

BRIEF COMMUNICATION

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A single amino acid substitution causes loss of expression of a *MICA* allele

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The human major histocompatibility complex (MHC) class I homologues *MICA* and *MICB* are stress-inducible surface molecules that are not associated with β_2 -microglobulin and peptides, are expressed in intestinal epithelium and epithelial tumors, and are recognized by $V_{\delta}1$ $\gamma\delta$ T cells, a subset of $\gamma\delta$ T cells that is enriched in epithelial sites (Bahram et al. 1994; Groh et al. 1996, 1998, 1999). Analogous to the interactions of MHC class I molecules with inhibitory or activating natural killer (NK) cell receptors that are expressed on NK cells and T cells (Lanier 1998), *MICA/B* are ligands for an activating receptor, NKG2D, which is expressed on most NK cells, $CD8^+$ $\alpha\beta$ T cells and $\gamma\delta$ T cells (Bauer et al. 1999).

MICA/B are variably expressed in some lung, breast, kidney, ovary, prostate, and colon carcinomas (Groh et al. 1999). While exploring this heterogeneity using cell lines, we identified two gastric epithelial tumor lines that lacked expression of *MICA* protein despite the presence of abundant mRNA. Analysis of this deficiency showed that both cell lines express a single allele of *MICA* (*MICA010*), which is defective because of a single amino acid substitution in the $\alpha 1$ domain that can be predicted to interfere with a stable protein fold.

Epithelial tumor cell lines were screened by flow cytometry for lack of expression of *MICA* and/or *MICB*, using monoclonal antibodies (mAbs) specific for

MICA (mAbs 2C10 and 3H5) or *MICA* and *MICB* (mAbs 6D4 and 6D5) (Groh et al. 1996, 1998). Two gastric tumor cell lines, AGS and KATO III, had little or no surface *MICA*, compared with the positive control HCT116 and Lovo colon carcinoma lines, although they contained equal or larger amounts of *MICA* mRNA. AGS cells expressed *MICB* mRNA and stained with the mAbs 6D4 and 6D5, whereas KATO III cells had little or no *MICB* mRNA (Fig. 1A,B; all cell lines were from the American Type Culture Collection). We examined whether the lack of *MICA* surface expression was due to a defect in protein processing in the secretory pathway. Immunoprecipitation with the mAbs 2C10 and 3H5 from lysates of metabolically labeled cells, *N*-glycanase treatment of immunocomplexes, and sodium dodecylsulfate-polyacrylamide gel electrophoresis (SDS-PAGE) detected the 43,000 *M_r* *MICA* polypeptide in HCT116 but not in AGS and KATO III cells (Fig. 1C). However, transfection of cDNA or of a cosmid encoding *MICA* (allele 004) restored surface *MICA* on KATO III cells (Fig. 2A). This indicated that expression of the endogenous gene was not impaired by a post-transcriptional or protein-processing defect, but was likely caused by a deleterious sequence alteration.

A substantial number of allelic variants of *MICA* have been described (Fodil et al. 1996), which have so far not been associated with differences in function. Neither the distribution of amino acid substitutions nor the crystal structure of *MICA* have offered potential explanations (Li et al. 1999). Using specific primers and reverse transcription-polymerase chain reaction, *MICA* mRNA sequences were derived from KATO III and AGS cells. Direct sequencing of amplicons identified a single sequence that was identical in both cell lines and corresponded to the *MICA010* allele, which has a proline for arginine substitution at position 6 in the first β strand of the $\alpha 1$ domain (Fig. 2B) (Fodil et al. 1996). Arginine at this position is conserved in all *MICA* and *MICB* alleles, as well as in homologous sequences from diverse nonhuman primate species (Ando et al. 1997;

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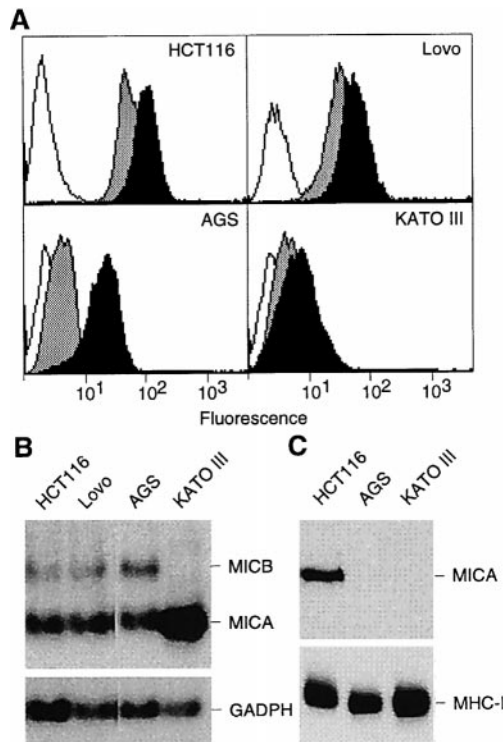


Fig. 1A-C Loss of MICA expression in KATO III and AGS cells. **A** Flow cytometry of HCT116, Lovo, AGS, and KATO III cells using monoclonal antibody (mAb) 2C10 (anti-MICA, gray profiles) and mAb 6D4 (anti-MICA and -MICB, black profiles). Open profiles are immunoglobulin isotype control stainings. **B** By blot hybridization, *MICA* mRNA was expressed in AGS and KATO III cells (upper panel). Lower panel shows glyceraldehyde 3-phosphate dehydrogenase (*GADPH*) control mRNA. **C** Immunoprecipitation and SDS-PAGE failed to detect MICA protein in [³⁵S]-methionine-labeled AGS and KATO III cells (Groh et al. 1996). Bottom panel shows control major histocompatibility complex class I (*MHC-I*) precipitations using mAb W6/32 (Parham et al. 1979). Immunocomplexes were treated with poly *N*-glycanase F

Steinle et al. 1998). Expression of cloned *MICA010* cDNA failed to produce significant amounts of surface MICA on numerous isolates of stably transfected C1R cells that were screened by flow cytometry, using mAbs specific for epitopes in the $\alpha 1\alpha 2$ (mAbs 2C10 and 6D4) or $\alpha 3$ domains of MICA (mAb 6D5) (Fig. 2C) (Groh et al. 1996, 1998). However, reversal of the proline substitution to arginine, by exchange of a 5'-end *SalI*-*Eco0109I* restriction fragment from *MICA004* cDNA, which differs at no other position in the $\alpha 1\alpha 2$ domains, restored surface expression of MICA on transfected C1R and KATO III cells (Fig. 2C). Thus, the single proline substitution abolished expression of the *MICA010* allele. In the crystal structure of MICA, this substitution blocks a β -sheet hydrogen bond with the histidine carbonyl at position 27 on the $\beta 2$ strand (Li et al. 1999). Moreover, this substitution is incompatible with β -sheet secondary structure, thus likely interfering with protein folding.

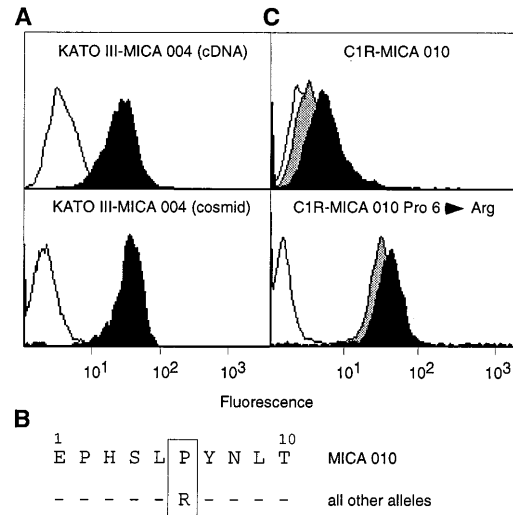


Fig. 2A-C AGS and KATO III cells express a single defective allele of *MICA*. **A** KATO III cells were able to express MICA after stable transfection with a cDNA or cosmid (cosmid M17A; Bahram et al. 1994) encoding *MICA004*. Fluorescence profiles show transfected (filled) and nontransfected (open) cells stained with mAb 2C10. **B** AGS and KATO III *MICA* mRNA corresponds to a single allele, *MICA010*, which has a proline for arginine substitution at position 6 in the $\alpha 1$ domain. **C** No significant expression of MICA was observed with numerous C1R cells stably transfected with *MICA010* cDNA cloned by reverse transcription-polymerase chain reaction from KATO III cells. Reversal of the proline to arginine substitution and transfection restored expression. Cells were stained with mAb 2C10 (black profiles) or mAb 6D4 (gray profiles). Open profiles are stainings of untransfected cells

There are only limited data on the frequencies of *MICA010* in human populations. In a study population of 242 Caucasians, the frequency of *MICA010* was 5% (Petersdorf et al. 1999), and among 114 unrelated Japanese, 12.5% (Komatsu-Wakui et al. 1999). In homozygotes, loss of MICA function may or may not be compensated by MICB, thus leaving open the question of potential immunological consequences in such individuals. However, *MICA010* is not the only loss-of-expression variant identified. The entire *MICA* gene appears to be deleted in Japanese individuals with an *HLA-B*4801* haplotype (Komatsu-Wakui et al. 1999). Interestingly, some of these also have a nonfunctional *MICB* gene due to a premature stop codon (Ando et al. 1997). This *MICA* and *MICB* loss haplotype occurs at a frequency of about 3.8% in Japanese (Komatsu-Wakui et al. 1999). Homozygous individuals are healthy, with no deficiency being immediately apparent. Thus, expression of MICA/B may not be essential for overall immunological fitness but may complement, and be redundant with, other arms of immune defense. However, subtle consequences of loss of *MICA* and/or *MICB* may become observable with knowledge of the physiological significance of these molecules and their interactions with NK and T cells. Information on expression variants of *MICA* and *MICB* may prove useful in that regard.

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