Autoantibodies in Melanoma-Associated Retinopathy Recognize an Epitope Conserved Between TRPM1 and TRPM3

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Melanoma-associated retinopathy (MAR) is a paraneoplastic syndrome associated with cutaneous malignant melanoma. Visual deficits include flickering photopsias, sudden night blindness, and a generalized constriction of visual fields. MAR is believed to be caused by an autoimmune response to antigens expressed by the tumor that are also present in the retina. Electroretinogram (ERG) recordings from MAR patients may contain autoantibodies that label both melanocytes and retinal bipolar cells. The goal of this study was to further map the antigenic epitope.

Methods. Patient sera were tested by immunofluorescence and Western blotting on HEK293 cells transfected with enhanced green fluorescent protein (EGFP)-TRPM1 fusion constructs and mouse retina sections.

Results. The epitope recognized by MAR patient sera was mapped to a region encoded by exons 9 and 10 of the human TRPM1 gene. This region of TRPM1 is highly conserved with TRPM3, and indeed MAR sera were found to cross-react with TRPM3, a closely related channel expressed in the retinal pigment epithelium (RPE).

Conclusions. These results indicate that TRPM1 autoantibodies in MAR patient sera recognize a short, intracellular segment of TRPM1. Cross-reactivity with TRPM3 in the RPE may account for other visual symptoms that are experienced by some MAR patients such as retinal and RPE detachments. We propose that TRPM1 autoantibodies are generated in response to abnormal TRPM1 polypeptides encoded by an alternate mRNA splice variant expressed by malignant melanocytes.

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the production of abnormal TRPM1 polypeptides that are seen as foreign by the immune system. Mapping the epitope or epitopes targeted by TRPM1 autoantibodies may yield insight into the mechanism by which TRPM1 becomes autoimmunogenic in melanoma, and may also provide insight into the array of visual symptoms associated with MAR. Previously, we have shown that TRPM1 autoantibodies in MAR patient sera bind to the intracellular, amino terminal domain of the channel. Here we show that MAR sera react not only with TRPM1, but also with the closely related family member TRPM3, which is expressed by the retinal pigment epithelium (RPE). Furthermore, we have narrowed the MAR epitope to amino acids encoded by exons 9 and 10 of human TRPM1, a region that is 82% identical in the respective human, mouse, and rat orthologs.

**METHODS**

**Expression Vectors**

A series of deletion constructs were generated from the full-length mouse TRPM1 (GenBank NM_001039104) and inserted between the KpnI and SmaI sites of pEGFP-C3 (Clontech, Mountain View, CA, USA). Restriction enzymes were used to remove N-terminal- and C-terminal-encoding segments as follows: The pEGFP-C3-TRPM1 plasmid was digested with BamHI and recircularized to generate the M1-G799 (BamHI) segment. Similarly, digestion with AccI and AgeI, followed by treatment with Klenow, and recircularization yielded the L1159 (AgeI)-C1622 segment. The M1-G550 (AccI) segment was generated by digesting the M1-G799 (BamHI) construct with AgeI and BamHI, T4 DNA polymerase treatment, and recircularization. The M1-I147 (EcoRV) segment was generated by digesting the pEGFP-C3-TRPM1 plasmid with EcoRV and recircularization. To generate the V149 (ApaLI)-V430 (AccI) construct, the 843-bp ApaLI-AccI fragment from M1-G550 (ApaI) was purified, treated with T4 DNA polymerase, and inserted into phosphatase-treated, SmaI-digested pEGFP-C3. Similarly the V149 (ApaLI)-Q283 (PstI) construct was generated by digesting the M1-G550 (ApaI) plasmid with ApaLI and PstI, T4 DNA polymerase treatment, and ligating the purified 399-bp fragment into SmaI-digested pEGFP-C3. The L282 (PstI)-G550 (ApaI) fragment was constructed from the M1-G550 (ApaI) plasmid, digested with PstI, and recircularized. Finally, digestion of the V149 (ApaLI)-V430 (AccI) construct with PstI followed by recircularization generated the L282 (PstI)-V430 (AccI) segment.

A human h109-JTRPM1 cDNA plasmid (GenBank NM_001252020) was used as template to amplify small TRPM1-encoding fragments using the following PCR primers (restriction site linkers in lowercase):

1. 5‘-ATGCCCTGAAAGACACATCTCTCT
2. 5‘-CCCTCGAGAACATGCAAACAG
3. 5‘-ggaattCTCTGTCGCTCTCGGGTGT
4. 5‘-TTCTCTACAGTACCTGTCGGCGAAGG
5. 5‘-ggaattCGACGAAACTGCATCACGC
6. 5‘-ggaatcGTAGCTCTGCTCTGTACG
7. 5‘-ccgattcTTTTCCTATTCGAC
8. 5‘-gtgacgtgCCATCGGAACGAGAATCTG
9. 5‘-gtcctctgTAGGACCTATCG

All PCR products were subcloned into pJET1.2 (Fermentas, Glen Burnie, MD, USA) and their nucleotide sequences were verified. The D189-F337 construct was amplified using primers 1 and 4. The resulting pJET1.2 plasmid was digested with XhoI and BglII, and the 465-bp fragment was subcloned into pEGFP-C3, digested with SalI and BamHI. The L275-I380 and L275-N407 constructs were prepared using primers 2 and 6, and 2 and 7, respectively. The PstI-BamHI fragments were subcloned into PstI-BamHI-digested pEGFP-C3. Similarly, the L288-N407 constructs were prepared using primers 3 and 6, and 3 and 7, and the EcoRI-BamHI fragments were subcloned into EcoRI-BamHI-digested pEGFP-C3. The M372-P435 and M372-L519 constructs were ampliﬁed using primers 5 and 8, and 5 and 9, subcloned into pJET1.2 and the EcoRI-AgeI fragments inserted into EcoRI-AgeI-digested pEGFP-N1 (Clontech). For the K361-P435 plasmids, the same EcoRI-AgeI fragments were inserted into pEGFP-C3 digested with EcoRI and Xmal.

**Animals**

Adult mice of both sexes were used in this study. All mice were maintained on a 12-hour light/dark cycle and provided food and water ad libitum. Retina sections from C57BL6 mice were used for initial screening of MAR serum immunoreactivity. For identifying the target of labeling in RPE, targeted TRPM3 knock-out mice (TRPM3tm1Lex, Texas Institute of Genomic Medicine, College Station, TX, USA) were used, and tissue from wild-type and knock-out littermates was compared. Mice were maintained and used for experiments in accordance with the ARVO Statement for the Use of Animals in Ophthalmic and Vision Research. All animal procedures were approved by the Oregon Health & Science University (OHSU) Institutional Animal Care and Use Committee.

**Patient Sera**

This study was approved by the OHSU Institutional Review Board and adhered to the tenets of the Declaration of Helsinki. One MAR serum sample (no. 1) was from a patient diagnosed at the National Eye Institute; the other serum sample (no. 2) was obtained from the Ocular Immunology Laboratory, OHSU. Thirty-eight control sera from normal healthy subjects were obtained from the Oregon Clinical and Translational Research Institute.

**Immunohistochemistry**

HEK293 cells were seeded onto polylysine-coated coverslips in 12- or 24-well tissue culture plates, transfected with pEGFP-C3 and -N1 expression plasmids encoding fragments of TRPM1 fused at the C- or N-terminus of enhanced green fluorescent protein (EGFP), using Effectene (Qiagen, Valencia, CA, USA), Lipofectamine (SignaGen, Rockville, MD, USA), or calcium phosphate coprecipitation. CHO-K1 cells were transfected with mouse TRPM3 (GenBank AE080504.1) in pcDNA3, using TransIT-CHO Transfection Kit (Mirus, Madison, WI, USA). Twenty-four to 36 hours after transfection, coverslips were removed from the wells, cells were fixed for 10 minutes by immersion in ice-cold 4% paraformaldehyde, and then processed for immunofluorescence as follows.

Freshly dissected mouse eyes were hemisected and the front of the eye and lens discarded. The remaining eyecup containing the retina was fixed by immersion in ice-cold 4% paraformaldehyde for 20 minutes, washed in ice-cold PBS, then cryoprotected by consecutive incubations in ice-cold 10%, 20%, and 30% sucrose. Vertical sections, 16 μm, were cut on a cryostat, air dried, and then stored at −80°C until use.

Transfected cells on coverslips and thawed retinal sections were processed for immunofluorescence confocal microscopy as described previously, with dilutions (1:100–1:2000) of the MAR serum instead of primary antibodies and anti-human IgG conjugated to Alexa Fluor 594 (1:1000; Invitrogen, Carlsbad, CA, USA) as the secondary antibody. Fluorescence images were
FIGURE 1. The MAR epitope is encoded by mouse TRPM1 exons 8 through 11. To map the MAR epitope, HEK cells were transfected with a series of EGFP-mouse TRPM1 deletion constructs and tested for immunofluorescence with MAR serum. (A) Top row: superimposition of GFP (green) and MAR serum 2 (red) immunofluorescence, with colocalization appearing yellow. Bottom row: MAR serum immunofluorescence alone. Scale bar: 10 μm. (B) Diagram of the mouse TRPM1 cDNA deletion constructs. Exon 2, which is alternatively spliced and encodes an alternative N-terminus, is not present in the plasmid constructs used. The first and last amino acids encoded by each construct are indicated. Positive immunofluorescence with MAR serum was graded as positive (+), or negative (−). MHR: TRPM homology regions. (C) HEK293 cells were transfected with plasmids encoding either mouse TRPM1-EGFP or human TRPM1-EGFP and then Western blotted with either MAR serum 1, MAR serum 2, an antibody to mouse TRPM1, or an antibody to GFP.
acquired with an Olympus FluoView FV1000 confocal microscope (Olympus, Waltham, MA, USA) using a ×60/1.42 oil immersion objective. Image brightness and contrast were enhanced using Adobe Photoshop (Adobe Systems, Inc., San Jose, CA, USA).

Western Blot Analysis

TRPM1-transfected HEK cells were collected in radio-immunoprecipitation assay (RIPA) buffer with protease inhibitor cocktail (Cell Signaling Technology, Danvers, MA, USA) for Western blot analysis. Lysates were electrophoresed on precast 4% to 12% polyacrylamide gradient gels (Novex; Invitrogen). The separated proteins were electrophoretically transferred to polyvinylidene difluoride (PVDF) membranes, which were then probed with human sera (1:1000), goat anti-GFP (1:1000), or sheep antibodies to mouse TRPM1 (amino acids 1423–1622). Anti-human IRDye 680CW, anti-sheep IRDye 680W, and anti-goat IRDye 800CW secondary antibodies (Li-Cor, Lincoln, NE, USA) were used at a dilution of 1:10,000 and visualized with an Odyssey infrared imaging system (Li-Cor).

RESULTS

The Epitope for TRPM1 Autoantibodies Is Located Near the Middle of the Cytoplasmic N-Terminal Domain

We previously found that MAR autoantibodies bind to a site within the predicted intracellular N-terminal domain of TRPM1.6 To localize the MAR epitope further, we subcloned successively smaller mouse TRPM1 cDNA restriction fragments and expressed them as EGFP fusion proteins in transfected HEK293 cells (Fig. 1). Transfected cells were then fixed and immunostained with two MAR antisera we previously described.6,25 Then, a fluorescent anti-human IgG was used to detect human autoantibodies. Following the transfection procedure, approximately 20% to 50% of the cells expressed the TRPM1–EGFP fusion proteins, as determined by the detection of EGFP (green) fluorescence. The untransfected cells (no EGFP fluorescence) served as a control for nonspecific immunofluorescence with the human sera (Fig. 1A). The two MAR sera showed similar patterns of immunoreactivity toward the TRPM1 fragments (not shown). The smallest immunoreactive fragment spans amino acids L282 to V430 (Fig. 1B). This region comprises the C-terminal 58 amino acids from the melastatin homology region (MHR)-2, 66 amino acids from the N-terminal part of MHR3, and a less conserved segment linking these two regions. This region of TRPM1 is 91% identical between the mouse and human sequences, and we have previously demonstrated that human MAR sera react with mouse TRPM1 by immunofluorescent labeling of mouse retina sections and CHO cells transfected with mouse TRPM1.6,25 Though both MAR sera react well with mouse TRPM1 by immunofluorescence, both sera reacted more strongly with human TRPM1 than mouse TRPM1 by Western blotting (Fig. 1C). This suggests that the sequence differences between human and mouse TRPM1 are not significant for binding of the autoantibodies to TRPM1 in its native conformation (i.e., immunofluorescent labeling of fixed cells or tissue), but do affect the binding affinity of the autoantibodies when TRPM1 is in a denatured state (i.e., Western blotting).

To further narrow the region of TRPM1 recognized by MAR autoantibodies, we used a human TRPM1 cDNA29 as template for PCR to generate a series of overlapping TRPM1–EGFP fusion constructs, spanning amino acids D189 to L519. This region is encoded by human exons 7 through 14 and encompasses the region corresponding to amino acids L282 to V450 of the mouse fragment identified in Figure 1. Protein
Transfected HEK293 cells were also seeded onto polylysine-coated coverslips, which were then fixed and immunostained using MAR sera 1 and 2. For both sera, the smallest immunopositive segment spanned human TRPM1 amino acids L288 to L380 (Fig. 3). Interestingly, MAR serum 1 did not react with the EGFP fusion construct containing amino acids K361 to P435 (Fig. 3A), whereas MAR serum 2 was positive for this construct (Fig. 3B). As negative control, sera from 38 healthy subjects were not reactive in these assays (not shown).

**TRPM1-Positive MAR Autoantibodies Cross-React With TRPM3**

The antigenic region of TRPM1 (human amino acids L288-L380) is 82% identical between TRPM1 and TRPM3 (Fig. 4A), suggesting that the MAR sera may react with both TRP channels. Labeling TRPM3-transfected cells with both MAR sera revealed that they indeed react with TRPM3 (Fig. 4B). TRPM3 mRNA has been shown to be abundantly expressed by the RPE.27 We detected MAR serum immunofluorescence in the RPE of wild-type mice that was markedly reduced in TRPM3 knockout mice, whereas immunofluorescence in the ON-bipolar cells, which express TRPM1, was unaffected in the TRPM3 knockout retina (Figs. 4C, 4D).

**DISCUSSION**

TRPM1 is expressed by both melanocytes and retinal bipolar cells,12,28 and it is downregulated in metastatic melanoma.29,30 Sera from melanoma patients diagnosed with MAR have been shown to react with TRPM1.6–8 The visual symptoms associated with MAR suggest that the TRPM1 autoantibodies inhibit channel function upon binding. Here, we mapped the immunogenic region of TRPM1 to a segment encoded by exons 9 and 10 of the human gene (corresponding to exons 7 and 8 in mouse), which is located in the cytoplasmic N-terminal domain of TRPM1. This region is 82% identical in TRPM3, a closely related channel that is expressed at high levels by the RPE in the eye,31 and is also expressed in pancreatic β-cells,32 dorsal root ganglia,33 and vascular smooth muscle cells.34 Indeed, we found that the MAR autoantibodies labeled TRPM3-expressing CHO cells, as well as the RPE in wild-type but not TRPM3 knockout mice. While inactivation of TRPM1 channels in the ON-bipolar cells by MAR autoantibodies is likely to account for the suppression of the ERG b-wave, cross-reactivity with TRPM3 may explain additional eye-related deficits seen in some cases of MAR, such as vitelliform lesions,35–37 character-ized by multiple sites of retinal detachment from the RPE. In these cases, it is possible that TRPM5 may be the primary autoantigen rather than TRPM1, particularly in patients with paraneoplastic vitelliform lesions but no classical MAR symptoms.37

It is noteworthy that both MAR sera reacted with the same small region of TRPM1, raising the question of what makes this region autoimmunogenic. Interestingly, a tumor suppressor microRNA, miR-211, is encoded within intron 8 of the TRPM1 gene (i.e., the intron between exons 8 and 9 of the human sequence).38–41 This microRNA is generated during processing of the TRPM1 pre-mRNA and is downregulated in advanced melanoma by an unknown mechanism. It is intriguing that intron 8 is located close to the TRPM1 region recognized by the MAR autoantibodies. A possible mechanism by which downregulation might occur is by alternative splicing of the TRPM1 pre-mRNA and is downregulated in advanced melanoma by an unknown mechanism. It is intriguing that intron 8 is located close to the TRPM1 region recognized by the MAR autoantibodies. A possible mechanism by which downregulation might occur is by alternative splicing of the TRPM1 pre-mRNA in a manner that prevents the generation of the microRNA. This aberrant mRNA splicing could also result in truncated TRPM1 polypeptides that may be recognized as non-self by the immune system and trigger an autoimmune response.
response. Indeed, alternate TRPM1 transcripts encoding truncated N-terminal TRPM1 polypeptides are more abundant than the transcript encoding full-length TRPM1 in pigmented metastatic melanoma cells.23 This is consistent with an RNA-seq analysis of TRPM1 transcripts in the melanoma cell line SK-Mel-30, which reveals much higher levels of transcripts encoding exons 2 to 11, than downstream exons.43 These shorter transcripts may include an alternative exon 9 donor site and encode a truncated protein. Examples of such cDNA clones and EST sequences are deposited in GenBank (e.g., BC033627). Indeed, the presence of truncated TRPM1 polypeptides has been reported in malignant melanocytes.24 We thus propose that such polypeptides are autoimmunogenic and cause MAR.

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References


FIGURE 4. MAR IgG cross-react with TRPM3. (A) Sequence alignment of the TRPM1 epitope and the corresponding region of TRPM3. Identical amino acids are indicated by colons, similar amino acids by periods. The minimal MAR epitope is boxed. (B) Immunofluorescent labeling of TRPM3-transfected CHO cells with MAR serum 2. (C, D) MAR serum 2 gave rise to strong immunofluorescence over the RPE in sections of TRPM3+/− mouse eyecups (IC upper image), but markedly reduced fluorescence over the RPE in TRPM3−/− eyes (ID upper image), whereas bipolar cell staining was strong in both TRPM3+/+ and TRPM3−/− retinas (IC lower image). RPE immunostaining is overlaid onto DIC images (IC, ID upper images). DIC images of the retina layers are shown to the left of the retina immunostaining (IC, ID lower images). The scale bars represent 10 µm in (B) and 20 µm in (D) (applies to both [C] and [D]). OPL, outer plexiform layer; INL, inner nuclear layer; IPL, inner plexiform layer.

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