Monoclonal Antibody Blockade of the Human Eag1 Potassium Channel Function Exerts Antitumor Activity

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Abstract

The potassium channel ether α-go-go has been directly linked to cellular proliferation and transformation, although its physiologic role(s) are as of yet unknown. The specific blockade of human Eag1 (hEag1) may not only allow the dissection of the role of the channel in distinct physiologic processes, but because of the implication of hEag1 in tumor biology, it may also offer an opportunity for the treatment of cancer. However, members of the potassium channel superfamily are structurally very similar to one another, and it has been notoriously difficult to obtain specific blockers for any given channel. Here, we describe and validate the first rational design of a monoclonal antibody that selectively inhibits a potassium current in intact cells. Specifically blocking hEag1 function using this antibody inhibits tumor cell growth both in vitro and in vivo. Our data provide a proof of concept that enables the generation of functional antagonistic monoclonal antibodies against ion channels with therapeutic potential. The particular antibody described here, as well as the technique developed to make additional functional antibodies to Eag1, makes it possible to evaluate the potential of the channel as a target for cancer therapy. [Cancer Res 2007;67(15):7343–9]

Introduction

There is compelling evidence that potassium channels play an important role in fundamental cellular processes such as excitability, muscle contraction, cell cycle progression, and cellular proliferation (1–3). Human Eag1 (hEag1) Kv10.1 in the International Union of Pharmacology nomenclature; ref. (4), encoded by the KCNH1 gene) is a voltage-gated potassium channel modulated throughout the cell cycle (5, 6) and has been suggested to be involved in tumorigenesis. It has been shown that ectopic expression of hEag1 favors tumor progression when transfected cells are injected in immunodepressed mice (7). Conversely, antisense or RNAi-mediated inhibition of hEag1 expression in tumor cell lines causes extensive reduction of cell proliferation (7, 8). Similarly, inhibition of hEag1-mediated currents by nonselective channel blockers like imipramine and astemizole has been suggested to decrease cell proliferation in melanoma and breast cancer cells (9, 10). In addition, the expression of human hEag1 has been detected in many tumor cell lines in vitro and in tumor tissues from cancer patients across all major tumor types (11–13), whereas the normal expression of hEag1 in healthy human tissues is preferentially confined to the central nervous system (7, 12, 14). These observations prompt the possibility that hEag1 channels participate in the progression of the malignant disease and thus represent a valid target for therapeutic intervention. A vast number of unspecific and nonselective drugs that modulate the activity of various types of potassium channels are available. However, the homogeneous structural features of the entire voltage-gated potassium channel superfamily make it difficult to identify selective blockers (15). Specifically, the closest homologue of hEag1 is human Eag2 (16), which displays 73% amino acid sequence identity with hEag1, the highest divergence being concentrated within the cytoplasmic COOH termini (16, 17). Moreover, an important member of the EAG channel family is the human ether α-go-go–related channel (HERG; ref. 18), the inhibition of which triggers well-characterized and dangerous cardiac consequences (19). Consequently, selectivity is a crucial feature for any potential anti-hEag1 therapy, as all currently known hEag1 blockers inhibit HERG to various degrees (20, 21).

Monoclonal antibodies represent a strategy to generate highly selective inhibitors against cell surface molecules, enabling a specific antigen to be distinguished from its closest homologues. Some polyclonal sera have been produced that effectively inhibit potassium currents in intact cells (15, 22). Unfortunately, polyclonal antibodies have the disadvantage that even after a serum has successfully been generated, there is no guarantee that another effective blocker can be produced using the same strategy (23, 24). The exquisite selectivity of monoclonal antibodies, however, could be exploited to generate molecules with the required target specificity, and advantageously, rational design processes can be incorporated into their development. Additionally, monoclonal antibodies can generally be produced in a recombinant system and modified to render them usable for therapeutic approaches. Therefore, we have designed a rational approach to produce the first monoclonal antibody that specifically inhibits a potassium channel in intact cells and thereby exerts antitumor effects.

Materials and Methods

Electrophysiology. For electrophysiologic experiments, monoclonal HEK293 cells expressing hEag1 (21) were grown for 24 to 72 h on poly-L-lysine–coated glass coverslips. All electrophysiologic experiments were done at room temperature. Macroscopic currents were recorded in the whole-cell configuration of the patch-clamp technique using an EPC-9 amplifier and Pulse software (HEKA). Patch pipettes with a tip resistance of 1.5 to 2 MΩ were made from Corning no. 0010 capillary glass (WPI). The internal solution contained 100 mmol/L of KCl, 45 mmol/L of N-methyl-D-glucamine, 10 mmol/L of 1,2-bis(2-aminoxyethane-N,N,N-triacetate) acid tetrapotassium salt (BAPTA-K4), and 10 mmol/L of HEPES/HC1 (pH 7.35). The control external solution contained 160 mmol/L of
NaCl, 2.5 mmol/L of KCl, 2 mmol/L of CaCl₂, 1 mmol/L of MgCl₂, 8 mmol/L of glucose, and 10 mmol/L of HEPES/NaOH (pH 7.4). Series resistance was determined using the automated capacity compensation of the amplifier and compensated by 60% to 80%. Data were analyzed using PulseFit and IgorPro (WaveMetrics). Data shown in text and legends represent mean ± SE for the indicated number of experiments. Statistical analysis was done using Student’s *t* test for a two-tailed distribution.

**Immunofluorescence.** Immunofluorescence was done on transfected CHO-K1 and HEK293 cells grown on glass coverslips. Cells were washed thrice with TBS (150 mmol/L NaCl, 20 mmol/L Tris-HCl; pH 7.5), fixed with 4% *p*-formaldehyde (4 °C for 4 min), and permeabilized with 1% Triton X-100 in TBS for 10 min. Nonspecific binding was blocked with 10% bovine serum albumin in TBS for 30 min. Primary antibody (1 μg/mL) incubation was done at room temperature for 2 h. AlexaFluor 546–labeled anti-mouse IgG antibody (Molecular Probes) was used as a secondary antibody. The coverslips were mounted using ProLong (Molecular Probes) and observed in a Zeiss LSM 510 laser-scanning confocal microscope.

**Site-directed mutagenesis.** Mutations on the epitope sequence of hEag1 were introduced with the QuickChange XL site-directed mutagenesis kit (Stratagene) using primers with the sequences: 5'-CAGTTTAATGGG-TCTGCCGGGATTTGGGAAGGTGGTCC and 5'-GGACCACCTTCCCAAATC-CCGGCAGACCCATTAAACTG. Afterwards, the complete coding sequence was confirmed to discard additional mutations.

** Colony formation assay.** Cells were preincubated with the corresponding antibody or vehicle and resuspended in 50 μL of 0.25% Noble agar (Difco) containing OptiMEM and 0.5% FCS. The suspension was plated on an agarose underlayer (OptiMEM with 20% FCS and 0.5% agarose, 50 μL) in quadruplicate wells of a 96-well plate. A 50 μL feeding layer (OptiMEM with 0.5% FCS) was plated on top of each well. Colonies were allowed to grow in the presence of antibody for 7 to 8 days and then stained with 50 μL of 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide (1 mg/mL in PBS) for 3 to 6 h. Viable colonies develop blue color through metabolization of 3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide and are thereby readily detectable. Wells were scanned in a Leica TCS Scanalyzer 3D System and the number of colonies was counted using the corresponding software.

**Animal experiments.** For in vivo tumor growth inhibition studies, we used xenograft implants in immunodeficient mice. In the MDA-MB-435S human breast cancer model, female CB17 Fox Chase severe combined immunodeficiency (SCID) mice (~20 g body weight) were implanted with 10⁷ cells in 200 μL of PBS. After measurable tumors developed, the animals were randomized into groups of 10 individuals with comparable average tumor size and body weight. After randomization, a loading mAb56 dose of 50 mg/kg, followed by weekly doses of 25 mg/kg was administered i.p. A negative control group received the same volume of PBS. As a positive control, cyclophosphamide (6.25 mg/kg) was administered orally. Tumor size was determined twice a week, always by the same operator, and tumor volume was estimated by multiplying the larger diameter by the square of the shorter diameter and the correction factor 0.52.

For the human pancreas carcinoma model PAXF1657, two groups of tumor-bearing nude mice (10 mice/group) received mAb56 or mAb33 i.p. at a loading dose of 50 mg/kg/d and follow-up dosing of 25 mg/kg/d on days 4,
Antibody generation. For the optimal immunogen design, we compared the sequences of hEag1, hEag2, and HERG in order to avoid cross-reactivity. We then concentrated on two regions of the channel, the linker between the fifth and sixth putative transmembrane segments (segment E3; Fig. 1A; ref. 15), and the COOH-terminal end. The E3 segment was chosen under the assumption that it should be the area closest to the ion permeation route from the extracellular side. This region has been successfully used to generate polyclonal antibodies against several ion channels (15, 22). The COOH-terminal end of the hEag1, putatively intracellular, should not play a direct role in the generation of a functional antibody, but it contains a segment that induces tetramerization (the tetramerizing coiled-coil; refs. 25, 26). This would mimic the structure of the natural channel because hEag1 is, like most potassium channels, a tetramer. The three-dimensional structure of the antigen can be very important in the immune process (27).

We thus generated a fusion protein containing two domains (Fig. 1A), residues 374 to 452, including the E3 segment, and residues 872 to 932, including the tetramerizing coiled-coil.

After immunization with this fusion protein and the generation of hybridomas using standard procedures (12), we defined a multilevel selection protocol to screen for functional antibodies. First, the supernatants showing highest affinity for the recombinant antigen in ELISA assays were tested by surface plasmon resonance (SPR; ref. 28) to determine which part of the immunogen contained the epitope. Those recognizing the E3 region were subsequently tested for their ability to distinguish between...
epitopes from hEag1 and hEag2 in ELISA and SPR. The hybridomas that qualified were then tested for functional inhibition of hEag1 currents in Xenopus oocytes (29). Only one of the supernatants (mAb56) reduced hEag1 currents significantly. The hybridoma was then re-cloned and the antibody produced was purified by double affinity chromatography (protein A and specific antigen). We then proceeded to a more detailed characterization of the properties of this particular antibody.

**Antibody characterization.** Epitope mapping using an array of overlapping peptides spanning the complete region of interest revealed that the region recognized by mAb56 was linear and corresponds to the sequence: GSGSGKWEG. Alignments to hEag2 (Fig. 1A) show that only four residues in the epitope are conserved between the two channels. BLAST searches using the epitope sequence did not reveal significant similarity with any other protein. When the performance of mAb56 was tested in immunofluorescence, we found clear positive signals in CHO, HEK293, and NIH3T3 cells expressing hEag1, which could be completely blocked by preincubation of the antibody with an excess of the peptide corresponding to the mAb56 epitope (Fig. 1B).

No signal was detected in immunofluorescence experiments on HEK293 cells overexpressing either hEag2 (Fig. 1C) or a mutant hEag1 channel derivative in which the mAb56 epitope had been mutated to the hEag2 sequence (Fig. 1D). Additionally, we have found no evidence for nonspecific bands using mAb56 in Western blots, although the antibody's sensitivity is relatively low in this assay. The lack of cross-reactivity in SPR, together with the low sequence similarity of the epitope and the immunofluorescence results, suggest a specific interaction with hEag1.

**Effects of mAb56 on hEag1 electrophysiology.** We subsequently tested the ability of mAb56 to inhibit hEag1 current expressed in HEK293 cells using whole-cell patch clamp (30). Superfusion of mAb56 (45 µg/mL, ~300 nmoi/L) induced an inhibition of ~40% of the current amplitude in 10 min (Fig. 2A), a period of time that did not induce remarkable rundown in the absence of the antibody. Both in HEK293 cells and in Xenopus oocytes, activation of the channel was required to observe antibody-mediated inhibition. When the cells were preincubated for 10 min after the addition of the antibody, and before applying a depolarizing pulse, the current amplitude was unaffected, indicating voltage-dependence of the blocking effect of the antibody (data not shown).

The ability to inhibit the ionic current is specific to mAb56. Another monoclonal antibody (mAb62; refs. 12, 31) raised against
the same region, and whose epitope is located only 23 residues upstream of that of mAb56 (Fig. 1A), failed to reduce the hEag1 current under the same conditions (Fig. 2). Sequential application of the antibodies revealed that mAb56 effectively reduced the current amplitude in cells that had shown no response to mAb62 (Fig. 2B), although mAb62 was able to bind to the channels in intact cells, as shown in immunofluorescence experiments (Fig. 2B, inset). These results strongly indicate that antibody recognition of the E3 region was necessary but not sufficient to achieve channel inhibition (15). Thus, some additional features were required to obtain functional antibodies. The slow time course of the block could follow the combination of a limited diffusion rate due to the relatively large molecular weight of the antibody, and the need for depolarization to achieve the block because pulses were applied at a frequency of 3 Hz.

Current inhibition by mAb56 showed dose-dependence. Because each antibody concentration required long incubation periods to reach steady state (at least 10 min), and because of the large amounts of antibody required for these experiments, we only estimated the concentration for half-maximal inhibition. A free fit of the average inhibition using the Hill equation gave an IC_{50} value of mAb56 in HEK293 cells of 73 ± 47 nmol/L (Fig. 2C).

Table 1. Overall level of inhibition mediated by mAb56 at the indicated concentration in different human tumor cell lines of various origins

<table>
<thead>
<tr>
<th>Origin</th>
<th>Cell line</th>
<th>Inhibition of colony formation (%)</th>
<th>Concentration (nmol/L)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Breast carcinoma</td>
<td>MDA-MB-435s</td>
<td>60</td>
<td>66</td>
</tr>
<tr>
<td></td>
<td>NCI-ADR</td>
<td>25</td>
<td>166</td>
</tr>
<tr>
<td>Melanoma</td>
<td>HT144</td>
<td>35</td>
<td>133</td>
</tr>
<tr>
<td></td>
<td>C8161</td>
<td>25</td>
<td>133</td>
</tr>
<tr>
<td></td>
<td>SKMe12</td>
<td>35</td>
<td>133</td>
</tr>
<tr>
<td>Ovarian carcinoma</td>
<td>SKOV3</td>
<td>40</td>
<td>133</td>
</tr>
<tr>
<td></td>
<td>OVCAR-3</td>
<td>25</td>
<td>133</td>
</tr>
<tr>
<td></td>
<td>SKOV-6</td>
<td>35</td>
<td>266</td>
</tr>
<tr>
<td></td>
<td>OVCAR-8</td>
<td>25</td>
<td>133</td>
</tr>
<tr>
<td>Cervical carcinoma</td>
<td>HeLa</td>
<td>40</td>
<td>133</td>
</tr>
<tr>
<td>Pancreas carcinoma</td>
<td>BxPC3</td>
<td>20–25</td>
<td>133</td>
</tr>
<tr>
<td>Colon carcinoma</td>
<td>HT29</td>
<td>30</td>
<td>66</td>
</tr>
<tr>
<td>Fibrosarcoma</td>
<td>HT1080</td>
<td>30–40</td>
<td>133</td>
</tr>
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</table>
To show that the effects of mAb56 depend on specific binding to the channel through the complementarity-determining regions, we measured the current amplitude in the presence of mAb56 that had been preincubated with a molar excess of a peptide with the sequence of the corresponding epitope (Fig. 2D). This treatment abolished the effects of mAb56 on hEag1 currents, indicating that the inhibition of the current was mediated by binding through the complementarity-determining regions and was therefore specific. Preincubation with a peptide with the mAb62 epitope sequence did not have any effect (Fig. 2D).

mAb56 blocks the native hEag1 current in neuroblastoma cells. To determine if mAb56 also blocks native currents and not only heterologously expressed channels, we selected the human neuroblastoma cell line SH-SY5Y. Eag1 and Eag2 show a remarkable dependence of the activation time constant on the prepulse potential (Cole-Moore shift). The magnitude of this shift is so unique that it can be taken as unequivocal identification of the current carried by Eag1 and Eag2. The potassium currents recorded from SH-SY5Y cells clearly show this property (32) and are reduced by antisense oligonucleotides (7). These cells abundantly express hEag1 mRNA, but no RNA encoding hEag2 is detectable. Therefore, native homomeric hEag1 channels are probably responsible for the observed currents. These endogenous hEag1 currents (Fig. 3A) were also inhibited by ~45% after 5 min of mAb56 perfusion (300 nmol/L), indicating that not only heterologously expressed, but also native hEag1 can be inhibited by mAb56.

mAb56 does not affect currents through HERG channels. Because HERG blockade is a major concern for all potential pharmacologic compounds and, even more acutely, for ion channel blockers (19), we tested whether mAb56 affects the amplitude of currents flowing through HERG channels.

Perfusion of mAb56 (~300 nmol/L) did not show any reduction on HERG currents expressed in HEK293 cells (Fig. 3B), showing that mAb56 selectively blocks ion channel flow mediated by hEag1 but not by HERG. Note that the small reduction in current seen in Fig. 3B is probably mere rundown because it occurs at the same rate in the presence or absence of antibody.

Therefore, mAb56 is the only known molecule able to inhibit hEag1 whereas leaving HERG unaffected. This finding reinforces the concept that monoclonal antibodies may represent an alternative to traditional ion channel blockers when blockade of a related molecule represents a concern.

mAb56 inhibits the growth of tumor cells. To analyze the biological consequences of hEag1 blockade by mAb56, we tested the effects of mAb56 on tumor cell growth under nonadherent culture conditions. The ability of tumor cells to form colonies in soft agar is an indication for the transformation of the cells because anchorage-independent cell growth is characteristic of tumor cells. As shown in Fig. 4A, mAb56 significantly impaired the ability of SKOV3 ovarian carcinoma cells to form colonies in soft agar in a concentration-dependent manner (Fig. 4B). The addition of PBS, a control isotype antibody (c-2b) or another monoclonal antibody against the COOH-terminal region of hEag1 (mAb33) did not influence colony formation (Fig. 4C), suggesting that mAb56-mediated hEag1 blockade exerts antiproliferative activity in vitro.

Similar experiments were done in several tumor cell lines from different types of cancer (all of which express abundant hEag1). mAb56 extensively reduced growth in all tested lines (Table 1). Together with the exquisite specificity against hEag1 shown by mAb56, these results reinforce the concept that hEag1 exerts a role in the proliferation of tumor cells.
anti-Eag1 antibody treatment was as efficacious as standard chemotherapy in reducing tumor growth (Fig. 5A). It should be noted that mAb56, which is cross-reactive with mouse and rat Eag1 (data not shown), did not cause any obvious side effects like weight loss or neurologic abnormalities in treated animals. In contrast with MDA-MB-435S xenografts, anti-Eag1 antibodies were not efficacious in SKOV3 ovarian cancer and BxPC3 pancreatic cancer xenograft studies (data not shown). It is interesting to note that the loading dose of 50 mg/kg, which represents 1 mg of antibody for a 20 g animal, will probably render plasma concentrations <20 mg/mL, which corresponds to the 300 nmol/L used in electrophysiology; further dosage exploration will be required in these models. Furthermore, at least in case of BxPC3 tumor cells, the lack of an in vivo antitumor effect correlated with very low expression levels of hEag1 in the xenograft tissue, which did not match the expression levels detected in vitro (data not shown).

We further investigated the antitumor activity of mAb56 in a primary model of human cancer. PAXF1657 tumors were derived directly from a human pancreatic cancer patient and were maintained continuously as s.c. xenografts in nude mice. Thus, PAXF1657 xenografts are assumed to closely resemble the malignant pancreatic cancer phenotype observed in the clinic. PAXF1657-bearing mice were treated with mAb56 and mAb33 (as a control) at a loading dose of 50 mg/kg followed by doses of 25 mg/kg on days 4, 7, and 11 of the study (i.p. injections). In this case, gemcitabine was included as a positive control. In this experiment, mAb56 inhibited tumor progression consistently in the range of 30% to 40% throughout the study duration (Fig. 5B). These results were confirmed in an additional independent PAXF1657 animal study (data not shown). These results further substantiate our finding that mAb56-mediated hEag1 ion channel current blockade exerts antitumor activity in vivo.

In conclusion, we have designed a rational strategy to generate a monoclonal antibody that functionally recognizes hEag1 ion channel protein and potently reduces hEag1 ion channel current. This strategy, which should be generally applicable, has produced the first monoclonal antibody able to inhibit an ion channel current in intact cells. The antibody is highly selective and does not bind to hEag2. Importantly, mAb56 does not affect HERG current. Therefore, mAb56 represents the first specific inhibitor of the hEag1 channel and will serve as a unique tool to elucidate the role of hEag1 channels in physiologic and pathologic processes. In addition, by blocking hEag1 ion channel activity, mAb56 effectively impairs tumor cell growth in vitro and in vivo, confirming the link between hEag1 expression and the proliferation properties of cancerous cells and tumor growth.

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References

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