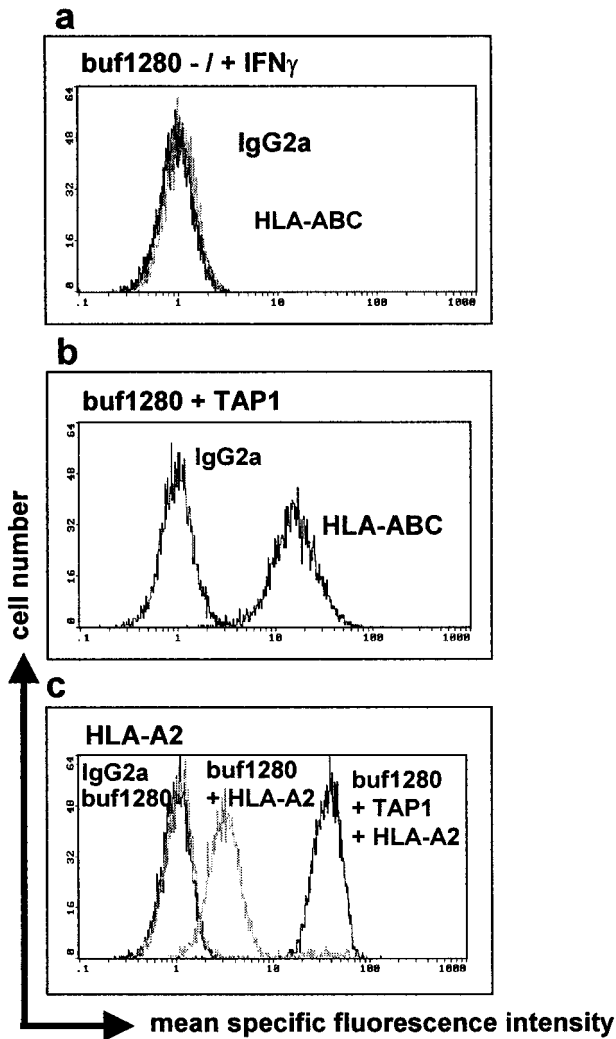
8648

Fig. 3. Correction of MHC class I surface expression by TAP1 gene transfer. Untreated and IFN-γ-treated buf1280 cells exhibit deficient MHC class I surface expression (*a*), which was partially restored upon *Tap1* gene transfer (*b*). The expression of HLA-A2 was not restored after *Tap1* gene transfer because of an insertion of 2 bp in the *HLA-A2* gene but was corrected by *HLA-A2* gene transfer (*c*).

perimental release − spontaneous release)/(Maximal release − spontaneous release).

Results and Discussion

Analysis of the Structural Integrity of TAP in Tumor Cell Lines. A panel of human tumor cell lines obtained from primary and metastatic melanoma and renal cell carcinoma were analyzed for structural abnormalities in the *Tap1* gene using genomic and RT-PCR followed by direct sequencing of respective amplification products. Sequence analyses of independent RT-PCR and genomic PCR products of 15 different tumor cell lines demonstrated, with the exception of the cell line buf1280 established from a metastatic melanoma lesion, the lack of sequence alterations in the samples analyzed. In contrast, buf1280 cells exhibit a bp deletion at position 1489 in the *TAP1* gene, which occurred within the first defined fold of the NBD, resulting in a frameshift and early stop codon. The existence of this alteration was independently confirmed by *BslI* digestion of uncloned genomic PCR products, because this deletion causes a distinct restriction enzyme cleavage pattern of wt and mutated *Tap1* (Fig. 1*a*).

Deficient Expression and Function of TAP Attributable to TAP1 Mutation. To evaluate the functional consequences of the TAP1 mutation in buf1280 melanoma cells, the expression of the TAP subunits, the peptide transport rate, as well as the level of MHC class I surface antigens was determined. RT-PCR analysis revealed TAP1 and TAP2 mRNA expression in the buf1280 cell line (Fig. 2*a*), whereas neither TAP1 nor TAP2 protein expression were detectable in these cells (Fig. 2, *b* and *c*). The impaired TAP protein expression was also accompanied by an inhibition of both peptide binding and peptide transport (Fig. 2, *d* and *e*). In addition, flow cytometric analysis using the anti-HLA class I antibody HLA-ABC-FITC revealed a lack of constitutive and IFN-γ-inducible MHC class I surface expression in the buf1280 cells (Fig. 3*a*). Thus, the bp deletion in the *Tap1* gene abrogates TAP protein expression and function, which is accompanied by MHC class I abnormalities.

Correction of the TAP-deficient Phenotype by *TAP* Gene Transfer. Stable gene transfer of wt *Tap1* into the melanoma cell line reconstituted the expression of both TAP subunits, the TAP1/TAP2 complex formation and the function of the peptide transporter as measured by peptide binding and peptide translocation into the endoplasmic reticulum (see Fig. 2, *b–e*). Furthermore, restoration of TAP function by *Tap1* gene transfer was accompanied by the expression of high levels of total MHC class I surface antigens on these cells (Fig. 3*a*).

CTL-mediated Immune Escape Attributable to Combined Structural Alterations of the *TAP1* and *HLA-A-2* Genes. To define whether there exists a correlation between the level of MHC class I surface expression and immune recognition, uninfected and MVA-tyr-infected TAP1^{−} and TAP1^{+} buf1280 cells were used as targets for HLA-A2-restricted tyrosinase-specific CTLs. Although total MHC class I surface expression was corrected by wt *TAP1* gene transfer, no recognition and killing of both parental TAP1^{−} and TAP1^{+} buf1280 cells were found, whereas the tyrosinase expressing, HLA-A2[+] melanoma cell line NA8 was efficiently lysed by these CTLs (Fig. 4). The lack of susceptibility to tyrosinase-specific lysis was attributable to abrogated expression of HLA-A2 surface antigens (Fig. 3*b*). Sequence analyses of genomic and RT-PCR products demonstrated a 2-bp insertion at position 890 in the *HLA-A2* gene, which was further confirmed by a distinct *BslI* digestion pattern of the genomic PCR products from parental buf1280 cells when compared with that of respective control cells (Fig. 1*b*). The impaired HLA-A2 expression could be overcome by wt *HLA-A2* gene transfer (Fig. 3*c*). The TAP1^{+}, HLA-A2^{+} buf1280 cells, but not the buf1280 HLA-A2[+] variants, were efficiently recognized by the HLA-A2-restricted tyrosinase-specific CTLs, demonstrating that the processing and presentation of HLA-A2-restricted, tyrosinase-specific peptides could be re-
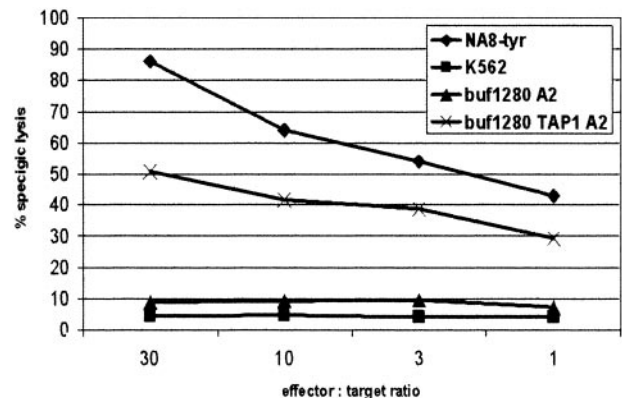

Fig. 4. Induction of CTL-specific lysis after *TAP1* and *HLA-A2* gene transfer. The TAP1^{−}, HLA-A2^{+} buf1280 cells were not lysed by tyrosinase-specific CTLs, whereas the TAP1^{+}, HLA-A2^{+} buf1280 cells were efficiently recognized with a 50% lysis. The cell line NA8-tyr served as positive control, and the cell line K562 served as a negative control.

8649

stored by cotransfection of both the wt *Tap1* and *HLA-A2* genes into the buf1280 melanoma cell line (Fig. 4).

Thus, we here describe for the first time the simultaneous occurrence of structural alterations in two components of the MHC class I APM, a 1-bp deletion within the first defined fold of the NBD of the *Tap1* subunit and a 2-bp insertion within the *HLA-A2* gene that are responsible for the lack of antigen processing and presentation as well as for MHC class I surface expression abnormalities. These data further suggest that the buf1280 cells evade the efficient CTL-mediated immune recognition by abrogating the presentation of both TAP-independent and TAP-dependent peptides in the context of the MHC class I molecules.

Mutations in the *Tap* genes have been found to severely affect MHC class I surface expression (18). To the best of our knowledge, no naturally occurring homozygous deletion resulting in the inactivation of TAP protein has been demonstrated in any murine and human tumor cell line. Chen *et al.* (11) demonstrated an R-to-Q substitution at residue 659 in the TAP1 subunit. This codon is located in the cytosolic domain of the ATP-binding region of the *Tap1* gene. These authors suggest that the ATP-binding ability of this novel allele may be affected by the substitution of an arginine to a glutamine. Recently, our group has identified specific sequences in the putative peptide binding domains that are essential for proper antigen processing without affecting the ATP-binding capability (19). These results argue for an influence of the conformation of these regions for proper peptide binding, suggesting that structural alterations near the NBD might negatively interfere with these properties. The TAP1$^-$ melanoma cell line buf1280 lacks TAP2 protein expression, although TAP2 mRNA was transcribed and no sequence alteration was detected. Because *Tap1* gene transfer also restores TAP2 protein expression, it is suggested that wt TAP1 stabilizes TAP2 protein and that both TAP subunits are coordinated regulated. Thus, a novel mechanism of TAP dysfunction and a newly identified phenotype of TAP mutations in human tumors have been identified.

Tumor cell lines of distinct origin often exhibit impaired expression and function of TAP, which could be often restored by IFN-γ treatment (10). In contrast to these studies, the TAP deficiency we defined in buf1280 cells cannot be overcome by IFN-γ treatment caused by a structural alteration in *Tap1*. Transfection of the wt *Tap1* gene restored the expression and ability to process and present antigens in the context of MHC class I molecules, demonstrating that this deletion is directly accompanied by deficient MHC class I surface expression and at least a TAP-dependent dysfunction of the antigen processing. The lack of induction of the HLA-A2-restricted, CTL-mediated recognition of the TAP1$^+$ melanoma cell line was attributable to an additional structural alteration in the *HLA-A2* gene of buf1280 cells and enables their escape from the TAP-independent immune response, because peptides also derived from signal sequences cannot be presented (20). The concomitant mutations in both *TAP1* and *HLA-A2* genes implicate an immune selection mediated also by CTL recognizing TAP-independent epitopes. Until now, a number of mutations have been reported in the *HLA-A2* gene ranging from point mutations, substitutions to bp insertions (7, 9), but the 2-bp insertion at position 890 of the *HLA-A2* gene demonstrated in buf1280 cells has not been described thus far. Thus, our data significantly extent the observations of others demonstrating: (*a*) a coordinated regulation of both TAP subunits; (*b*) a novel TAP mutant phenotype; and (*c*) the first description of a combined structural alteration of two distinct APM components causing a concomitant loss of the TAP-independent and TAP-dependent antigen presentation function in human tumors.

Acknowledgments

References

1. Pamer, E., and Cresswell, P. Mechanisms of MHC class I-restricted antigen processing. Annu. Rev. Immunol., *16:* 323–358, 1998.
2. Momburg, F., Roelse, J., Hämmerling, G., and Neefjes, J. J. Peptide size selection by the major histocompatibility complex-encoded peptide transporter. J. Exp. Med., *179:* 1613–1618, 1994.
3. Ljunggren, H. G., and Karre, K. Host resistance directed selectivity against H-2-deficient lymphoma variants. Analysis of mechanism. J. Exp. Med., *162:* 1745–1759, 1985.
4. Hill, A., and Ploegh, H. Getting the inside out: the transporter associated with antigen processing (TAP) and the presentation of viral antigen. Proc. Natl. Acad. Sci. USA, *92:* 341–343, 1995.
5. van Kaer, L., Ashton-Rickardt, P. G., Ploegh, H. L., and Tonegawa, S. TAP1 mutant mice are deficient in antigen presentation, surface class I molecules, and CD4$-$8$+$ T cells. Cell, *71:* 1205–1209, 1992.
6. Garrido, F., Ruiz-Cabello, F., Cabrera, T., Perez-Villar, J. J., Lopez-Botet, M., Duggan-Keen, M., and Stern, P. L. Implications for immunosurveillance of altered HLA class I phenotypes in human tumours. Immunol. Today, *18:* 89–95, 1997.
7. Marincola, F. M., Jaffee, E. M., Hicklin, D. J., and Ferrone, S. Escape of human solid tumors from T cell recognition: molecular mechanisms and functional significance. Adv. Immunol., *74:* 181–185, 2000.
8. Koopman, L. A., Corver, W. E., van der Slik, A. R., Giphar, M. J., and Fleuren, G. J. Multiple genetic alterations cause frequent and heterogeneous human histocompatibility leukocyte antigen class I loss in cervical cancer. J. Exp. Med., *191:* 961–965, 2000.
9. Elsner, H. A., Drabek, J., Rebmann, V., Ambruzova, Z., Grosse-Wilde, T., and Blaszcyk, R. Non-expression of HLA-B*5111N is caused by an insertion into the cytosine island at exon 4 creating a frameshift stop codon. Tissue Antigens, *57:* 369–375, 2001.
10. Seliger, B., Maeurer, M. J., and Ferrone, S. Antigen-processing machinery breakdown and tumor growth. Immunol. Today, *21:* 455–462, 2000.
11. Chen, H. L., Gabrilovich, D., Tampe, R., Girgis, K. R., Nadaf, S., and Carbone, D. P. A functionally defective allele of TAP1 results in loss of MHC class I antigen presentation in a human lung cancer. Nat. Genet., *13:* 210–213, 1996.
12. Kallfelz, M., Jung, D., Hilmes, C., Knuth, A., Jaeger, E., Huber, C., and Seliger, B. Induction of immunogenicity of a human renal-cell carcinoma cell line by *TAP*-gene transfer. Int. J. Cancer, *81:* 125–129, 1999.
13. Wölfel, T., Schneider, J., Meyer zum Buschenfelde, K. H., Rammensee, H. G., Rotzschke, O., and Falk, K. Isolation of naturally processed peptides recognized by cytolytic T lymphocytes on human melanoma cells in association with HLA-A2.1. Int. J. Cancer, *57:* 413–418, 1994.
14. Neefjes, J. J., Momburg, F., and Hämmerling, G. J. Selective and ATP-dependent translocation of peptides by MHC-encoded transporter. Science (Wash. DC), *261:* 769–774, 1994.
15. Meyer T. H., van Endert, P. M., Uebel, S., Ehring, B., and Tampé, R. Functional expression and purification of the ABC transporter complex-associated with antigen-processing (TAP) in insect cells. FEBS Lett., *351:* 443–447, 1994.
16. van Endert, P. M., Tampé, R., Meyer, T. H., Tisch, R., Bach, J. F., and McDevitt, H. O. A sequential model for peptide binding and transport by the transporters associated with antigen processing. Immunity, *1:* 491–500, 1994.
17. Drexler, I., Antunes, E., Schmitz, M., Wolfel, T., Huber, C., Erfle, V., Rieber, P., Theobald, M., and Sutter, G. Modified vaccinia virus Ankara for delivery of human tyrosinase as melanoma-associated antigen: induction of tyrosinase- and melanoma-specific human leukocyte antigen A*0201-restricted cytotoxic T cells *in vitro* and *in vivo*. Cancer Res., *59:* 4955–4963, 1999.
18. de la Salle, H., Houssaint, E., Peyrat, M. A., Arnold, D., Salamero, J., Pinczon, T., Stevanovic, S., Bausinger, H., Fricker, D., Gomard, E., Biddison, W., Lehner, P., UytdeHaag, F., Sasportes, M., Donato, L., Rammensee, H. G., Cazenave, J. P., Hanau, D., Tongio, M. M., and Bonneville, M. Human peptide transporter deficiency. J. Immunol., *158:* 4555–4563, 1997.
19. Ritz, U., Momburg, F., Pircher, H. P., Strand, D., Huber, C., and Seliger, B. Identification of sequences in the human peptide transporter subunit TAP1 required for transporter associated with antigen processing (TAP) function. Int. Immunol., *13:* 31–41, 2001.
20. Wei, M. L., and Cresswell, P. HLA-A2 molecules in an antigen processing mutant cell contain signal sequence-derived peptides. Nature (Lond.), *356:* 443–446, 1992.

Immune Escape of Melanoma: First Evidence of Structural Alterations in Two Distinct Components of the MHC Class I Antigen Processing Pathway

Barbara Seliger, Ulrike Ritz, Rupert Abele, et al.

Updated version	Access the most recent version of this article at: http://cancerres.aacrjournals.org/content/61/24/8647

Cited articles	This article cites 20 articles, 6 of which you can access for free at: http://cancerres.aacrjournals.org/content/61/24/8647.full#ref-list-1
Citing articles	This article has been cited by 37 HighWire-hosted articles. Access the articles at: http://cancerres.aacrjournals.org/content/61/24/8647.full#related-urls

E-mail alerts	Sign up to receive free email-alerts related to this article or journal.
Reprints and Subscriptions	To order reprints of this article or to subscribe to the journal, contact the AACR Publications Department at pubs@aacr.org.
Permissions	To request permission to re-use all or part of this article, use this link http://cancerres.aacrjournals.org/content/61/24/8647. Click on "Request Permissions" which will take you to the Copyright Clearance Center's (CCC) Rightslink site.