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(54) **DIAGNOSIS OF MALIGNANT NEOPLASMS**

DIAGNOSE VON MALIGNEN NEOPLASMEN

DIAGNOSTIC DE TUMEURS MALIGNES

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- **INCE N ET AL: "Overexpression of human aspartyl (asparaginyl) beta - hydroxylase is associated with malignant transformation." CANCER RESEARCH, (2000 MAR 1) 60 (5) 1261-6., XP001002102**

Remarks:

The file contains technical information submitted after the application was filed and not included in this specification

Description

[0001] The present invention relates to an ex vivo method for diagnosing a malignant neoplasm in a mammal. The present invention also comprehends an ex vivo method of prognosis of such a malignant neoplasm.

[0002] Primary malignant central nervous system (CNS) neoplasms, particularly glioblastomas, are highly fatal due to their aggressive and widespread infiltration of the brain and resistance to anti-cancer treatments. Although progress has been made in unraveling the pathological mechanisms underlying CNS cancers as well as other cancer types, tumor specific therapeutic approaches and methods of diagnosis have been largely elusive.

[0003] Lavaissiere, et al. (J. Clin. Invest., 1996; 98(6):1313-1323) disclose that aspartyl (asparaginyl) beta-hydroxylase (AAH) is expressed on the cell surface of a number of hepatocellular caranomas and cholangiocarcinamas. Lavaissiere, et al. disclose the sequence of cDNA encoding human AAH and the deduced amino acid sequence and the production of monoclonal antibodies to such HAAH.

[0004] According to one aspect of the present invention there is provided a method for diagnosing a malignant neoplasm in a mammal as claimed in claim 1 below.

[0005] Malignant neoplasms detected in this manner include those derived from endodermal tissue, e.g., colon cancer, breast cancer, pancreatic cancer, liver cancer, and cancer of the bile ducts. Neoplasms of the central nervous system (CNS) such as primary malignant CNS neoplasms of both neuronal and glial cell origin and metastatic CNS neoplasms are also detected. Bodily fluids such as a CNS-derived bodily fluid, blood, serum, urine, saliva, sputum, lung effusion, and ascites fluid, may be contacted with an HAAH-specific antibody in accordance with the invention.

[0006] The assay format is also useful to generate temporal data used for prognosis of malignant disease.

[0007] According to another aspect of the present invention therefore there is provided a method of prognosis of a malignant neoplasm as claimed in claim 2 below.

[0008] The antibody preferably binds to a site in the carboxyterminal catalytic domain of HAAH. Alternatively, the antibody binds to an epitope that is exposed on the surface of the cell. The antibody is a polyclonal antisera or monoclonal antibody. The invention encompasses the use of not only an intact monoclonal antibody, but also of an immunologically-active antibody fragment, e. g. , a Fab or $(Fab)_2$ fragment; an engineered single chain Fv molecule; or a chimeric molecule, e.g., an antibody which contains the binding specificity of one antibody, e.g., of murine origin, and the remaining portions of another antibody, e.g., of human origin. Preferably the antibody is a monoclonal antibody such as FB50, 5C7, 5E9, 19B, 48A, 74A, 78A, 86A, HA238A, HA221, HA 239, HA241, HA329, or HA355. Antibodies which bind to the same epitopes as those monoclonal antibodies are also within the invention.

[0009] An HAAH-specific intrabody is a recombinant single chain HAAH-specific antibody that is expressed inside a target cell, e.g., tumor cell. Such an intrabody binds to endogenous intracellular HAAH and inhibits HAAH enzymatic activity or prevents HAAH from binding to an intracellular ligand. HAAH-specific intrabodies inhibit intracellular signal transduction, and as a result, inhibit growth of tumors which overexpress HAAH.

[0010] A further embodiment relates to the in vitro use of a kit as claimed in independent claim 12.

[0011] Disclosed is also a kit for diagnosis of a tumor in a mammal contains an HAAH-specific antibody. The diagnostic assay kit is preferentially formulated in a standard two-antibody binding format in which one HAAH-specific antibody captures HAAH in a patient sample and another HAAH-specific antibody is used to detect captured HAAH. For example, the capture antibody is immobilized on a solid phase, e.g., an assay plate, an assay well, a nitrocellulose membrane, a bead, a dipstick, or a component of an elution column. The second antibody, i.e., the detection antibody, is typically tagged with a detectable label such as a colorimetric agent or radioisotope.

[0012] HAAH is a protein belonging to the (alpha-ketoglutarate dependent dioxygenase family of prolyl and lysyl hydroxylases which play a key role in collagen biosynthesis. This molecule hydroxylates aspartic acid or asparagine residues in EGF-like domains of several proteins in the presence of ferrous iron. These EGF-like domains contain conserved motifs, that form repetitive sequences in proteins such as clotting factors, extracellular matrix proteins, LDL receptor, NOTCH homologues, or NOTCH ligand homologues.

[0013] The alpha-ketoglutarate-dependent dioxygenase aspartyl (asparaginyl) beta-hydroxylase (AAH) specifically hydroxylates one aspartic or asparagine residue in EGF-like domains of various proteins. The 4.3-kb cDNA encoding the human AspH (hAspH) hybridizes with 2.6 kb and 4.3 kb transcripts in transformed cells, and the deduced amino acid sequence of the larger transcript encodes an protein of about 85 kDa. Both *in vitro* transcription and translation and Western blot analysis also demonstrate a 56-kDa protein that may result from posttranslational cleavage of the catalytic C-terminus.

[0014] A physiological function of AAH is the post-translational beta-hydroxylation of aspartic acid in vitamin K-dependent coagulation proteins. However, the abundant expression of AAH in several malignant neoplasms, and low levels of AAH in many normal cells indicate a role for this enzyme in malignancy. The AAH gene is also highly expressed in cytotrophoblasts, but not syncytiotrophoblasts of the placenta. Cytotrophoblasts are invasive cells that mediate placental implantation. The increased levels of AAH expression in human cholangiocarcinomas, hepatocellular carcinomas, colon cancers, and breast carcinomas were primarily associated with invasive or metastatic lesions. Moreover, overexpression

of AAH does not strictly reflect increased DNA synthesis and cellular proliferation since high levels of AAH immunoreactivity were observed in 100 percent of cholangiocarcinomas, but not in human or experimental disease processes associated with regeneration or nonneoplastic proliferation of bile ducts. AAH overexpression and attendant high levels of beta hydroxylase activity lead to invasive growth of transformed neoplastic cells. Detection of an increase in HAAH expression is useful for early and reliable diagnosis of the cancer types which have now been characterized as overexpressing this gene product.

Diagnosis of malignant tumors

[0015] HAAH is overexpressed in many tumors of endodermal origin and in at least 95% of CNS tumors compared to normal noncancerous cells. An increase in HAAH gene product in a patient-derived bodily fluid may be detected according to the present invention using standard methods, e.g., by Western blot assays or a quantitative assay such as ELISA. For example, a standard competitive ELISA format using an HAAH-specific antibody is used to quantify patient HAAH levels. Alternatively, a sandwich ELISA using a first antibody as the capture antibody and a second HAAH-specific antibody as a detection antibody is used.

[0016] Methods of detecting HAAH include contacting a component of a bodily fluid with an HAAH-specific antibody bound to solid matrix, e.g., microtiter plate, bead, dipstick. For example, the solid matrix is dipped into a patient-derived sample of a bodily fluid, washed, and the solid matrix is contacted with a reagent to detect the presence of immune complexes present on the solid matrix.

[0017] Proteins in a test sample are immobilized on (e.g., bound to) a solid matrix. Methods and means for covalently or noncovalently binding proteins to solid matrices are known in the art. The nature of the solid surface may vary depending upon the assay format. For assays carried out in microtiter wells, the solid surface is the wall of the microtiter well or cup. For assays using beads, the solid surface is the surface of the bead. In assays using a dipstick (i.e., a solid body made from a porous or fibrous material such as fabric or paper) the surface is the surface of the material from which the dipstick is made. Examples of useful solid supports include nitrocellulose (e.g., in membrane or microtiter well form), polyvinyl chloride (e.g., in sheets or microtiter wells), polystyrene latex (e.g., in beads or microtiter plates, polyvinylidine fluoride (known as IMMULON™), diazotized paper, nylon membranes, activated beads, and Protein A beads. The solid support containing the antibody is typically washed after contacting it with the test sample, and prior to detection of bound immune complexes. Incubation of the antibody with the test sample is followed by detection of immune complexes by a detectable label. For example, the label is enzymatic, fluorescent, chemiluminescent, radioactive, or a dye. Assays which amplify the signals from the immune complex are also known in the art, e.g., assays which utilize biotin and avidin.

[0018] An HAAH-detection reagent, e.g., an antibody, is packaged in the form of a kit, which contains one or more HAAH-specific antibodies, control formulations (positive and/or negative), and/or a detectable label. The assay may be in the form of a standard two-antibody sandwich assay format known in the art.

[0019] Anti-HAAH antibodies may be obtained by techniques well known in the art. Such antibodies are polyclonal or monoclonal. Polyclonal antibodies may be obtained using standard methods, e.g., by the methods described in Ghose et al., Methods in Enzymology, Vol. 93, 326-327, 1983. An HAAH polypeptide, or an antigenic fragment thereof, was used as the immunogen to stimulate the production of polyclonal antibodies in the antisera of rabbits, goats, sheep, or rodents. Antigenic polypeptides for production of both polyclonal and monoclonal antibodies useful as immunogens include polypeptides which contain an HAAH catalytic domain. For example, the immunogenic polypeptide is the full-length mature HAAH protein or an HAAH fragment containing the carboxyterminal catalytic domain e.g., an HAAH polypeptide containing the His motif of SEQ ID NO: 1.

Table 1: Amino acid sequence of HAAH

MAQRKNAKSS GNSSSSGSGS GSTSAGSSSP GARRETKHGG HKNGRKGGLS GTSFFTWFMV 61
IALLGVWTSV AVVWFDLVDY EEVLGKLGIY DADGDGDFDV DDAKVLLGLK ERSTSEPAVP 121
PEEAEPHTEP EEQVPVEAEP QNIEDEAKEQ IQSLLHEMVH AEHVEGEDLQ QEDGPTGEPQ 181
QEDDEFLMAT DVDDRFETLE PEVSHEETEH SYHVEETVSQ DCNQDMEEMM SEQENPDSSE 241
PVVEDERLHH DTDDVTYQVY EEQAVYEPLE NEGIEITEVT APPEDNPVED SQVIVEEVSI 301
FPVEEQQEVP PETNRKTDDP EQKAKVKKKK PKLLNKFDKT IKAELDAAEK LRKRGKIEEA 361
VNAFKELVRK YPQSPRARYG KAQCEDDLAE KRRSNEVLRG AIETYQEVAS LPDVPADLLK 421
LSLKRRSDRQ QFLGHMRGSL LTLQRLVQLF PNDTSLKNDL GVGYLLIGDN DNAKKVYEEV 481
LSVTPNDGFA KVHYGFILKA QNKIAESIPY LKEGIESGDP GTDDGRFYFH LGDAMQRVGN 541
KEAYKWYELG HKRGHFASVW QRSLYNVNGL KAQPWWTPKE TGYTELVKSL ERNWKLIRDE 601
GLAVMDKAKG LFLPEDENLR EKGDWSQFTL WQQGRRNENA CKGAPKTCTL LEKFPETTGC 661
RRGQIKYSIM HPGTHVWPHT GPTNCRLRMH LGLVIPKEGC KIRCANETRT WEEGKVLIFD 721
DSFEHEVWQD ASSFRLIFIV DVWHPELTPQ QRRSLPAI (SEQ ID NO:2; GENBANK Accession No. S83325; His motif is underlined; conserved sequences within the catalytic domain are designated by bold type)

[0020] Antibodies which bind to the same epitopes as those antibodies disclosed herein are identified using standard methods, e.g., competitive binding assays, known in the art.

[0021] Monoclonal antibodies may be obtained by standard techniques. Ten μg of purified recombinant HAAH polypeptide was administered to mice intraperitoneally in complete Freund's adjuvant, followed by a single boost intravenously (into the tail vein) 3-5 months after the initial inoculation. Antibody-producing hybridomas were made using standard methods. To identify those hybridomas producing antibodies that were highly specific for an HAAH polypeptide, hybridomas were screened using the same polypeptide immunogen used to immunize. Those antibodies which were identified as having HAAH-binding activity are also screened for the ability to inhibit HAAH catalytic activity using the enzymatic assays described below. Preferably, the antibody has a binding affinity of at least about 10^8 liters/mole and more preferably, an affinity of at least about 10^9 liters/mole.

[0022] Monoclonal antibodies may be humanized by methods known in the art, e.g, MAbs with a desired binding specificity can be commercially humanized (Scotgene, Scotland; Oxford Molecular, Palo Alto, CA).

[0023] HAAH-specific intrabodies are produced as follows. Following identification of a hybridoma producing a suitable monoclonal antibody, DNA encoding the antibody is cloned. DNA encoding a single chain HAAH-specific antibody in which heavy and light chain variable domains are separated by a flexible linker peptide is cloned into an expression vector using known methods (e.g., Marasco et al., 1993, Proc. Natl. Acad. Sci. USA 90:7889-7893 and Marasco et al., 1997, Gene Therapy 4:11-15). Such constructs are introduced into cells, e.g., using standard gene delivery techniques for intracellular production of the antibodies. Intracellular antibodies, i.e., intrabodies, are used to inhibit signal transduction by HAAH. Intrabodies which bind to a carboxyterminal catalytic domain of HAAH inhibit the ability of HAAH to hydroxylate EGF-like target sequences.

[0024] Methods of linking HAAH-specific antibodies (or fragments thereof) which bind to cell surface exposed epitopes of HAAH on the surface of a tumor cell are linked to known cytotoxic agents, e.g, ricin or diptheria toxin, using known methods.

[0025] Following is a description by way of example only with reference to the accompanying drawings of materials and methodologies that may be made in the present invention.

[0026] In the drawings:

Fig. 1 is a bar graph showing colony formation induced by transient transfection of NIH-3T3 cells with various aspartyl (asparaginyl) beta-hydroxylase (AAH) cDNAs. Colony formation was induced by transient transfection with 10 μg DNA. In contrast, the mutant murine AAH construct without enzymatic activity has no transforming activity. The data is presented as mean number of transformed foci ± SEM.

Fig. 2 is a bar graph showing the results of a densitometric analysis of a Western blot assay of proteins produced by various murine AAH stably transfected cell clones. In clones 7 and 18, there was a modest increase in HAAH gene expression, while the overexpression was to a lesser degree in clone 16.

Figs. 3A-B are bar graphs showing colony formation in soft agar exhibited by HAAH stably transfected clones compared to HAAH enzymatic activity. Fig. 3A shows a measurement of murine AAH enzymatic activity in clones

7, 16 and 18, and Fig. 3B shows colony formation exhibited by clones 7, 16 and 18. Data is presented as mean number of colonies 10 days after plating ± SEM. All three clones with modest increases in HAAH enzymatic activity, that correlated with protein expression, exhibited anchorage independent growth.

Fig. 4 is a bar graph showing tumor formation in nude mice injected with transfected clones overexpressing murine AAH. Tumor growth was assessed after 30 days. Mean tumor weight observed in mice injected with clones 7, 16 and 18 as compared to mock DNA transfected clone. All animals, which were injected with clones overexpressing HAAH, developed tumors.

Figs. 5A-D are bar graphs showing increased AAH expression in PNET2 (Fig. 5A, 5C) and SH-Sy5y (Fig. 5B) cells treated with retinoic acid (Figs. 5A, 5B) or phorbol ester myristate (PMA; Fig. 5C) to induce neurite outgrowth as occurs during tumor cell invasion. The cells were treated with 10 μM retinoic acid or 100 nM PMA for 0, 1, 2, 3, 4, or 7 days. Cell lysates were analyzed by Western blot analysis using an HAAH-specific monoclonal antibody to detect the 85 kDa AAH protein. The levels of immunoreactivity were measured by volume densitometry (arbitrary units). The graphs indicate the mean ± S.D. of results obtained from three separate experiments. In Fig. 5D, PNET2 cells were treated for 24 hours with sub-lethal concentrations of H_2O_2 to induce neurite retraction. Viability of greater than 90% of the cells was demonstrated by Trypan blue dye exclusion. Similar results were obtained for SH-Sy5y cells.

Fig. 6 is a bar graph showing the effects of AAH over-expression on the levels of anti-apoptosis (Bcl-2), cell cycle-mitotic inhibitor (p16 and p21/Wafl), and proliferation (proliferating cell nuclear antigen; PCNA) molecules. PNET2 neuronal cells were stably transfected with the full-length human cDNA encoding AAH (pHAAH) or empty vector (pcDNA). AAH gene expression was under control of a CMV promoter. Western blot analysis was performed with cell lysates prepared from cultures that were 70 to 80 percent confluent. Protein loading was equivalent in each lane. Replicate blots were probed with the different antibodies. Bar graphs depict the mean S.D.'s of protein expression levels measured in three experiments. All differences are statistically significant by Student T-test analysis ($P<0.01$-$P<0.001$).

Fig. 7 is a diagram of showing the components of the IRS-1 signal transduction pathway.

Example 1: Increased expression of HAAH is associated with malignant transformation

[0027] HAAH is a highly conserved enzyme that hydroxylates EGF-like domains in transformation associated proteins. The HAAH gene is overexpressed in many cancer types including human hepatocellular carcinomas and cholangiocarcinomas. HAAH gene expression was found to be undetectable during bile duct proliferation in both human disease and rat models compared to cholangiocarcinoma. Overexpression of HAAH in NIH-3T3 cells was associated with generation of a malignant phenotype, and enzymatic activity was found to be required for cellular transformation. The data described below indicate that overexpression of HAAH is linked to cellular transformation of biliary epithelial cells.

[0028] To identify molecules that are specifically overexpressed in transformed malignant cells of human hepatocyte origin, the FOCUS hepatocellular carcinoma (HCC) cell line was used as an immunogen to generate monoclonal antibodies (mAb) that specifically or preferentially recognize proteins associated with the malignant phenotype. A lambda GT11 cDNA expression library derived from HepG2 HCC cells was screened, and a HAAH-specific mAb produced against the FOCUS cell line was found to recognize an epitope on a protein encoded by an HAAH cDNA. The HAAH enzyme was found to be upregulated in several different human transformed cell lines and tumor tissues compared to adjacent human tissue counterparts. The overexpressed HAAH enzyme in different human malignant tissues was found to be catalytically active.

[0029] HAAH gene expression was examined in proliferating bile ducts and in NIH 3T3 cells. Its role in the generation of the malignant phenotype was measured by the formation of transformed foci, growth in soft agar as an index of anchorage independent growth and tumor formation in nude mice. The role of enzymatic activity in the induction of transformed phenotype was measured by using a cDNA construct with a mutation in the catalytic site that abolished hydroxylase activity. The results indicated that an increase in expression of HAAH gene is associated with malignant transformation of bile ducts.

[0030] The following materials and methods were used to generate the data described below.

Antibodies

[0031] The FB50 monoclonal antibody was generated by cellular immunization of Balb/C mice with FOCUS HCC cells. A monoclonal anti-Dengue virus antibody was used as a non-relevant control. The HBOH2 monoclonal antibody was generated against a 52 kDa recombinant HAAH polypeptide and recognizes the catalytic domain of beta-hydroxylase from mouse and human proteins. Polyclonal anti-HAAH antibodies cross-react with rat hydroxylase protein. Control antibody anti-Erk-1 was purchased from Santa Cruz Biotechnology, Inc., CA. Sheep anti-mouse and donkey anti-rabbit antisera labeled with horseradish peroxidase were obtained from Amersham, Arlington Heights, IL.

Constructs

[0032] The murine full length AAH construct (pNH376) and the site-directed mutation construct (pNH376-H660) with abolished catalytic activity were cloned into the eukaryotic expression vector pcDNA3 (Invitrogen Corp., San Diego, CA). The full length human AAH was cloned into prokaryotic expression vector pBC-SK+ (Stratagene, La Jolla, CA). The full length human AAH (GENBANK Accession No. S83325) was subcloned into the EcoRI site of the pcDNA3 vector.

Animal model of bile duct proliferation

[0033] Rats were divided into 9 separate groups of 3 animals each except for group 9, which contained 5 rats. Group 1 was the non-surgical control group, and group 2 was the sham-operated surgical control. The remaining groups underwent common bile duct ligation to induce intrahepatic bile duct proliferation and were evaluated at 6, 12, 24, 48 hours and 4, 8 and 16 days as shown in Table 3. Animals were asphyxiated with CO_2, and liver samples were taken from left lateral and median lobes, fixed in 2 % paraformaldehyde and embedded in paraffin. Liver samples (5 m) were cut and stained with hematoxylin and eosin to evaluate intrahepatic bile duct proliferation. Immunohistochemistry was performed with polyclonal anti-HAAH antibodies that cross-react with the rat protein to determine levels of protein expression.

Bile duct proliferation associated with primary sclerosing cholangitis (PSC)

[0034] Liver biopsy samples were obtained from 7 individuals with PSC and associated bile duct proliferation. These individuals were evaluated according to standard gastroenterohepatological protocols. Patients were 22-46 years of age and consisted of 4 males and 3 females. Four had associated inflammatory bowel disease (3 ulcerative colitis and 1 Crohn's colitis). All patients underwent a radiological evaluation including abdominal ultrasonography and endoscopic retrograde cholangiopancreaticography to exclude the diagnosis of extrahepatic biliary obstruction. Tissue sections were prepared from paraffin embedded blocks and were evaluated by hematoxylin and eosin staining for bile duct proliferation. Expression of HAAH was determined by immunohistochemistry using an HAAH-specific monoclonal antibody such as FB50.

Immunohistochemistry

[0035] Liver tissue sections (5 μm) were deparaffinized in xylene and rehydrated in graded alcohol. Endogenous peroxidase activity was quenched by a 30-minute treatment with 0.6 % H_2O_2 in 60% methanol. Endogenous biotin was masked by incubation with avidin-biotin blocking solutions (Vector Laboratories, Burlingame, CA). The FB50 mAb (for PSC samples) and polyclonal anti-HAAH-hydroxylase antibodies (for rat liver samples) were added to slides in a humidified chamber at 4°C overnight. Immunohistochemical staining was performed using a standard avidin-biotin horseradish peroxidase complex (ABC) method using Vectastain Kits with diaminobenzidine (DAB) as the chromogen according to manufacturer's instructions (Vector Laboratories, Inc., Burlingame, CA). Tissue sections were counterstained with hematoxylin, followed by dehydration in ethanol. Sections were examined by a light microscopy for bile duct proliferation and HAAH protein expression. Paraffin sections of cholangiocarcinoma and placenta were used as positive controls, and hepatosteatosis samples were used as a negative controls. To control for antibody binding specificity, adjacent sections were immunostained in the absence of a primary antibody, or using non-relevant antibody to Dengue virus. As a positive control for tissue immunoreactivity, adjacent sections of all specimens were immunostained with monoclonal antibody to glyceraldehyde 3-phosphate dehydrogenase.

Western blot analysis

[0036] Cell lysates were prepared in a standard radioimmunoprecipitation assay (RIPA) buffer containing protease inhibitors. The total amount of protein in the lysates was determined by Bio-Rad colorimetric assay (Bio Rad, Hercules, CA) followed by 10% sodium dodecyl sulphate-polyacrylamide gel electrophoresis (SDS-PAGE), transferred to PVDF membranes, and subjected to Western blot analysis using FB50, HBOH2, anti-Erk-1 (used as an internal control for protein loading) as primary, sheep anti-mouse and donkey anti-rabbit antisera labeled with horseradish peroxidase as secondary antibodies. Antibody binding was detected with enhanced chemiluminescence reagents (SuperSignal, Pierce Chemical Company, Rockford, IL) and film autoradiography. The levels of immunoreactivity were measured by volume densitometry using NIH Image software.

Enzymatic activity assay

[0037] AAH activity was measured in cell lysates using the first EGF-like domain of bovine protein S as substrate where ^{14}C-labeled alpha-ketogluterate hydroxylates the domain releasing ^{14}C containing CO_2 according to standard methods, e.g., those described by Jia et al., 1992, J. Biol. Chem. 267:14322-14327; Wang et al., 1991, J. Biol. Chem. 266:14004-14010; or Gronke et al., 1990, J. Biol. Chem. 265:8558-8565. Incubations were carried out at 37°C for 30 min in a final volume of 40 μl containing 48 μg of crude cell extract protein and 75 μM EGF substrate.

Cell transfection studies

[0038] The NIH-3T3 cells were cultured in Dulbecco's modified Eagle's medium (DMEM; Mediatech, Washington, DC) supplemented with 10 % heat-inactivated fetal calf serum (FCS; Sigma Chemical Co., St.Louis, MO), 1% L-glutamine, 1% non-essential amino acids and 1% penicillin-streptomycin (GIBCO BRL, Life Technologies, Inc., Grand Island, NY). Subconfluent NIH-3T3 cells (3 x 10^5 cells/60-mm dish) were transfected with 10 μg of one of the following plasmids: 1) non-recombinant pcDNA3 vector (Invitrogen Corp., San Diego, CA) as a negative control; 2) pNH376-H660, the murine AAH cDNA that was mutated in the catalytic domain and cloned into the pcDNA3 vector driven by a CMV promoter; 3) pNH376, the wild type murine AAH cDNA cloned into the pcDNA3 vector; 4) pCDHH, wild type human AAH cDNA cloned into the pcDNA3 vector; or 5) pLNCX-UP 1, a cDNA that encodes v-Src oncogene (positive control). Cells were transfected using the calcium phosphate transfection kit according to manufacturer's instructions (5 Prime - 3 Prime, Inc., Boulder, CO). Comparison of cellular transfection efficiency was assessed with the various constructs. For this procedure, confluent plates obtained 48 hours after transfection were split and reseeded into 12 separate 6-cm dishes, and 6 of them were made to grow in the presence of 400 μg/ml G-418 (GIBCO BRL, Life Technologies, Inc., Grant Island, NY) containing medium. The number of G-418 resistant foci was determined at 14 days after transfection and used to correct for any variability in transfection efficiency.

Transformation assay

[0039] The NIH-3T3 cells were transfected with the various constructs and allowed to reach confluence after 48 hours as described above. Each 6 cm dish was split and seeded into 12 different 6 cm dishes. While 6 of them were made to grow in the presence of G-418 to detect transfection efficiency, the other six were grown in complete medium without G-418 and with a medium change every 4th day. The number of transformed foci were counted in these plates without G-418 and expressed as transformed foci per μg transfected DNA.

Anchorage-independent cell growth assay

[0040] A limiting dilution technique (0.15 cell/well of a flat bottom 96-well-plate) was performed on transfectants grown in G-418 in order to isolate cell clones with different levels of HAAH activity as measured by Western blot analysis and enzymatic assay of hydroxylase activity. Cloned cell lines (1.0 x 10^4 cells) were suspended in complete medium containing 0.4 % low-melting agarose (SeaPlaque GTG Agarose; FMC Bioproducts, Rockland, Maine) and laid over a bottom agar mixture consisting of complete medium with 0.53 % low-melting agarose. Each clone was assayed in triplicate. The clones were seeded under these conditions and 10 days later the size (positive growth > 0.1 mm in diameter) and number of foci were determined.

Tumorigenicity in nude mice

[0041] The same clones as assessed in the anchorage independent growth assay were injected into nude mice and observed for tumor formation. Tumorigenicity was evaluated using 10 animals in each of 4 groups (Charles River Labs., Wilmington, MA). Group 1 received 1 x 10^7 cells stably transfected with mock DNA, Group 2-4 received 1 x 10^7 cells of clones stable transfected with pNH376 and expressing various levels of murine HAAH protein. Nude mice were kept under pathogen-free conditions in a standard animal facility. Thirty days after tumor cell inoculation, the animals were sacrificed using isofluorane (Aerrane, Anaquest, NJ) containing chambers and the tumors were carefully removed and weight determined.

Animal model of bile duct proliferation

[0042] Following ligation of the common bile duct, intrahepatic bile duct proliferation was evident at 48 hours. Tissue samples obtained 8 and 16 days following common bile duct ligation revealed extensive bile duct proliferation as shown in Table 3.

Table 3: Bile duct proliferation and HAAH expression at different intervals after common bile duct ligation

Group	Surgical Procedure	Microscopy*	Immunohistochemistry
1	no surgery	normal	negative
2	sham surgery	normal	negative
3	6 hours post ligation	normal	negative
4	12 hours post ligation	normal	negative
5	24 hours post ligation	normal	negative
6	48 hours post ligation	minimal bile duct prolif.	negative
7	4 days post ligation	moderate bile duct prolif.	negative
8	8 days post ligation	extensive bile duct prolif.	negative
9	16 days post ligation	extensive bile duct prolif.	negative
* Investigation was performed under light microscopy following a hematoxylin and eosin staining.			

[0043] Immunohistochemical staining failed to detect presence of HAAH in proliferating bile ducts at any time. Analysis of HAAH expression in bile ducts derived from sham surgical controls was also negative, while all samples exhibited positive immunoreactivity with control antibodies to glyceraldehyde 3-phosphate dehydrogenase. Thus, bile duct proliferation was not associated with increased HAAH expression in this standard animal model system.

HAAH expression in PSC

[0044] The liver biopsy specimens from patients with PSC exhibited bile duct proliferation accompanied by periductal fibrosis and a mononuclear inflammatory cell infiltrate without evidence of dysplasia. Adjacent sections immunostained with the an HAAH-specific monoclonal antibody had no detectable HAAH immunoreactivity in proliferating bile ducts. In contrast, sections of cholangiocarcinoma that were immunostained simultaneously using the same antibody and detection reagents manifested intense levels of HAAH immunoreactivity in nearly all tumor cells, whereas adjacent sections of the cholangiocarcinomas exhibited a negative immunostaining reaction with monoclonal antibody to Dengue virus. These findings indicate that HAAH expression was associated with malignant transformation rather than non-cancerous cellular proliferation of intrahepatic bile ducts.

HAAH associated transformation of NIH-3T3 cells

[0045] The transforming capability of the murine and human AAH genes, as well as the murine AAH mutant construct without enzymatic activity were compared to mock DNA (negative control) and v-Src transfected NIH-3T3 cells (positive control). The transforming capability of murine AAH was found to be 2-3 times that of vector DNA control as shown in Fig. 1. The transforming capacity of the human gene was greater than that observed with the murine AAH (32 ± 1.5 versus 13 ± 2.6 transformed foci, respectively). The murine and human AAH transfected cells formed large foci, resembling those of v-Src transfected fibroblasts, compared to the occasional much smaller foci observed in cells transfected with vector DNA that displayed the contact inhibition of fibroblast cell lines. Parallel experiments performed using the mutant pNH376-H660 construct without enzymatic activity revealed no transforming activity. This finding indicates that the enzymatic activity of HAAH is required for the transforming activity exhibited by the HAAH gene.

Anchorage-independent cell growth assay

[0046] After transient transfection with the murine AAH construct, several different transformed foci were isolated for dilutional cloning experiments to establish stable transfected cell clones with different levels of HAAH gene expression. Nine different cloned cell lines were selected for further study. The expression level of the HAAH protein was determined by Western blot analysis. Clones 7 and 18 had a modest increase in HAAH protein expression, yet formed large colonies in soft agar (Fig. 2). Protein loading was equivalent in all lanes as shown by immunoblotting of the same membranes with an anti-Erk-1 monoclonal antibody. The increased protein expression was associated with increased enzymatic activity as shown in Fig. 3. The capability of these clones to exhibit anchorage independent cell growth in soft agar is presented in Fig. 3. All 3 clones with increased HAAH gene expression demonstrated anchorage independent cell growth

compared to the mock DNA transfected clone.

Tumor formation in nude mice

[0047] The 3 clones with increased HAAH gene expression were evaluated for the ability to form tumors in nude mice. Tumor size in the mouse given clone 18 was compared to a mock DNA transfected clone. Clones 7, 16 and 18 were highly transformed in this assay and produced large tumors with a mean weight of 2.5, 0.9 and 1.5 grams, respectively (Fig. 4). These data indicate that overexpression of HAAH contributes to induction and maintenance of the malignant phenotype *in vivo.*

High level HAAH expression is indicative of malignancy

[0048] In order to determine if HAAH expression was associated with malignancy rather than increased cell turnover, two models of bile duct proliferation were studied. In the animal model, ligation of the common bile duct induced extensive intrahepatic bile duct proliferation, yet there was no evidence of HAAH gene expression under these experimental conditions as shown in Table 3. Similarly, HAAH gene expression was assessed in a human disease model associated with bile duct proliferation since PSC is an autoimmune liver disease associated with destruction as well as proliferation of the intra and extrahepatic bile ducts. PSC is premalignant disease, and a significant proportion of affected individuals will eventually develop cholangiocarcinoma. However, no evidence for increased HAAH gene expression in the presence of extensive bile duct proliferation.

[0049] Having established that HAAH protein levels were elevated in cholangiocarcinoma and not in normal or proliferating bile ducts, the role of HAAH in the generation of a malignant phenotype was studied. The HAAH gene was transfected into NIH-3T3 cells and cellular changes, e.g., increased formation of transformed foci, colony growth in soft agar and tumor formation in nude mice associated with malignant transformation, were evaluated. The full-length murine and human AAH genes were cloned into expression constructs and transiently transfected into NIH-3T3 cells. An increased number of transformed foci was detected in cells transfected both with the murine and human AAH genes as compared to mock DNA transfected controls. The increased number of transformed foci, after controlling for transfection efficiency, was not as high compared to v-Src gene transfected cells used as a positive control. The enzymatic activity of the HAAH gene was required for a malignant phenotype because a mutant construct which abolished the catalytic site had no transforming properties. Several stable transfectants and cloned NIH-3T3 cell lines with a modest increase in HAAH protein levels and enzymatic activity were established. Such cell lines were placed in soft agar to examine anchorage independent cell growth as another property of the malignant phenotype. All cell lines grew in soft agar compared to mock DNA transfected control, and there was a positive correlation between the cellular level of HAAH gene expression and the number and size of colonies formed. Three of these cloned cell lines formed tumors in nude mice. All three cell lines with increased HAAH expression were oncogenic as shown by the development of large tumors as another well-known characteristic of the transformed phenotype.

[0050] To determine whether cellular changes induced by overexpression of HAAH were related to the enzymatic function, a site-directed mutation was introduced into the gene that changed the ferrous iron binding site from histidine to lysine at 660th position of mouse HAAH thereby abolishing hydroxylase activity of the murine HAAH. A corresponding mutation in HAAH is used as a dominant negative mutant to inhibit HAAH hydroxylase activity. The pNH376-H660 construct had no transformation activity indicating cellular changes of the malignant phenotype induced by overexpression depends on the enzymatic activity of the protein.

[0051] Notch receptors and their ligands have several EGF-like domains in the N-terminal region that contain the putative consensus sequence for beta-hydroxylation. Notch ligands are important elements of the Notch signal transduction pathway and interaction of Notch with its ligands occurs by means of EGF-like domains of both molecules. Point mutations affecting aspartic acid or asparagine residues in EGF-like domains that are the targets for beta-hydroxylation by HAAH reduce calcium binding and protein-protein interactions involved in the activation of downstream signal transduction pathways. Overexpression of HAAH and Notch protein hydroxylation by HAAH contributes to malignancy. Tumor growth is inhibited by decreasing Notch protein hydroxylation by HAAH.

[0052] The data presented herein is evidence that high-level HAAH expression is linked to malignant transformation. An increase in expression of the HAAH cDNA in NIH-3T3 cells induced a transformed phenotype manifested by increased numbers of transformed foci, anchorage-independent growth, and tumorigenesis in nude mice. In addition, intact HAAH-enzyme was found to be required for HAAH-associated transformation. Accordingly, inhibition of as little as 20% of endogenous HAAH enzymatic activity or expression confers a therapeutic benefit. For example, clinical benefit is achieved by 50%-70% inhibtion of HAAH expression or activity after administaration of an HAAH inhibitory compound compared to the level associated with untreated cancer cell or a normal noncancerous cell.

[0053] HAAH is regulated at the level of transcription. Only modest increases in HAAH expression and enzyme activity were required for cellular transformation. These results indicate that increased HAAH gene expression and enzyme

activity contribute to the generation or maintenance of the transformed phenotype and that decreasing transcription of the HAAH gene or decreasing enzymatic activity of the HAAH gene product leads to a decrease in malignancy. Accordingly, HAAH transcription is inhibited by administering compounds which decrease binding of Fos and/or Jun (elements which regulate HAAH transcription) to HAAH promoter sequences.

[0054] Since HAAH is up-regulated with malignant transformation of bile duct epithelium, and HAAH immunoreactivity is detectable on tumor cell surface membranes, HAAH is also a molecule to which to target a cytotoxic agent, e.g., by linking the cytotoxic agent to a compound that binds to HAAH expressed on the surface of a tumor cell. Assay of HAAH protein levels in biological fluids such as bile is a diagnostic marker of human cholangiocarcinoma.

Example 2: Expression of AAH and growth and invasiveness of malignant CNS neoplasms

[0055] AAH is abundantly expressed in carcinomas and trophoblastic cells, but not in most normal cells, including those of CNS origin. High levels of AAH expression were observed in 15 of 16 glioblastomas, 8 of 9 anaplastic oligodendrogliomas, and 12 of 12 primitive neuroectodermal tumors (PNETs). High levels of AAH immunoreactivity were primarily localized at the infiltrating edges rather than in the central portions of tumors. Double-label immunohistochemical staining demonstrated a reciprocal relationship between AAH and tenascin, a substrate for AAH enzyme activity. PNET2 neuronal cell lines treated with phorbol ester myristate or retinoic acid to stimulate neuritic extension and invasive growth exhibited high levels of AAH expression, whereas H_2O_2-induced neurite retraction resulted in down-regulation of AAH. PNET2 neuronal cells that stably over-expressed the human AAH cDNA had increased levels of PCNA and Bcl-2, and reduced levels of p21/Wafl and p16, suggesting that AAH overexpression results in enhanced pathological cell proliferation, cell cycle progression, and resistance to apoptosis. In addition, the reduced levels of p16 observed in AAH-transfectants indicate that AAH over-expression confers enhanced invasive growth of neoplastic cells since deletion or down-regulation of the p16 gene correlates with more aggressive and invasive in vivo growth of glioblastomas. Increased AAH immunoreactivity was detected at the infiltrating margins of primary malignant CNS neoplasms, further indicating a role of HAAH in tumor invasiveness.

[0056] The following materials and methods were used to generate the data described below.

Analysis of AAH Immunoreactivity in Primary Human Malignant CNS Neoplasms:

[0057] AAH immunoreactivity was examined in surgical resection specimens of glioblastoma (N=16), anaplastic oligodendroglioma (N=9), and primitive neuroectodermal tumor (PNET; supratentorial neuroblastomas (N=3) and medulloblastomas (N=9). The histopathological sections were reviewed to confirm the diagnoses using standard criteria. Paraffin sections from blocks that contained representative samples of viable solid tumor, or tumor with adjacent intact tissue were studied. Sections from normal adult postmortem brains (N=4) were included as negative controls. AAH immunoreactivity was detected using qn HAAH-specific monoclonal antibody. Immunoreactivity was revealed by the avidin-biotin horseradish peroxidase complex method (Vector ABC Elite Kit; Vector Laboratories, Burlingame, CA) using 3-3' diaminobenzidine (DAB) as the chromogen (24) and hematoxylin as a counterstain.

[0058] Tenascin and laminin are likely substrates for AAH due to the presence of EGF-like repeats within the molecules. Double-immunostaining studies were performed to co-localize AAH with tenascin or laminin. The AAH immunoreactivity was detected by the ABC method with DAB as the chromogen, and tenascin or laminin immunoreactivity was detected by the avidin-biotin alkaline phosphatase complex method (Vector Laboratories, Burlingame, CA) with BCIP/NBT as the substrate. As positive and negative controls, adjacent sections were immunostained with monoclonal antibody to glial fibrillary acidic protein (GFAP) and Hepatitis B surface antigen. All specimens were batch immunostained using the same antibody dilutions and immunodetection reagents.

Cell Lines and Culture Conditions

[0059] Studies were conducted to determine whether AAH expression was modulated with neurite (filopodia) extension (sprouting) as occurs with invasive growth of malignant neoplasms. Human PNET2 CNS-derived and SH-Sy5y neuroblastoma cells were cultured and stimulated for 0, 1, 2, 3, 5, or 7 days with 100 nM phorbol 12-ester 13-acetate or 10 μM retinoic acid to induce sprouting. In addition, to examine the effects of neurite retraction on AAH expression, subconfluent cultures were treated for 24 hours with low concentrations (10-40 μM) of H_2O_2. For both studies, AAH expression was evaluated by Western blot analysis using the an HAAH-specific antibody.

Generation of PNET2 AAH-transfected Clones

[0060] The full-length human AAH cDNA (SEQ ID NO:3) was ligated into the pcDNA3.1 mammalian expression vector in which gene expression was under the control of a CMV promoter (Invitrogen Corp., San Diego, CA). PNET2 cells

were transfected with either pHAAH or pcDNA3 (negative control) using Cellfectin reagent (Gibco BRL, Grand Island, NY). Neomycin-resistant clones were selected for study if the constitutive levels of AAH protein expression were increased by at least two-fold relative to control (pcDNA3) as detected by Western blot analysis. To determine how AAH overexpression altered the expression of genes that modulate the transformed phenotype, the levels of proliferating cell nuclear antigen (PCNA), p53, p21/Wafl, Bcl-2, and p16 were measured in cell lysates prepared from subconfluent cultures of AAH (N=5) and pcDNA3 (N=5) stably transfected clones. PCNA was used as marker of cell proliferation. p53, p21/Wafl, and Bcl-2 levels were examined to determine whether cells that over-expressed AAH were more prone to cell cycle progression and more resistant to apoptosis. The levels of p16 were assessed to determine whether AAH over-expression has a role in tumor invasiveness.

Table 2: HAAH cDNA sequence

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cggaccgtgc aatggcccag cgtaagaatg ccaagagcag cggcaacagc agcagcagcg 61
gctccggcag cggtagcacg agtgcgggca gcagcagccc cggggcccgg agagagacaa 121
agcatggagg acacaagaat gggaggaaag gcggactctc gggaacttca ttcttcacgt 181
ggtttatggt gattgcattg ctgggcgtct ggacatctgt agctgtcgtt tggtttgatc 241
ttgttgacta tgaggaagtt ctaggaaaac taggaatcta tgatgctgat ggtgatggag 301
attttgatgt ggatgatgcc aaagttttat taggacttaa agagagatct acttcagagc 361
cagcagtccc gccagaagag gctgagccac acactgagcc cgaggagcag gttcctgtgg 421
aggcagaacc ccagaatatc gaagatgaag caaaagaaca aattcagtcc cttctccatg 481
aaatggtaca cgcagaacat gttgagggag aagacttgca acaagaagat ggacccacag 541
gagaaccaca acaagaggat gatgagtttc ttatggcgac tgatgtagat gatagatttg 601
agaccctgga acctgaagta tctcatgaag aaaccgagca tagttaccac gtggaagaga 661
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cagtttcaca agactgtaat caggatatgg aagagatgat gtctgagcag gaaaatccag 721
attccagtga accagtagta gaagatgaaa gattgcacca tgatacagat gatgtaacat 781
accaagtcta tgaggaacaa gcagtatatg aacctctaga aaatgaaggg atagaaatca 841
cagaagtaac tgctcccccc gaggataatc ctgtagaaga ttcacaggta attgtagaag 901
aagtaagcat ttttcctgtg gaagaacagc aggaagtacc accagaaaca aatagaaaaa 961
cagatgatcc agaacaaaaa gcaaaagtta agaaaaagaa gcctaaactt ttaaataaat 1021
ttgataagac tattaaagct gaacttgatg ctgcagaaaa actccgtaaa aggggaaaaa 1081
ttgaggaagc agtgaatgca tttaaagaac tagtacgcaa ataccctcag agtccacgag 1141
caagatatgg gaaggcgcag tgtgaggatg atttggctga gaagaggaga agtaatgagg 1201
tgctacgtgg agccatcgag acctaccaag aggtggccag cctacctgat gtccctgcag 1261
acctgctgaa gctgagtttg aagcgtcgct cagacaggca acaatttcta ggtcatatga 1321
gaggttccct gcttaccctg cagagattag ttcaactatt tcccaatgat acttccttaa 1381
aaaatgacct tggcgtggga tacctcttga taggagataa tgacaatgca aagaaagttt 1441
atgaagaggt gctgagtgtg acacctaatg atggctttgc taaagtccat tatggcttca 1501
tcctgaaggc acagaacaaa attgctgaga gcatcccata tttaaaggaa ggaatagaat 1561
ccggagatcc tggcactgat gatgggagat tttatttcca cctgggggat gccatgcaga 1621
gggttgggaa caaagaggca tataagtggt atgagcttgg gcacaagaga ggacactttg 1681
catctgtctg gcaacgctca ctctacaatg tgaatggact gaaagcacag ccttggtgga 1741
ccccaaaaga aacgggctac acagagttag taaagtcttt agaaagaaac tggaagttaa 1801
tccgagatga aggccttgca gtgatggata aagccaaagg tctcttcctg cctgaggatg 1861
aaaacctgag ggaaaaaggg gactggagcc agttcacgct gtggcagcaa ggaagaagaa 1921
atgaaaatgc ctgcaaagga gctcctaaaa cctgtacctt actagaaaag ttccccgaga 1981
caacaggatg cagaagagga cagatcaaat attccatcat gcaccccggg actcacgtgt 2041
ggccgcacac agggcccaca aactgcaggc tccgaatgca cctgggcttg gtgattccca 2101
aggaaggctg caagattcga tgtgccaacg agaccaggac ctgggaggaa ggcaaggtgc 2161
tcatctttga tgactccttt gagcacgagg tatggcagga tgcctcatct ttccggctga 2221
tattcatcgt ggatgtgtgg catccggaac tgacaccaca gcagagacgc agccttccag 2281
caatttagca tgaattcatg caagcttggg aaactctgga gaga
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(SEQ ID NO:3 ; GENBANK Accession No. S83325; codon encoding initiating methionine is underlined).

Western blot analysis

[0061] Cells grown in 10 cm^2 dishes were lysed and homogenized in a standard radioimmunoprecipitation assay RIPA buffer containing protease and phosphatase inhibitors. The supernatants collected after centrifuging the samples at 12,000 x g for 10 minutes to remove insoluble debris were used for Western blot analysis. Protein concentration was measured using the BCA assay (Pierce Chemical Co, Rockford, IL). Samples containing 60 μg of protein were electrophoresed in sodium dodecyl sulfate polyacrylamide gels (SDS-PAGE) and subjected to Western blot analysis. Replicate blots were probed with the individual antibodies. Immunoreactivity was detected with horseradish peroxidase conjugated IgG (Pierce Chemical Co, Rockford, IL) and enhanced chemiluminescence reagents. To quantify the levels of protein expression, non-saturated autoradiographs were subjected to volume densitometry using NIH Image software, version 1.6. Statistical comparisons between pHAAH and pcDNA3 transfected cells were made using Student T tests.

Antibodies

[0062] HAAH-specific monoclonal antibody generated against the FOCUS hepatocellular carcinoma cells were used to detect AAH immunoreactivity. Monoclonal antibodies to tenascin, and glial fibrillary acidic protein, and rabbit polyclonal antibody to laminin were purchased from Sigma Co. (St. Louis, MO). Rabbit polyclonal antibody to human p16 was purchased from Santa Cruz Biotechnology Inc. (Santa Cruz, CA). The 5C3 negative control monoclonal antibody to

Hepatitis B surface antigen was generated using recombinant protein and used as a negative control.

AAH immunoreactivity in primary malignant brains tumors

[0063] AAH immunoreactivity was detected in 15 of 16 glioblastomas, 8 of 9 anaplastic oligodendrogliomas, and all 12 PNETs. AAH immunoreactivity was localized in the cytoplasm, nucleus, and cell processes. The tissue distribution of AAH immunoreactivity was notable for the intense labeling localized at the interfaces between tumor and intact brain, and the conspicuously lower levels of immunoreactivity within the central portions of the tumors. High levels of AAH immunoreactivity were also observed in neoplastic cells distributed in the subpial zones, leptomeninges, Virchow-Robin perivascular spaces, and in individual or small clusters of neoplastic cells that infiltrated the parenchyma. In contrast, AAH immunoreactivity was not detectable in normal brain. The distribution of AAH immunoreactivity appeared not to be strictly correlated with DNA synthesis since the density of nuclei in mitosis (1-5%) was similar in the central and peripheral portions of the tumors.

Relationship between AAH and tenascin immunoreactivity in glioblastomas

[0064] Tenascin is an extracellular matrix-associated antigen expressed in malignant gliomas. Tenascin contains EGF-like domains within the molecule, a substrate for HAAH hydroxylation. To localize AAH in relation to tenascin immunoreactivity in malignant brain tumors, double-label immunohistochemical staining was performed in which AAH was detected using a brown chromogen (DAB), and tenascin, a blue chromogen (BCIP/NBT). Adjacent sections were similarly double-labeled to co-localize AAH with laminin, another EGF domain containing extracellular matrix molecule expressed in the CNS. Intense levels of tenascin immunoreactivity were observed in perivascular connective tissue and in association with glomeruloid proliferation of endothelial cells. The double-labeling studies demonstrated a reciprocal relationship between AAH and tenascin immunoreactivity such that high levels of AAH were associated with low or undetectable tenascin, and low levels of AAH were associated with abundant tenascin immunoreactivity. Although laminins are also likely substrates for AAH enzyme activity due to the EGF repeats within the molecules, double labeling studies revealed only low levels of laminin immunoreactivity throughout the tumors and at interfaces between tumor and intact tissue.

Analysis of AAH expression in neuronal cell lines treated with PMA or RA

[0065] Neuritic sprouting/filopodia extension marks invasive growth of neoplastic neuronal cells. PMA activates protein kinase C signal transduction pathways that are involved in neuritic sprouting. Retinoic acid binds to its own receptor and the ligand-receptor complex translocates to the nucleus where it binds to specific consensus sequences present in the promoter/enhancer regions of target genes involved in neuritic growth. Both PNET2 and SH-Sy5y cells can be induced to sprout by treatment with PMA (60-120 nM) or retinoic acid (5-10 μM). Figs. 5A-D depict data from representative Western blot autoradiographs; the bar graphs correspond to the mean $\pm$ S.D. of results obtained from three experiments. Western blot analysis with the FB50 antibody detected doublet bands corresponding to protein with an molecular mass of approximately 85 kDa. Untreated PNET2 cells had relatively low levels of AAH immunoreactivity (Fig. 5A), whereas untreated SH-Sy5y cells had readily detected AAH expression (Fig. 5B). Untreated PNET2 cells exhibited polygonal morphology with coarse, short radial cell processes, whereas SH-Sy5y cells were slightly elongated and spontaneously extend fine tapered processes. Both cell lines manifested time-dependent increases in the levels of AAH immunoreactivity following either RA (Figs. 5A and 5B) or PMA (Fig. 5C) stimulation and neurite extension. In PNET2 cells, the levels of AAH protein increased by at least two-fold 24 hours after exposure to RA or PMA, and high levels of AAH were sustained throughout the 7 days of study. In SH-Sy5y cells, the RA- or PMA-stimulated increases in AAH expression occurred more gradually and were highest after 7 days of treatment (Fig. 5B).

[0066] To examine the effect of AAH expression on neurite retraction, PNET2 and SH-Sy5y cells were treated with low concentrations (8-40 μM) of H_2O_2. After 24 hours exposure to up to 40 μM H_2O_2, although most cells remained viable (Trypan blue dye exclusion), they exhibited neurite retraction and rounding. Western blot analysis using the FB50 antibody demonstrated H_2O_2 dose-dependent reductions in the levels of AAH protein (Fig. 5D).

Effects of AAH over-expression in PNET2 cells

[0067] To directly assess the role of AAH overexpression in relation to the malignant phenotype, PNET2 cells were stably transfected with the human full-length cDNA with gene expression under control of a CMV promoter (pHAAH). Neomycin-resistant clones that had at least two-fold higher levels of AAH immunoreactivity relative to neomycin-resistant pcDNA3 (mock) clones were studied. Since aggressive behavior of malignant neoplasms is associated with increased DNA synthesis, cell cycle progression, resistance to apoptosis, and invasive growth, the changes in phenotype associated

with constitutive over-expression of AAH were characterized in relation to PCNA, p21/Waf1, p53, Bcl-2, and p16. PCNA was used as an index of DNA synthesis and cell proliferation. p21/Waf1 is a cell cycle inhibitor. Expression of the p53 tumor-suppressor gene increases prior to apoptosis, whereas bc1-2 inhibits apoptosis and enhances survival of neuronal cells. p16 is an oncosuppressor gene that is often either down-regulated or mutated in infiltrating malignant neoplasms.

[0068] Five pHAAH and 5 pcDNA3 clones were studied. Increased levels of AAH expression in the pHAAH transfected clones was confirmed by Western (Fig. 6) and Northern blot analyses. Western blot analysis using cell lysates from cultures that were 70 to 80 percent confluent demonstrated that constitutively increased levels of AAH expression (approximately 85 kDa; $P<0.05$) in pHAAH-transfected cells were associated with significantly increased levels of PCNA (approximately 35 kDa; $P<0.01$) and Bcl-2 (approximately 25 kDa; $P<0.05$), and reduced levels ofp21/Wafl (approximately 21 kDa; $P<0.001$) and p16 (approximately 16 kDa; $P<0.001$) (Fig. 6). However, the pHAAH stable transfectants also exhibited higher levels of wild-type p53 (approximately 53-55 kDa). Although AAH expression (85 kDa protein) in the stable transfectants was increased by only 75 to 100 percent, the levels of p16 and p21/Waf1 were sharply reduced, and PCNA increased by nearly two-fold (Fig. 6).

Increased AAH expression is indicative of growth and invasiveness of malignant CNS neoplasms

[0069] The data described herein demonstrates that AAH overexpression is a diagnostic tool by which to identify primary malignant CNS neoplasms of both neuronal and glial cell origin. Immunohistochemical staining studies demonstrated that AAH overexpression was detectable mainly at the interfaces between solid tumor and normal tissue, and in infiltrating neoplastic cells distributed in the subpial zones, leptomeninges, perivascular spaces, and parenchyma. *In vitro* experiments demonstrated that AAH gene expression was modulated with neurite (filopodium) extension and invasiveness and down-regulated with neurite retraction. In addition, PNET2 cells stably transfected with the AAH cDNA exhibited increased PCNA and bcl-2, and reduced Wafl/p21 and p16 expression. Therefore, AAH overexpression contributes to the transformed phenotype of CNS cells by modulating the expression of other genes that promote cellular proliferation and cell cycle progression, inhibit apoptosis, or enhance tumor cell invasiveness.

[0070] The data demonstrated readily detectable AAH mRNA transcripts (4.3 kB and 2.6 kB) and proteins (85 kDa and 50-56 kDa) in PNET2 and SH-Sy5y cells, but not in normal brain. Correspondingly, high levels of AAH immunoreactivity were observed in 35 of the 37 in malignant primary CNS-derived neoplasms studied, whereas the 4 normal control brains had no detectable AAH immunoreactivity. The presence of high-level AAH immunoreactivity at the infiltrating margins and generally not in the central portions of the tumors indicates that AAH overexpression is involved in the invasive growth of CNS neoplasms. Administration of compounds which decrease AAH expression or enzymatic activity inhibits proliferation of CNS tumors which overexpress AAH, as well as metastases of CNS tumors to other tissue types.

[0071] The AAH enzyme hydroxylates EGF domains of a number of proteins. Tenascin, an extracellular matrix molecule that is abundantly expressed in malignant gliomas, contains EGF-like domains. Since tenascin promotes tumor cell invasion, its abundant expression in glioblastomas represents an autocrine mechanism of enhanced tumor cell growth vis-a-vis the frequent overexpression of EGF or EGF-like receptors in malignant glial cell neoplasms. Analysis of the functional domains of tenascins indicated that the mitogenic effects of this family of molecules are largely mediated by the fibronectin domains, and that the EGF-like domains inhibit growth, cell process elongation, and matrix invasion. Therefore, hydroxylation of the EGF-like domains by AAH represents an important regulatory factor in tumor cell invasiveness.

[0072] Double-label immunohistochemical staining studies demonstrated a reciprocal relationship between AAH and tenascin immunoreactivity such that high levels AAH immunoreactivity present at the margins of tumors were associated with low levels of tenascin, and low levels of AAH were often associated with high levels of tenascin. These observations indicated that AAH hydroxylation of EGF-like domains of tenascin alters the immunoreactivity of tenascin protein, and in so doing, facilitates the invasive growth of malignant CNS neoplasms into adjacent normal tissue and perivascular spaces.

[0073] AAH immunoreactivity was examined in PNET2 and SH-Sy5y neuronal cells induced to undergo neurite extension with PMA or retinoic acid, or neurite retraction by exposure to low doses of H_2O_2. AAH expression was sharply increased by PMA- or retinoic acid-induced neurite (filopodium) extension, and inhibited by H_2O_2-induced neurite retraction and cell rounding. Neurite or filopodium extension and attachment to extracellular matrix are required for tumor cell invasion in the CNS. The EGF-like domains of tenascin inhibit neuritic and glial cell growth into the matrix during development.

[0074] To directly examine the role of AAH overexpression in relation to the transformed phenotype, genes modulated with DNA synthesis, cell cycle progression, apoptosis, and tumor invasiveness were examined in neuronal cell clones that stably over-expressed the human AAH cDNA. The findings of increased PCNA and reduced Wafl/p21 immunoreactivity indicated that AAH overexpression enhances cellular proliferation and cell cycle progression. In addition, the finding of increased Bcl-2 expression indicated that AAH overexpression contributes to the transformed phenotype by

increasing cellular resistance to apoptosis. The apparently contradictory finding of higher levels of p53 in the cells that overexpressed AAH is explained by the observation that high levels of wildtype p53 in immature neuronal cells were associated with neuritic growth (invasiveness) rather than apoptosis. Levels of p16 were reduced (compared to normal cells) or virtually undetectable in cells that constitutively overexpressed AAH; a deletion mutation of the p 16 gene has been correlated with invasive growth and more rapid progression of malignant neoplasms, including those of CNS origin. These data indicate that p16 expression is modulated by AAH.

Example 3: Increased HAAH production and IRS-mediated signal transduction

[0075] IRS-1 mediated signal transduction pathway is activated in 95% of human HCC tumors compared to the adjacent uninvolved liver tissue. HAAH is a downstream effector gene involved in this signal transduction pathway. HAAH gene upregulation is closely associated with overexpression of IRS-1 in HCC tumors as revealed by immunohistochemical staining and Western blot analysis. A high level of HAAH protein is expressed in HCC and cholangiocarcinoma compared to normal hepatocytes and bile ducts. Both of these tumors also exhibit high level expression of IRS-1 by immunohistochemical staining. FOCUS HCC cell clones stably transfected with a C-terminal truncated dominant negative mutant of IRS-1, which blocks insulin and IGF- 1 stimulated signal transduction, was associated with a striking reduction in HAAH gene expression in liver. In contrast, transgenic mice overexpressing IRS-1 demonstrate an increase in HAAH gene expression by Western blot analysis. Insulin stimulation of FOCUS HCC cells (20 and 40 U) in serum free medium and after 16 hr of serum starvation demonstrated upregulation of HAAH gene expression. These data indicate that HAAH gene expression is a downstream effector of the IRS-1 signal transduction pathway.

Example 4: Effects of HAAH expression levels on the characteristics of the malignant phenotype

[0076] Overexpression of IRS-1 in NIH 3T3 cells induces transformation. The full-length murine HAAH construct was cloned into the pcDNA3 eukaryotic expression vector. A second murine construct encoded HAAH with abolished catalytic activity due to a site directed mutation. The full-length human HAAH cDNA was cloned into the pcDNA3 expression vector as well as a plasmid that encodes v-src which was used as a positive control for transformation activity. Standard methods were used for transfection of NIH 3T3 cells, control for transfection efficiency, assays of HAAH enzymatic activity, transformation by analysis of foci formation, anchorage-independent cell growth assays and analysis of tumorigenicity in nude mice. The data indicated that HAAH overexpression is associated with generation of a malignant phenotype.

Table 4: Overexpression of enzymatically active HAAH indicates malignancy

cDNA	# of foci ± S.D.[b]	NIH 3T3 clone	# of colonies[e]
pcDNA3 (mock)	6.0 ± 3.3	PcDNA (mock)	0.4 ± 0.5
murine HAAH	14.0 t 2.9	clone 18[d]	6.2 ± 2.9
mutant murine HAAH[a]	1.6 ± 1.0	clone 16[e]	4.7 ± 6.5
human HAAH	32.0 ± 5.4		
v-scr	98.0 ± 7.1		

a. enzymatically inactive HAAH
b. P<0.01 compared to mock and mutant murine HAAH
c. P<0.001 compared to mock
d. Clone 18 is a stable cloned NIH 3T3 cell line that overexpression human HAAH by approximately two fold.
e. Clone 16 is a stable cloned NIH 3T3 cell line that overexpresses human HAAH by about 50%.

[0077] These data indicate that overexpression of HAAH is associated with formation of transformed foci. Enzymatic activity is required for cellular transformation to occur. Cloned NIH 3T3 cell lines with increased human HAAH gene expression grew as solid tumors in nude mice. HAAH is a downstream effector gene of the IRS-1 signal transduction pathway.

Claims

1. An ex vivo method for diagnosing a malignant neoplasm in a mammal, said method comprising contacting a bodily fluid from said mammal with an antibody or fragment thereof which binds to an aspartyl (asparaginyl) beta-ltydxoxylase (AAH) polypeptide under conditions sufficient to form an antigen-anitbody complex and detecting the antigen-antibody complex.

2. An ex vivo method for prognosis of a malignant neoplasm of a mammal, said method comprising the method according to claim 1 and
wherein said method generates temporal data used for prognosis of malignant disease.

3. The method of claim 1 or 2, wherein the patient is human.

4. The method of claim 1, 2 or 3 wherein said neoplasm is derived from endodermal tissue.

5. The method of claim 1,2 or 3, wherein said neoplasm is selected from colon cancer, breast cancer, pancreatic cancer, liver cancer and cancer of the bile ducts.

6. The method of claim 1, 2 or 3 wherein said neoplasm is a cancer of the central nervous system (CNS).

7. The method of claim 1, 2 or 3, wherein said bodily fluid is selected from a CNS-derived bodily fluid, blood, serum, urine, saliva, sputum, lung effusion and ascites fluid.

8. The method of any preceding claim, wherein the antigen-antibody complex is detected by a label selected from an enzymatic label, a fluorescent label, a chemiluminescent label, a radioactive label and a dye label.

9. The method of any preceding claim, wherein said neoplasm is selected from a hepatocellular carcinoma, a cholangiocarcinoma, a glioblastoma and a neuroblastoma.

10. The method of any preceding claim, wherein said antibody binds to an epitope within a catalytic site of AAH.

11. The method of claim 9, wherein said antibody is a single chain Fv molecule.

12. An in vitro use of a kit which comprises a detectably-labelled antibody that binds to an AAH, wherein the use is to aid in diagnosis of a neoplasm detectable in the bodily fluid of a mammal.

Patentansprüche

1. Ex vivo-Methode zum Diagnostizieren eines malignen Neoplasmas in einem Säuger, welche Methode das Kontaktieren einer Körperflüssigkeit von dem Säuger mit einem Antikörper oder Fragment davon, welcher an ein Aspartyl-(Asparaginyl)-beta-Hydroxylase-(AAH)-Polypeptid unter Bedingungen bindet, die ausreichend sind, um einen Antigen-Antikörper-Komplex zu bilden, und Nachweisen der Antigen-Antikörper-Komplexes umfasst.

2. Ex vivo-Methode zum Prognostizieren eines malignen Neoplasmas eines Säugers, wobei die Methode die Methode nach Anspruch 1 umfasst und wobei die Methode zeitliche Daten generiert, die zum Prognostizieren der malignen Erkrankung verwendet werden.

3. Methode nach Anspruch 1 oder 2, wobei der Patient ein Mensch ist.

4. Methode nach Anspruch 1, 2 oder 3, wobei das Neoplasma von endodermalen Gewebe stammt.

5. Methode nach Anspruch 1, 2 oder 3, wobei das Neoplasma ausgewählt ist aus Dickdarmkrebs, Brustkrebs, Bauchspeicheldrüsenkrebs, Leberkrebs und Krebs der Gallengänge.

6. Methode nach Anspruch 1, 2 oder 3, wobei das Neoplasma ein Krebs des Zentralen Nervensystems (ZNS) ist.

7. Methode nach Anspruch 1, 2 oder 3, wobei die Körperflüssigkeit ausgewählt ist aus einer ZNS-abgeleiteten Kör-

perflüssigkeit, Blut, Serum, Urin, Speichel, Auswurf, Lungeneffusion und Aszitesflüssigkeit.

8. Methode nach jedem der vorangehenden Ansprüche, wobei der Antigen-Antikörper-Komplex mittels einer Markierung nachgewiesen wird, ausgewählt aus einer enzymatischen Markierung, einer fluoreszierenden Markierung, einer chemilumineszierenden Markierung, einer radioaktiven Markierung und einer Farbstoff-Markierung.

9. Methode nach jedem der vorangehenden Ansprüche, wobei das Neoplasma ausgewählt ist aus einem hepatozellulärem Karzinom, einem Cholangiokarzinom, einem Glioblastom und einem Neuroblastom.

10. Methode nach jedem der vorangehenden Ansprüche, wobei der Antikörper an ein Epitop innerhalb einer katalytischen Stelle von AAH bindet.

11. Methode nach Anspruch 9, wobei der Antikörper ein einzelkettiges Fv-Molekül ist.

12. In vitro-Verwendung eines Kits, welches einen nachweisbar markierten Antikörper umfasst, der an eine AAH bindet, wobei die Verwendung zur Unterstützung des Diagnostizierens eines in der Körperflüssigkeit eines Säugers detektierbaren Neoplasmas dient.

Revendications

1. Procédé *ex vivo* de diagnostic d'un néoplasme malin chez un mammifère, ledit procédé comprenant la mise en contact d'un liquide corporel provenant dudit mammifère avec un anticorps ou un fragment de celui-ci qui se lie à un polypeptide d'aspartyl (asparaginyl)-bêta-hydroxylase (AAH) dans des conditions suffisantes pour former un complexe antigène-anticorps et la détection du complexe antigène-anticorps.

2. Procédé *ex vivo* de pronostic d'un néoplasme malin d'un mammifère, ledit procédé comprenant le procédé selon la revendication 1 et
où ledit procédé génère des données temporaires utilisées pour le pronostic d'une maladie maligne.

3. Procédé selon la revendication 1 ou 2, où le patient est un homme.

4. Procédé selon la revendication 1, 2 ou 3, où ledit néoplasme est dérivé du tissu endodermique.

5. Procédé selon la revendication 1, 2 ou 3, où ledit néoplasme est choisi parmi un cancer du côlon, un cancer du sein, un cancer pancréatique, un cancer du foie et un cancer des conduits biliaires.

6. Procédé selon la revendication 1, 2 ou 3, où ledit néoplasme est un cancer du système nerveux central (SNC).

7. Procédé selon la revendication 1, 2 ou 3, où ledit liquide corporel est choisi parmi un liquide corporel dérivé du SNC, le sang, le sérum, l'urine, la salive, un crachat, un épanchement pulmonaire et un liquide d'ascite.

8. Procédé selon l'une quelconque des revendications précédentes, dans lequel le complexe antigène-anticorps est détecté par un marqueur choisi parmi un marqueur enzymatique, un marqueur fluorescent, un marqueur chimioluminescent, un marqueur radioactif et un marqueur colorant.

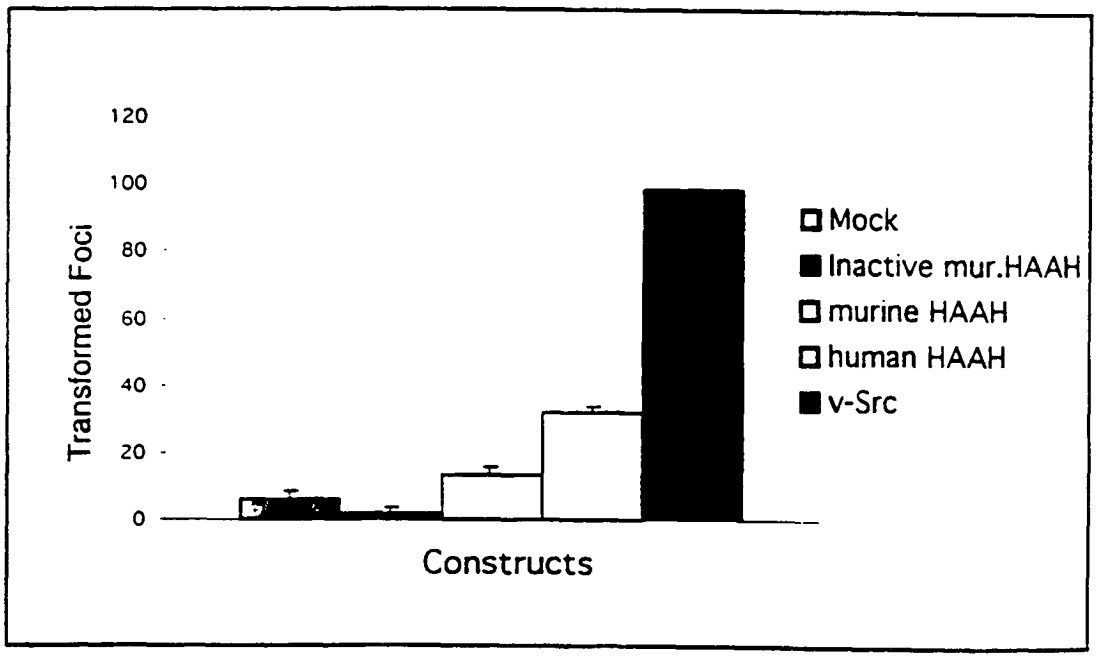
9. Procédé selon l'une quelconque des revendications précédentes, où ledit néoplasme est choisi parmi un carcinome hépatocellulaire, un cholangiocarcinome, un glioblastome et un neuroblastome.

10. Procédé selon l'une quelconque des revendications précédentes, dans lequel ledit anticorps se lie à un épitope au sein d'un site catalytique d'AAH.

11. Procédé selon la revendication 9, dans lequel ledit anticorps est une molécule de Fv à chaîne unique.

12. Utilisation in vitro d'un kit qui comprend un anticorps marqué de manière détectable qui se lie à une AAH, où l'utilisation consiste à aider au diagnostic d'un néoplasme détectable dans le liquide corporel d'un mammifère.

Fig. 1


120
100
80
60
40
20
0
Transformed Foci
Constructs
Mock
Inactive mur.HAAH
murine HAAH
human HAAH
v-Src

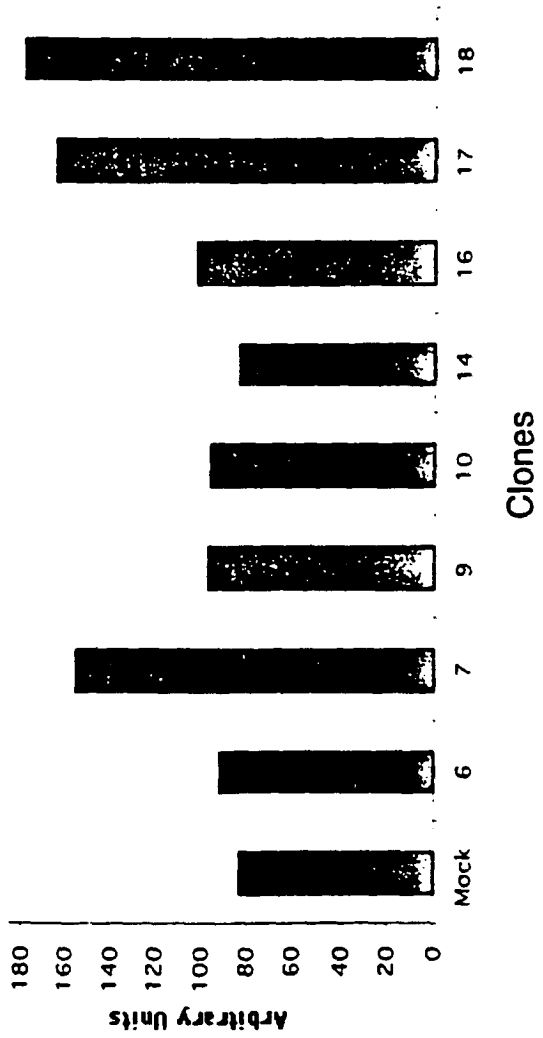

Arbitrary Units
0
20
40
60
80
100
120
140
160
180
Mock
6
7
9
10
14
16
17
18
Clones

Fig. 2

Fig. 3a

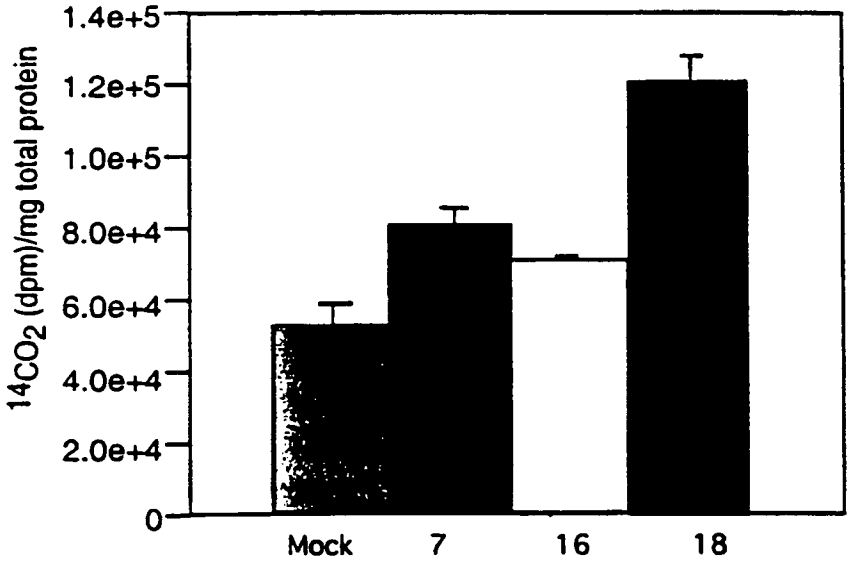
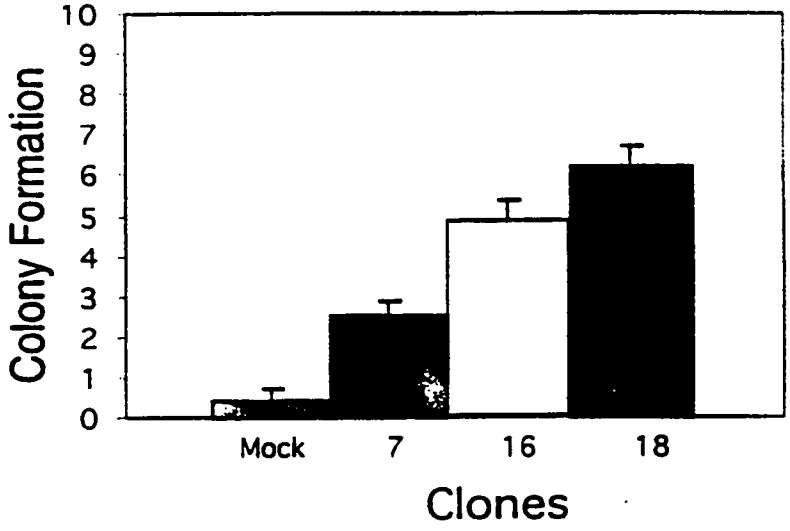

1.4e+5
1.2e+5
1.0e+5
8.0e+4
6.0e+4
4.0e+4
2.0e+4
0
$^{14}CO_2$ (dpm)/mg total protein
Mock
7
16
18

Fig. 3b


10
9
8
7
6
5
4
3
2
1
0
Colony Formation
Mock
7
16
18
Clones

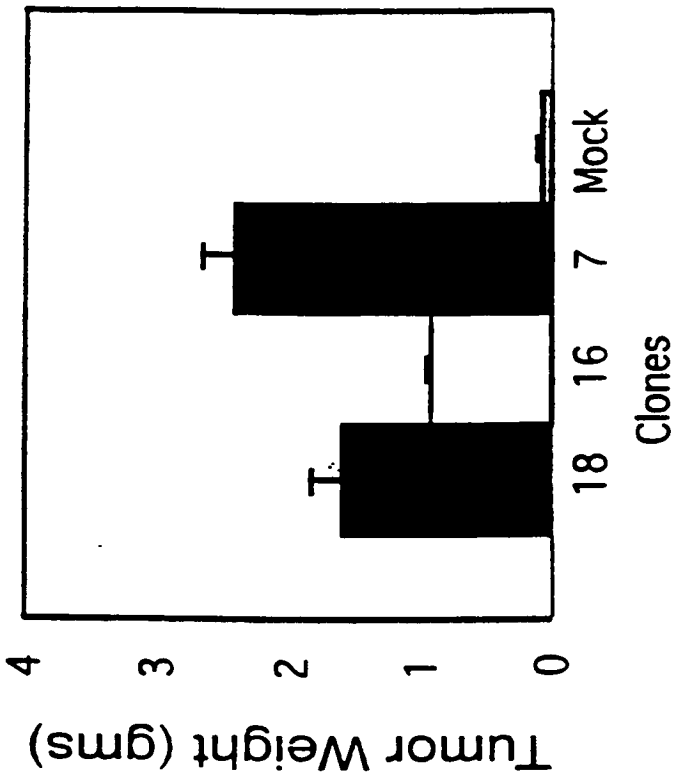


Fig. 4

Fig. 5a

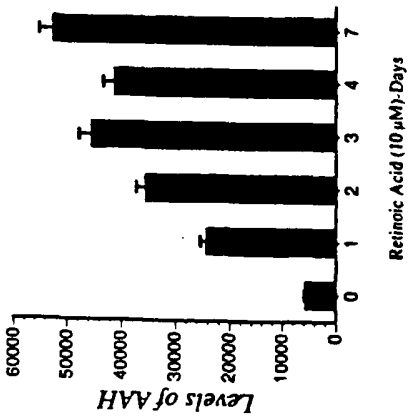


Fig. 5b

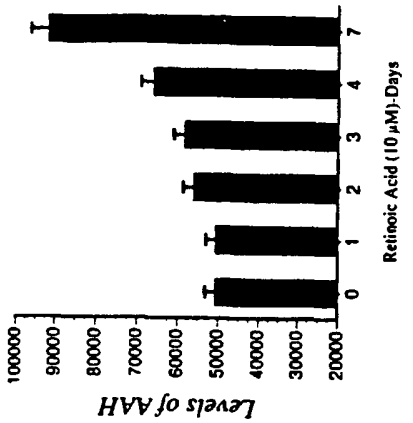


Fig. 5c

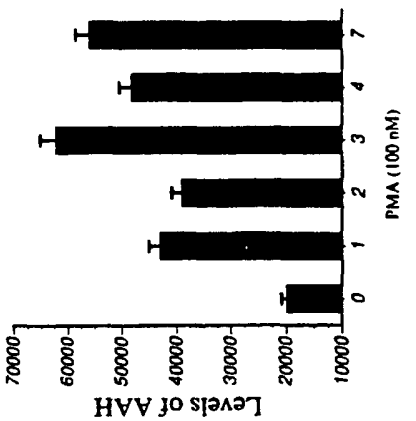


Fig. 5d

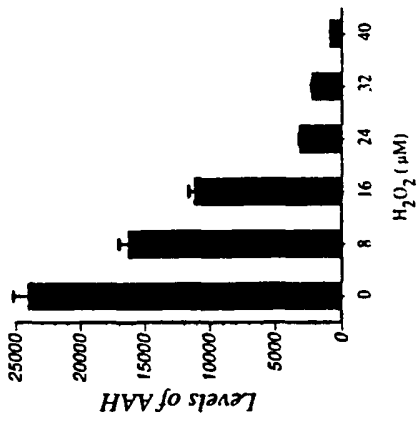
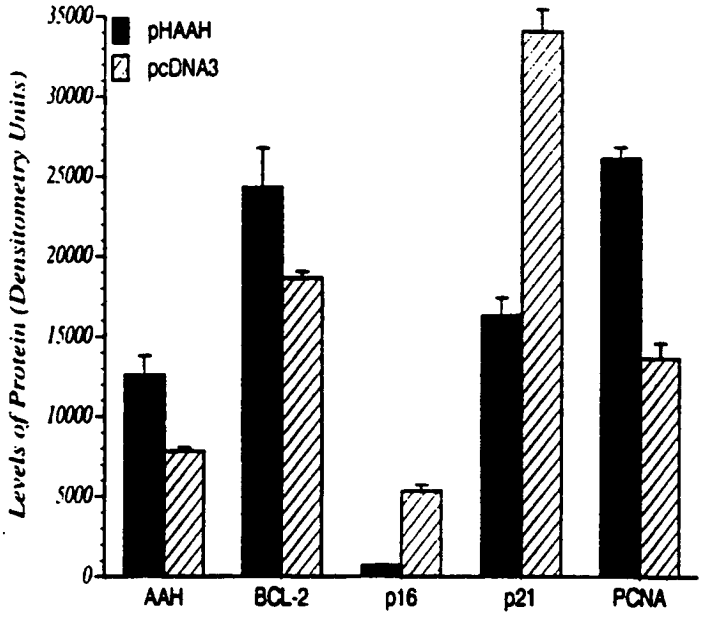


Fig. 6


pHAAH
pcDNA3
Levels of Protein (Densitometry Units)
35000
30000
25000
20000
15000
10000
5000
0
AAH
BCL-2
p16
p21
PCNA

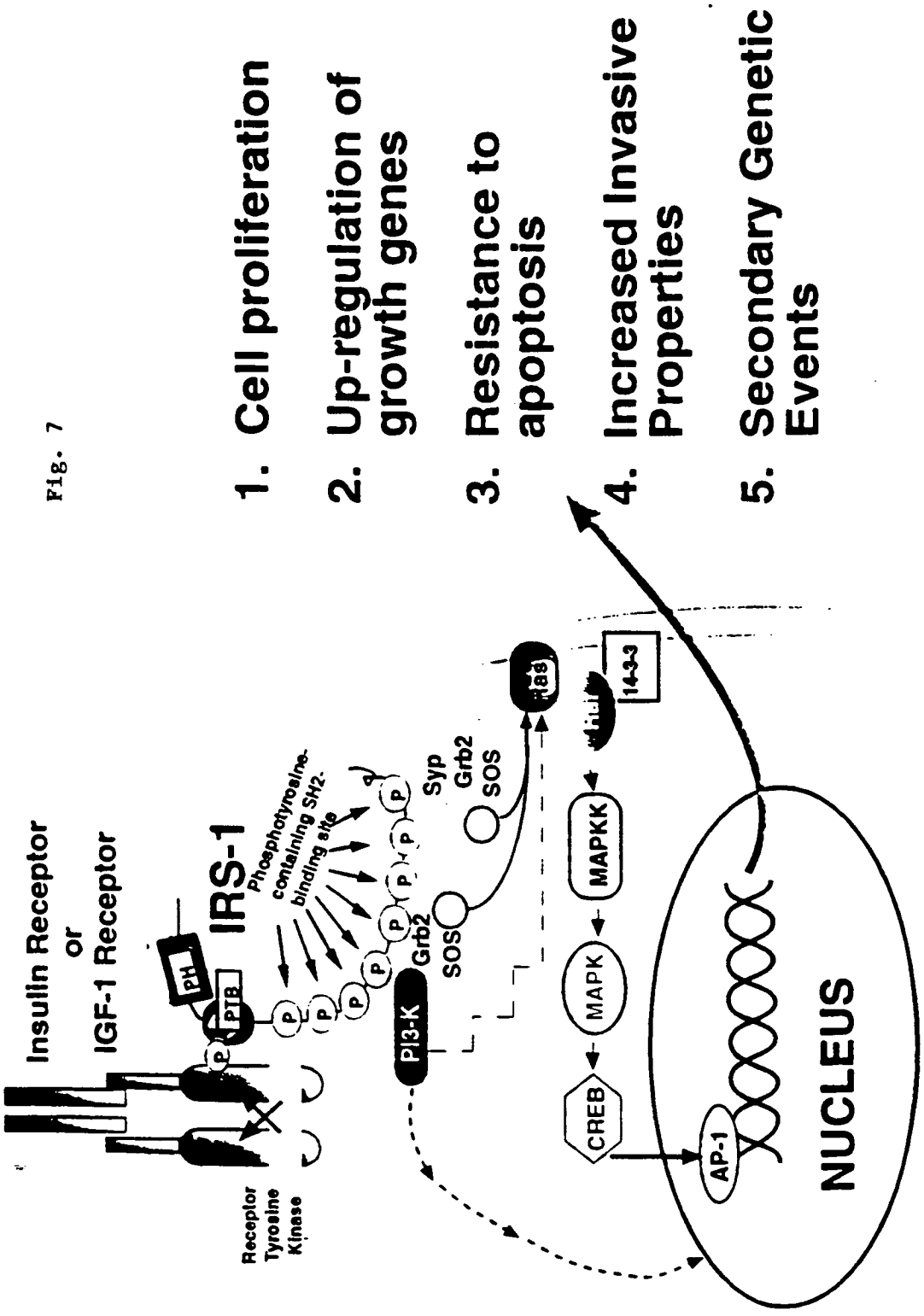

1. Cell proliferation
2. Up-regulation of growth genes
3. Resistance to apoptosis
4. Increased Invasive Properties
5. Secondary Genetic Events
Insulin Receptor
or
IGF-1 Receptor
Receptor Tyrosine Kinase
PH
PTB
IRS-1
Phosphotyrosine-containing SH2-binding site
Grb2
SOS
PI3-K
Syp
Grb2
SOS
ras
14-3-3
MAPKK
MAPK
CREB
AP-1
NUCLEUS

Fig. 7

Fig. 8

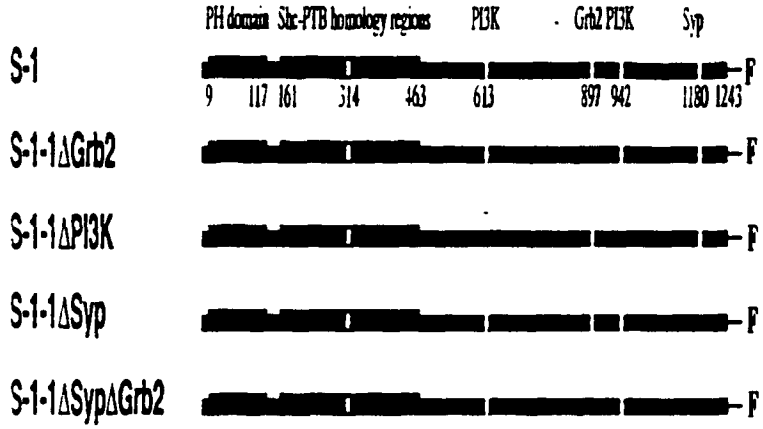

PH domain
Shc-PTB homology regions
PI3K
Grb2 PI3K
Syp
S-1
9
117
161
314
463
613
897
942
1180
1243
F
S-1-1ΔGrb2
S-1-1ΔPI3K
S-1-1ΔSyp
S-1-1ΔSypΔGrb2

Fig. 9

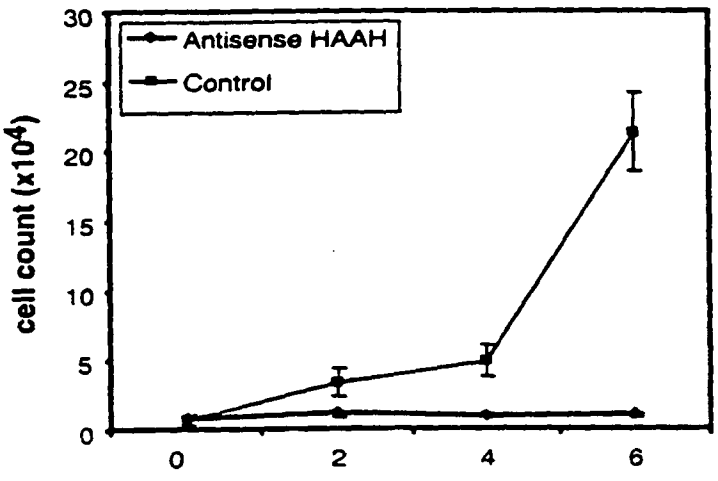


Fig. 1)

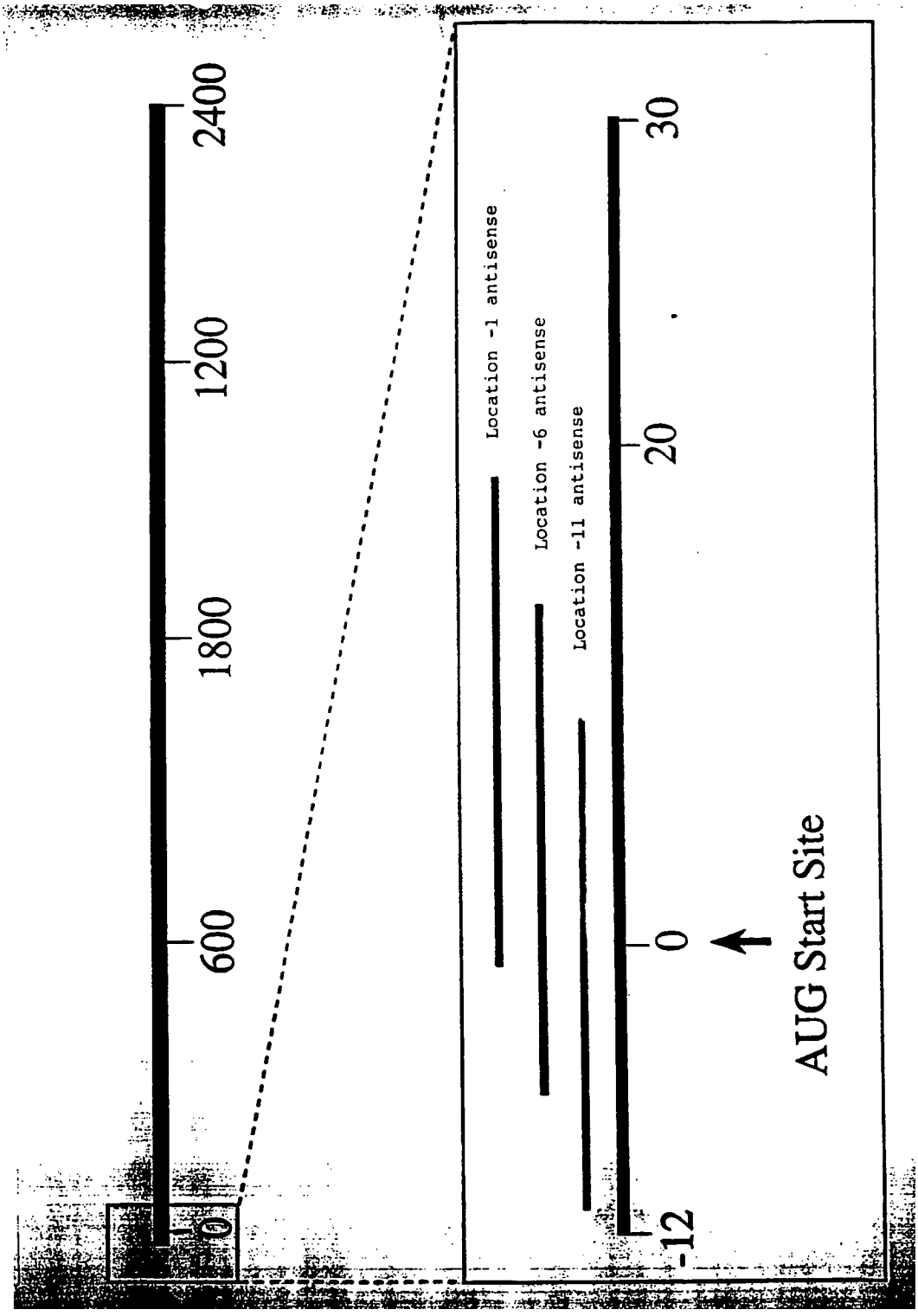

2400
1200
1800
600
0
-12
20
30
Location -1 antisense
Location -6 antisense
Location -11 antisense
AUG Start Site

Fig. 11

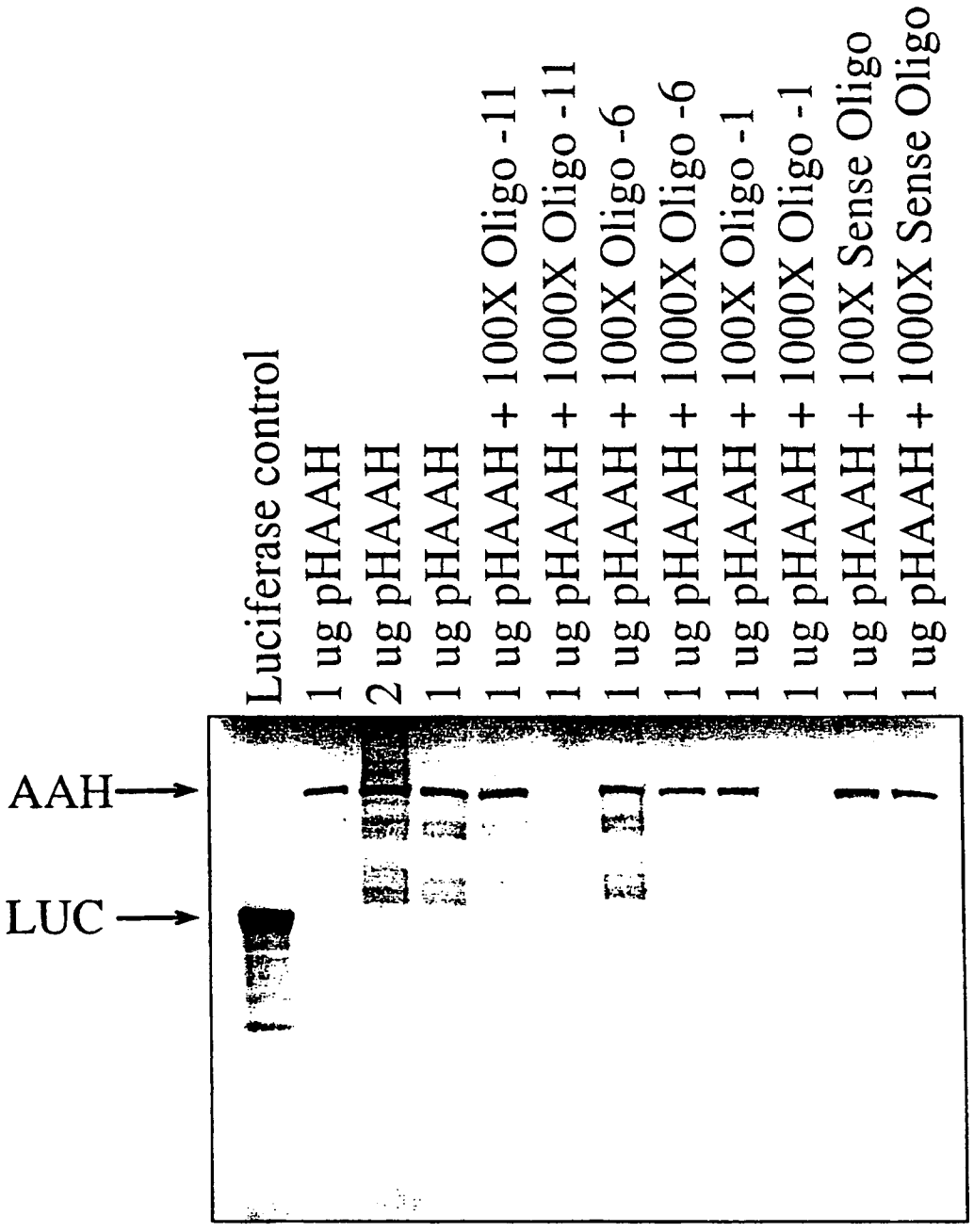
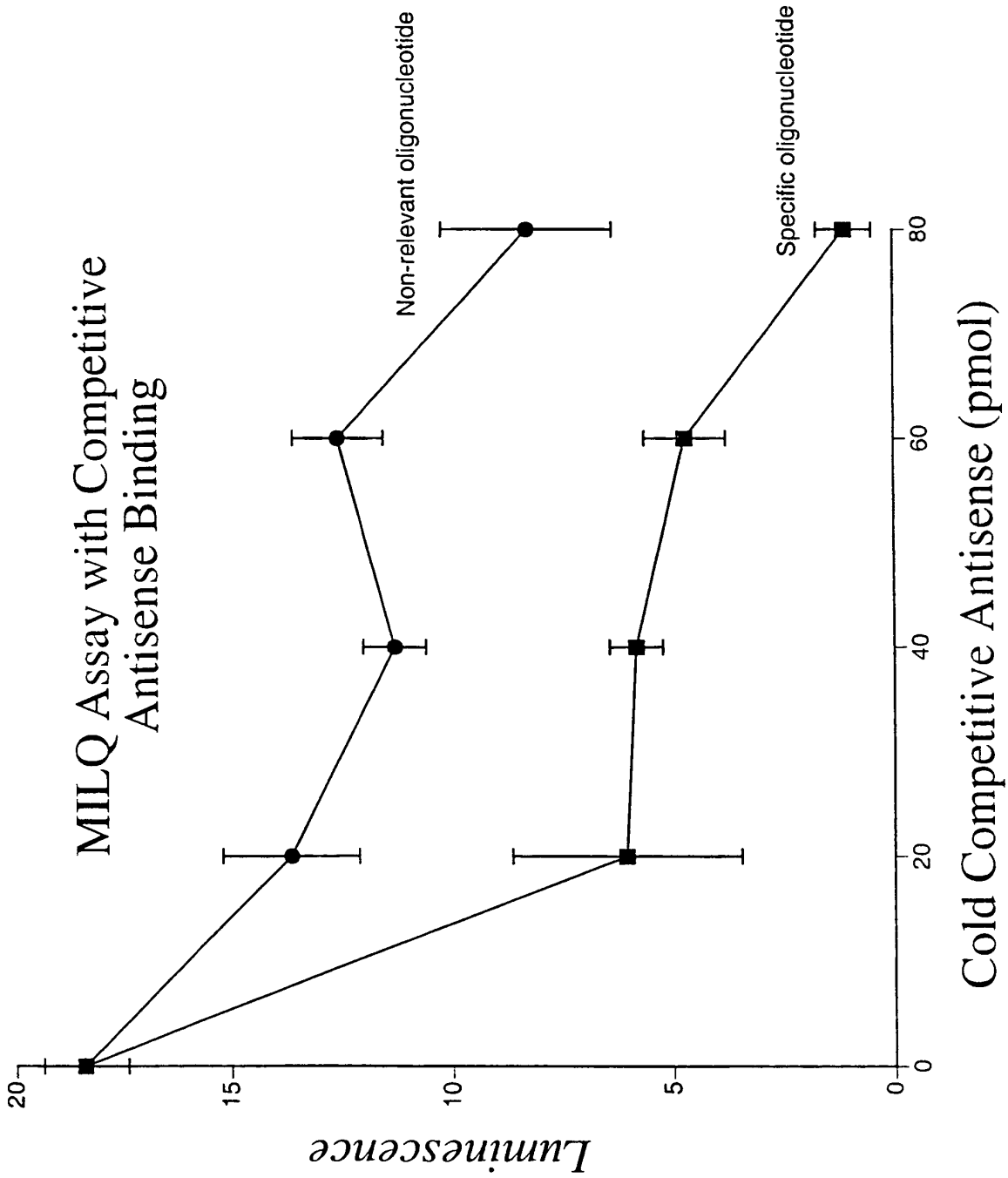

Luciferase control
1 ug pHAAH
2 ug pHAAH
1 ug pHAAH
1 ug pHAAH + 100X Oligo -11
1 ug pHAAH + 1000X Oligo -11
1 ug pHAAH + 100X Oligo -6
1 ug pHAAH + 1000X Oligo -6
1 ug pHAAH + 100X Oligo -1
1 ug pHAAH + 1000X Oligo -1
1 ug pHAAH + 100X Sense Oligo
1 ug pHAAH + 1000X Sense Oligo
AAH
LUC

Fig. 12


MILQ Assay with Competitive Antisense Binding
Non-relevant oligonucleotide
Specific oligonucleotide
Luminescence
Cold Competitive Antisense (pmol)
0
5
10
15
20
0
20
40
60
80

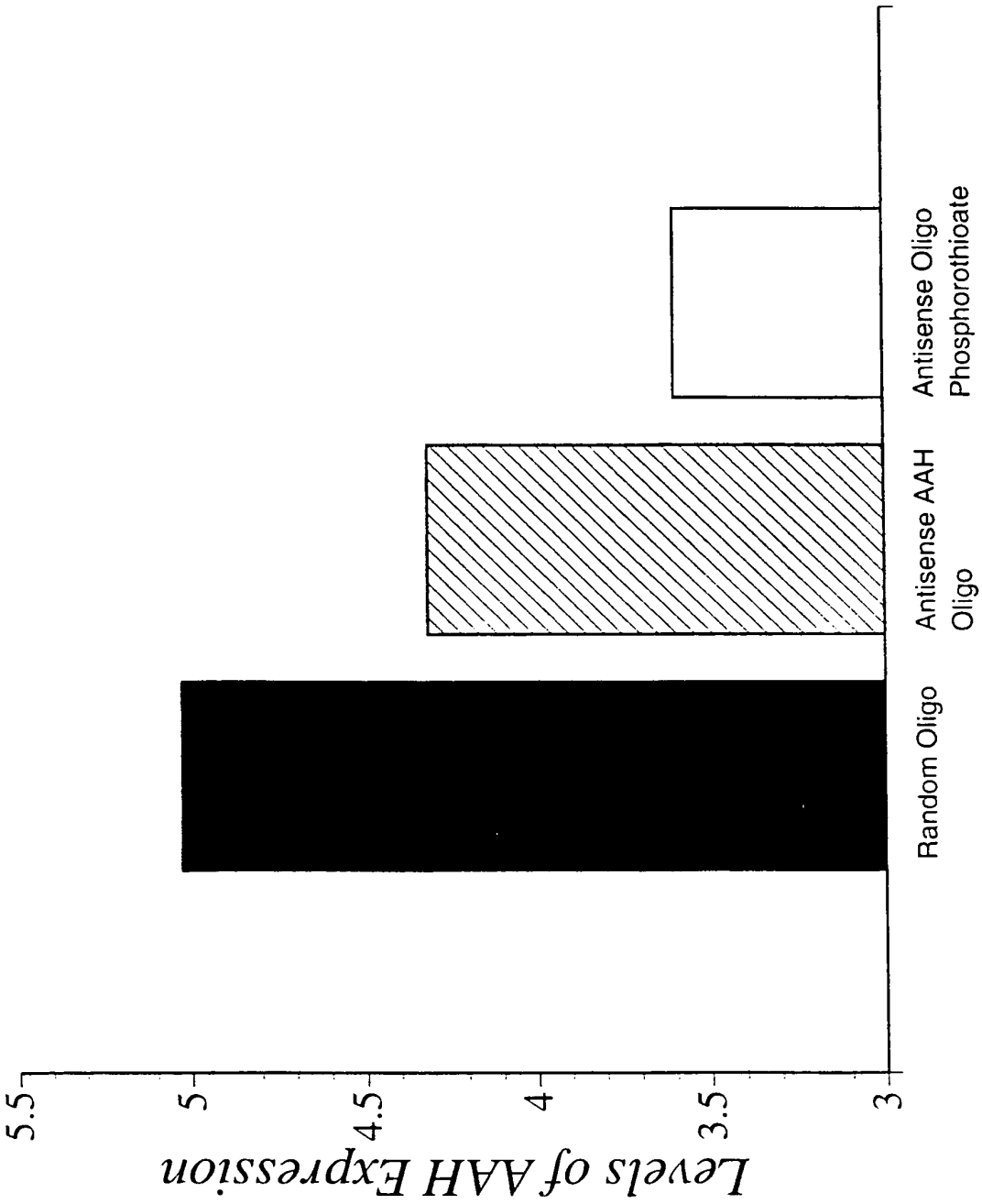

Levels of AAH Expression
5.5
5
4.5
4
3.5
3
Random Oligo
Antisense AAH Oligo
Antisense Oligo Phosphorothioate

Fig 13

Fig.14 A

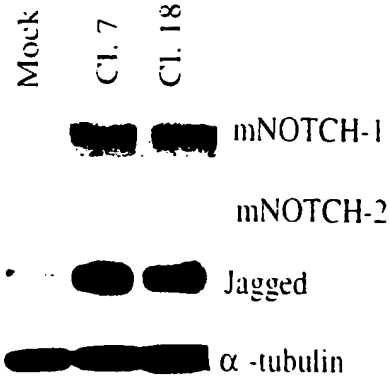


Fig. 14 B

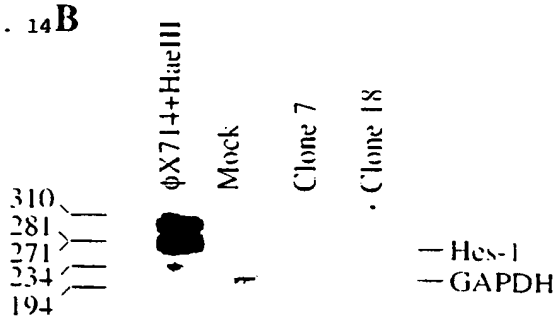
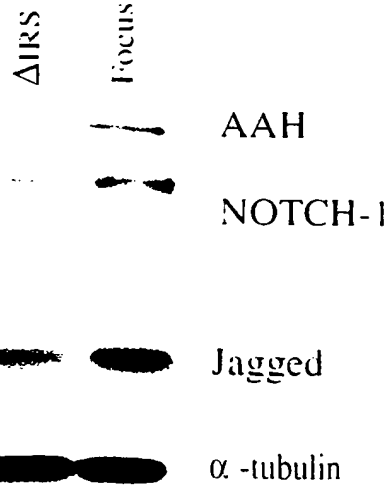


Fig. 14 C



专利名称(译)	恶性肿瘤的诊断		
公开(公告)号	EP1259813B1	公开(公告)日	2007-04-25
申请号	EP2000978436	申请日	2000-11-08
申请(专利权)人(译)	罗德岛医院，的寿命合作伙伴		
当前申请(专利权)人(译)	罗德岛医院		
[标]发明人	WANDS JACK R DE LA MONTE SUZANNE M INCE NEDIM CARLSON ROLF I		
发明人	WANDS, JACK, R. DE LA MONTE, SUZANNE, M. INCE, NEDIM CARLSON, ROLF, I.		
IPC分类号	G01N33/574 G01N33/573 A61K31/7088 A61K31/713 C12N15/11 A61K38/44 A61K31/44 A61K47/48 C07K16/40 C12Q1/26 A61P35/00 A61K31/00 A61K31/4412 A61K31/45 A61K38/43 A61K39/395 A61K45/00 A61K48/00 C07K14/47 C12N9/02 C12N15/09 C12N15/113 C12P21/08 C12Q1/02 G01N33/53 G01N33/577		
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优先权	09/436184 1999-11-08 US		
其他公开文献	EP1259813A2		
外部链接	Espacenet		

摘要(译)

本发明的特征在于一种通过使来自哺乳动物的体液与结合人天冬氨酰（天冬酰胺酰）β-羟化酶（HAAH）多肽的抗体接触以及通过抑制HAAH治疗恶性肿瘤的方法来诊断哺乳动物的恶性肿瘤的方法。还包括通过使肿瘤细胞与HAAH反义核酸接触来抑制肿瘤生长的方法。

Table 1: Amino acid sequence of HAAH

MAQRKNAKSS GNSSSSGSGS GSTSAGSSSP GARRETKHGG HKNGRKGGLS GTSFFTWFMV 61
IALLGVWTSV AVVWFDLVDY EEVLGKLGIY DADGDGDFDV DDAKVLLGLK ERSTSEPAVP 121
PEEAEPHTEP EEQVPVEAEP QNIEDEAKEQ IQSLLHEMVH AEHVEGEDLQ QEDGPTGEPQ 181
QEDDEFLMAT DVDDRFETLE PEVSHEETEH SYHVEETVSQ DCNQDMEEMM SEQENPDSSE 241
PVVEDERLHH DTDDVTYQVY EEQAVYEPLE NEGIEITEVT APPEDNPVED SQVIVEEVSI 301
FPVEEQQEVP PETNRKTDDP EQKAKVKKKK PKLLNKFDKT IKAELDAAEK LRKRGKIEEA 361
VNAFKELVRK YPQSPRARYG KAQCEDDLAE KRRSNEVLRG AIETYQEVAS LPDVPADLLK 421
LSLKRRSDRQ QFLGHMRGSL LTLQRLVQLF PNDTSLKNDL GVGYLLIGDN DNAKKVYEEV 481
LSVTPNDGFA KVHYGFILKA QNKIAESIPY LKEGIESGDP GTDDGRFYFH LGDAMQRVGN 541
KEAYKWYELG HKRGHFASVW QRSLYNVNGL KAQPWWTPKE TGYTELVKSL ERNWKLIRDE 601
GLAVMDKAKG LFLPEDENLR EKGDWSQFTL WQQGRRNENA CKGAPKTCTL LEKFPETTGC 661
RRGQIKYSIM HPGTHVWPHT GPTNCRLRMH LGLVIPKEGC KIRCANETRT WEEGKVLIFD 721

DSFEHEVWQD ASSFRLIFIV DVWHPELTPQ QRRSLPAI (SEQ ID NO:2; GENBANK Accession No. S83325; His motif is underlined; conserved sequences within the catalytic domain are designated by bold type)