Genome-wide gene expression analysis of chemoresistant pulmonary carcinoid cells

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Purpose: Carcinoids are highly chemoresistant tumors associated with a dismal prognosis. This study involved a comparison of the genome-wide gene expression pattern of a chemoresistant and a chemosensitive pulmonary carcinoid cell line to reveal factors that contribute to the resistant phenotype.

Materials and methods: Gene expression of UMC-11 chemoresistant carcinoid cells as assessed by 32 K microarray was compared with H835 chemosensitive carcinoid cells, and the genes that were differentially expressed and expected to be related to chemoresistance were selected.

Results: Drug-resistant UMC-11 cells exhibited increased expression of transcripts known to confer resistance to different cytostatics such as P-glycoprotein, multidrug resistance-associated proteins 2 and 3, effectors of the glutathione detoxification and xenobiotics degradation pathways, and ion transporters including Na⁺/K⁺-adenosine triphosphatase. In addition, enhanced transcription of several S100 proteins, capable of suppressing apoptosis, regulation of topoisomerase I (topo I) expression by antisense transcripts from TOPO1 pseudogenes, and alterations of the cytoskeleton seem to contribute to the multidrug-resistant phenotype. A multitude of epidermal growth factor (EGF)-related and neuropeptide growth factors, overexpression of proteases, and appearance of aerobic glycolytic metabolism complement the malignant phenotype of the UMC-11 cells.

Conclusion: The multidrug-resistant phenotype of the UMC-11 pulmonary carcinoid cell line seems to be mediated by classical efflux pumps, drug metabolization or conjugation systems, and, possibly, modulation of apoptotic cell death by S100 proteins and topo I expression by pseudogene transcripts. Autocrine or paracrine stimulation by a host of EGF-related and neuropeptide growth factors, as well as high metastatic potency indicated by increased expression of components of aerobic glycolysis and proteolytic enzymes, may furthermore account for the failure of therapeutic interventions.

Keywords: neuroendocrine tumor, drug resistance, microarray, drug transporter, apoptosis

Introduction

Pulmonary carcinoid tumors are considered low-grade malignant neoplasms of the neuroendocrine cells, originating from the Kulchitsky cells of the bronchial mucosa layer, and represent about 1%–5% of all lung tumors.¹-³ Ninety percent of these tumors termed typical carcinoids are well differentiated and characterized by a small degree of mitosis, pleomorphism, and necrosis.⁴,⁵ The remaining 10% of the tumors with increased mitotic activity, nuclear pleomorphism, and cellular irregularity are classified as aggressive atypical carcinoids.⁶,⁷ The patients with lung carcinoids can be cured by surgical resection, but a fraction of tumors gives rise to widespread metastasis within
several years after primary treatment. In contrast to the more indolent, well-differentiated neuroendocrine tumors exhibiting metastases in less than 15% of cases and revealing a 5-year survival rate of more than 90%, well-differentiated neuroendocrine carcinomas are more aggressive, develop metastases in 30%–50% of cases, and yield a 5-year survival rate between 40% and 60%. Almost all recurrences of either typical or atypical carcinoids involve distant sites. Finally, patients with malignant carcinoids show a 5-year survival rate of about 20% and a median survival of 2 years in the presence of liver metastases. Medical treatment of metastatic disease includes somatostatin (SST) analogs, α-interferons, and chemotherapy. Basically, chemotherapy can be considered for patients with carcinoids progredient under nontoxic therapy, provided that they have significant symptoms and poor prognosis. Clinical trials demonstrated that the response rates to single-agent chemotherapy limited to approximately 20%, and for multiagent chemotherapy, the response rates are invariably less than 40%. Moreover, these responses are frequently short-lived and rarely translate to prolonged survival. In contrast, responses of rapidly proliferating, poorly differentiated (atypical or small cell-like) carcinoid tumors to chemotherapy are high but the duration of response is extremely short. In these studies, doxorubicin, 5-fluorouracil (5-FU), dacarbazine, streptozotocin, cyclophosphamide, cisplatin, and etoposide were used either in the following gene expression analysis. The aim of this study was to compare the transcriptome of the highly chemoresistant UMC-11 with the sensitive H835 cell line to delineate candidate genes possibly conferring multidrug resistance to pulmonary carcinoids.

Materials and methods

Chemicals and cell lines

Unless otherwise noted, all chemicals and solutions were obtained from Sigma-Aldrich (St. Louis, MO). UMC-11 and H835 pulmonary carcinoid cell lines were purchased from the American Tissue Culture Collection (Manassas, VA). Cells were cultured in RPMI-1640 medium supplemented with 10% fetal bovine serum (Seromed, Berlin, Germany), 4 mM glutamine, and antibiotics. UMC-11 was subcultured by trypsinization (2.5% trypsin in EDTA solution; Boehringer Mannheim, Germany), and H835 cells growing in suspension were maintained by replacement of the medium and dispersed by trypsin treatment.

Cell proliferation assay

Cells were harvested, counted, and distributed into the wells of flat-bottomed 96-well microtiter plates at a density of 1 × 10^4 cells/well in 100 µL medium. 100 µL of appropriate dilutions of test compounds was added to each well, and the plates were incubated under tissue culture conditions for 4 days. Stock solutions of the compounds were prepared in either 70% ethanol or dimethyl sulfoxide and diluted more than 100-fold for use in chemosensitivity assays. Solvent-control wells were included in all tests. Dose–response curves were obtained by the assessment of cell growth at 2-fold drug dilutions in triplicate and used for the calculation of the half maximal inhibitory concentration (IC_{50}) values. Cell proliferation was quantified using a modified tetrazolium dye (3-(4,5-dimethylthiazol-2-yl)-2,5-diphenyltetrazolium bromide) assay (EZ4U; Biomedica, Vienna, Austria).

Genome-wide gene expression analysis

Lysates of 30 × 10^6 cells (extraction buffer: 4 M guanidine isothiocyanate, 0.5% sodium N-lauroyl sarcosinate, 10 mM EDTA, 5 mM sodium citrate, and 100 µM β-mercaptoethanol; 30 minutes, 4°C) were added to cesium trifluoroacetate and centrifuged (46,000 rpm, 15°C, 20 h). Supernatant containing DNA was removed and RNA was precipitated with ice-cold 96% ethanol. Pellets were washed and, following removal of ethanol, resuspended in sterile water. RNA content was measured photometrically.

Gene expression analysis was performed using the Applied Biosystems (ABI) Human Genome Survey Microarray V2.0 (Applied Biosystems, Foster City, CA) according to the manufacturer’s instructions. Therefore, 2–5 µg mRNA (20–50 µg total RNA) was reversely transcribed (RT) to first-strand cDNA (MyCycler thermocycler; Bio-Rad, Hercules, CA). The RT mixture was labeled on ice and
purified according to the manufacturer’s instructions for the Applied Biosystems 1700 RT Labeling Kit v002 (Applied Biosystems). Hybridization of cDNA and microarray analysis (Applied Biosystems 1700) were carried out following the manufacturer’s chemiluminescence detection kit protocol. Data for each cell line (n = 2) were filtered, normalized, and log2-transformed before further processing was done using Microsoft Excel software (Microsoft, Redmond, WA) or Statistical Analysis of Microarray (false discovery rate of 10%; Stanford University, Stanford, CA). ABI 1700 gene identities can be accessed via the Panther classification system (www.pantherdb.org).

Results

We previously reported the following IC50 values (IC50 in UMC-11/IC50 H835, mean ± standard deviation) for a range of drugs that were obtained for UMC-11 and H835 cells in chemosensitivity assays: vinblastine (ng/mL), 2 ± 0.35/2 ± 0.3; taxol (ng/mL), 10 ± 4.4/9 ± 3.9; camptothecin (nM), 18 ± 5.0/6.5 ± 4.3; 5-FU (µM), 30 ± 4.6/45 ± 8.7; doxorubicin (nM), 370 ± 72/73 ± 2.4; gemcitabine (nM), 833 ± 103/30.0 ± 20; tamoxifen (µM), 9 ± 3.3/7 ± 2.4; cisplatin (µM), 33 ± 15/33 ± 7.0; oxaliplatin (µM), 5 ± 0.25/6 ± 0.51; carboplatin (µM), 36 ± 7.1/36 ± 9.9; mitomycin (ng/mL), 156 ± 15/35 ± 9.0; streptozotocin (µg/mL), 180 ± 33/60 ± 19; etoposide (µg/mL), 45 ± 12.3/30.25 ± 0.02; and dacarbazine (µg/mL), 4 ± 2.3/16 ± 3.9. Thus, UMC-11 cells were resistant to taxol, camptothecin, 5-FU, doxorubicin, gemcitabine, tamoxifen, cisplatin, streptozotocin, and etoposide (IC50 exceeding peak plasma concentration).16

Genome-wide expression analysis was performed for chemoresistant UMC-11 and chemosensitive H835 pulmonary carcinoid cells, and the genes that were significantly overexpressed more than 4-fold in the former cell line compared with the latter were grouped according to their cellular functions and pathways (Table 1). Genes were furthermore selected in regard to their possible relation with the resistant phenotype of the UMC-11 cells. The low number of genes with lower expression in UMC-11 compared with H835 cells was not included in this analysis because of the absence of transcripts with a connection to chemoresistance. After filtering of the 1,520 transcripts that were overexpressed more than 4-fold in UMC-11 compared with H835 carcinoid cells, 386 were annotated to the corresponding genes, and 102 of these are expected to be involved in proliferation, metastasis, and drug resistance of the carcinoid cells, as listed in Table 1.

In UMC-11 cells, enzymes mainly involved in glucose and energy metabolism that were preferentially expressed included lactate dehydrogenase (LDH/LDH), glyceraldehyde 3-phosphate dehydrogenase (GAPDH), hexokinase 1 (HK1), citrate synthetase (CS), and pyruvate dehydrogenase kinase 4 (PDK4), indicating differences in glucose uptake and utilization between the 2 cell lines. Increased expression of hypoxia-inducible gene domain family member 1A (HIGD1A) and argyrosine receptor nuclear translocator 2 (ARNT2) together with the changes in regard to glucose metabolism pointed to the presence of an increased rate of aerobic glycolysis (Warburg effect) in UMC-11 cells. Furthermore, in these cells, a number of proteases and protease inhibitors were highly expressed, including serine proteases 1–3 (PRSS1-3), serine protease inhibitors (SERPINS A2, E2, B6, and A10), cathepsin L (CTSL), matrix metalloproteinase 13 (MMP13, identical to collagenase 3), and the corresponding tissue inhibitors of metalloproteinase 1 and 3 (TIMP1 and 3). Hypoxia is known to select for an aggressive cancer phenotype characterized by an increased capacity to infiltrate tissues.

In addition, UMC-11 cells showed higher expression of a large number of membrane transporters compared with H835 cells, thus comprising Na+/K+-adenosine triphosphatase ([ATPase], ATP1B1), the FXYD regulatory subunit 2 (FXYD2), and ion pumps regulating intracellular Ca2+ concentration (ATP2A2, ATP2B1, and ATP2C2). The subfamily members of ATP-binding cassette (ABC) transporters (ABC1, C2, and C3) resemble the classical resistance proteins P-glycoprotein (P-gp) and multidrug resistance-associated proteins (MRPs) 2 and 3. Furthermore, the 2 solute carrier organic anion transporters (SLCO1A2 and SLCO2A1), shuttling bile acids, prostaglandins (PGs), and other anions, and a number of solute carriers transporting aspartate/glutamate (SLC1A6), biogenic amines (SLC18A1), anions (SLC4A2), sodium (SLC4A11), potassium chloride (SLC12A7), sodium phosphate (SLC20A2), and guanosine diphosphate-fucose (SLC35C1) were found to be upregulated.

Moreover, a large number of growth factors and receptors were overexpressed in UMC-11 compared with H835 cells, including members of the epidermal growth factor (EGF) family, insulin-like growth factor (IGF) family, neurotrophins, and others. In particular, EGF receptor (EGFR), v-erb-b2 erythroblastic leukemia viral oncogene homolog 3 (ERBB3), transforming growth factors (TGFβ1, β1, and β2), ephrin (ERG), and amphiregulin (AREG) constitute a growth regulatory system, with heat shock protein 90 (Hsp90) and sprouty 2 (SPRY2) as modulators. A second independent growth factor pathway was provided by IGF2 and regulatory binding proteins (IGFBP1, 3, 5, 6, and
Table 1: Relative mRNA expression of selected genes in UMC-11 and H835 carcinoid cell lines

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(Continued)
IGF2BP2), supplemented by a number of neuropeptides, namely vasointestinal peptide (VIP), neurotensin (NTS), VGF (VGF nerve growth factor inducible), and neuropeptide W (NPW). Interleukin-8 (IL-8), calcitonin-related polypeptide β (CALCB), angiotensin (AGT), and fibroblast growth factor 12 (FGF12) may in addition be involved in the regulation of cell proliferation, with SST as inhibitor. Increased overexpression of adenylate cyclase (ADCY2) pointed to an important role of this enzyme in signal transduction pathways of the growth stimulators.

S100 proteins regulate intracellular processes, such as cell growth and motility, cell cycle regulation, transcription, and differentiation. Twenty members have been identified so far, and altogether, S100 proteins represent the largest subgroup of the EF-hand Ca²⁺-binding protein family. A unique feature of these proteins is that individual members are localized in specific cellular compartments from where some are able to relocate upon Ca²⁺ activation, thus transducing the Ca²⁺ signal temporally and spatially by interacting with different targets highly specific for each S100 protein. Some of the S100 Ca²⁺-binding proteins overexpressed in the UMC-11 cells, namely A2, A4, A6, A10, P, A14, and A16, seem to have important functions in Ca²⁺ homeostasis, growth, and apoptosis. Differences in the expression of cytoskeleton constituents comprised type I keratins (KRT18 and KRT19), type II keratins (KRT7 and KRT8), cadherin 1 (CDH1), villin 1 (VIL1), claudins (CLDN4, 7, and 20), tubulin β3 (TUBB3), thymosin β4, X-linked chromosome (TMSB4X), and stromal interaction molecule 2 (STIM2).

Finally, detoxification of xenobiotics may be mediated by conjugation to sulphur-containing compounds, and the corresponding enzymes comprising glutathione S-transferase θ1 (GSTT1), glutathione S-transferase π1 (GSTP1), glutaredoxin (GRX), arylsulfatase (ARSE/D/SULF2), glutathione S-transferase Ω2 (GSTO2), and thiosulfatase (TST) were found to be overexpressed in UMC-11 cells. Other mechanisms for the metabolism of drugs in UMC-11 cells included the cytochrome P450 (CYP) oxidoreductases (CYP26B and CYP12B6) that are regulated by the consistently overexpressed aryl hydrocarbon receptor (AHR), aldehyde dehydrogenase 7A1 (ALDH7A1), and aldo-keto reductase 7A3 (AKR7A3). Topoisomeraseases are important targets of a range of cytotoxic drugs, in particular (topol) for camptothecin derivatives like irinotecan and topotecan. Although TOP1 expression was elevated in UMC-11 cells, increased amounts of anti-sense transcripts stemming from TOPP1 and TOPP2 are expected to downregulate TOP1 to induce drug resistance.

Discussion

Neuroendocrine lung tumors are highly refractory to chemotherapy, but the detailed mechanisms resulting in chemoresistance have not been fully characterized so far. In contrast to the typical carcinoids, where multidrug resistance (MDR) is mediated by P-gp but not MRP, the atypical carcinoids exhibit cellular detoxification by P-gp, MRP, and GST-π expression. Both Bcl-2 and p53 proteins appear unchanged in carcinoids, suggesting that the apoptotic capacity conferred by these two gene products is not involved in chemoresistance. The chemoresistance of typical carcinoids was questioned, in general, based on their sensitivities observed in in vitro tests using these well-differentiated tumors. We recently compared the chemosensitivity profiles of the three carcinoid cell lines UMC-11, H727, and H835 and demonstrated marked chemoresistance to a wide range of cytotoxic drugs in UMC-11 cells in contrast to the other two chemosensitive cell lines. In this study, genome-wide gene expression analysis was used to search for candidate genes overexpressed in UMC-11 cells compared with H835 cells, and that would possibly hold the potential to confer chemoresistance.

Expression of hexokinase (HK1), an enzyme that traps glucose inside the cell by catalyzing phosphorylation to glucose 6-phosphate, and thus, maintains the downhill concentration gradient permitting facilitated glucose transport into cells for utilization, was higher in UMC-11 than in H835 cells. GAPDH catalyzes the conversion of glyceraldehyde 3-phosphate to D-glyceraldehyde 1,3-bisphosphate during the sixth step of glycolysis. LDH/LDHB catalyzes the conversion of l-lactate and nicotinamide adenine dinucleotide (NAD) to pyruvate and NADH in the final step of anaerobic glycolysis. This enzyme normally converts pyruvate, the final product of glycolysis, to lactate under hypoxic conditions. PDK4 is a member of the PDK/BCKDK protein kinase family and encodes a mitochondrial protein with a histidine kinase domain. This protein inhibits the PD complex (PDC) by phosphorylating one subunit, which contributes to the regulation of glucose metabolism. The PDC converts pyruvate to acetyl coenzyme A (acetyl-CoA) by decarboxylation. Acetyl-CoA may then enter into the citric acid cycle for cellular respiration, thereby the glycolytic metabolic pathway is linked to the citric acid cycle and energy released in the form of NADH PD. In summary, high expression of these enzymes may indicate a shift of the cellular metabolism to increased uptake and catabolization of glucose.

Tumor cells exhibit aerobic glycolysis frequently (Warburg effect), and according to our results, the increased expression of a number of relevant genes corroborate
this metabolic shift. Unlike in H835 cells, HIGD1A is overexpressed in UMC-11 cells. HIG1 was found as a novel gene, with unknown function induced by hypoxia and glucose deprivation in human cervical epithelial cells in vitro.\textsuperscript{20} Hypoxia-induced transcription of the HIF-target genes HIGD1A, egl nine homolog 1 (EGLN1), Bcl2-interacting-protein 3 (BNIP3), and phosphofructokinase 1 is independent of the CH1 domain of CBP/p300, whereas stanniocalcin 1 and SLC2A1 (glucose transporter 1) were moderately affected by SLCO1A2 expression, abundant transcripts of ARNT2, a member of the basic-helix-loop-helix-Per-Arnt-Sim (bHLH-PAS) superfamily of transcription factors that was observed in UMC-11 cells, heterodimerize with HIF-1 in the nucleus and, thus, promote expression of oxygen-responsive genes. In contrast to HK1, GAPDH is known to be induced by hypoxia or nickel.\textsuperscript{21,22} Therefore, UMC-11 cells clearly showed signs of aerobic glycolysis and induction of hypoxia-induced genes under aerobic conditions.\textsuperscript{25}

Most cancers exhibit elevated protease levels that contribute to certain aspects of tumor behavior in regard to growth, metastasis, and angiogenesis. Increased expression of the CTSs of the cysteine protease family, such as CTSL, correlates with invasion and migration of highly metastatic B16 melanoma cells.\textsuperscript{26} Trypsin 1 and 2, serine protease 3 (PRSS1, 2, and 3), and MMP13 were preferentially expressed in UMC-11 but not in H835 cells. Trypsin is implicated in colorectal carcinogenesis and promotes growth and dissemination of various cancers.\textsuperscript{27} Furthermore, trypsin expression is an indicator of poor prognosis and shorter disease-free survival of colorectal cancer patients. Trypsin seems to act directly by the digestion of type I collagen or indirectly by the activation of other protease cascades like MMPs. Stimulated by trypsin, both MMPs and protease-activated receptor 2 may activate the mitogen-activated protein kinase–extracellular signal-regulated protein kinase (MAPK-ERK) pathway through EGFR. MMPs may play an important role in both transformation from adenoma to carcinoma and initiation of invasion and metastasis. Upregulation of MMP13 at the tumor-bone interface is crucial for tumor-induced osteolysis, which suggests that MMP13 is a potential therapeutic target for breast cancer bone metastasis.\textsuperscript{28} Tumor cell proteases are under tight regulation by protease inhibitors like TIMP2 and 3, both acting on MMP13.\textsuperscript{29} Moreover, the highly expressed serpins (serine protease inhibitors) A1, A10, E2, and F1 are proteins with similar structures that were first identified as inhibitors.\textsuperscript{30} SERPINA10 was one of the six novel marker genes for neuroendocrine carcinoma cells comprising paraneoplastic antigen MA2 and testican 1 precursor (SPOCK1) among others.\textsuperscript{31} Overexpression of these proteases in conjunction with their regulatory inhibitors in UMC-11 cells pointed to a highly metastatic and aggressive phenotype.

The solute carrier, human organic anion transporting polypeptide SLCO1A2 is highly expressed in the intestine, kidney, cholangiocytes, and the blood–brain barrier.\textsuperscript{32} This localization suggests that the transporter may be crucial for the distribution of clinically important drugs, besides shutting bile acids. SLCO2A1 transports PGs like PGE2 that was identified as the principal prostanoid promoting cell growth and survival in colorectal tumors by increasing Bcl-2 expression, which promotes cell survival under hypoxic conditions.\textsuperscript{33} The other solute carriers overexpressed in UMC-11 cells are involved in the maintenance of ion homeostasis (Na\textsuperscript{+}, K\textsuperscript{+}, H\textsuperscript{+}, and others), with no clear relation to chemoresistance.

MDR of tumor cells against a whole group of cytotoxic compounds is mediated by ABC efflux pumps.\textsuperscript{34} P-gp (ABCB1), encoded by the MDR1 gene, was the first such transporter detected. Determination of MDR1 mRNA in human cancers revealed elevated expression in untreated, intrinsically drug-resistant tumors, including those derived from carcinoid tumors.\textsuperscript{35} Further studies resulted in the characterization of the MRPs in some drug-selected cancer cell lines.\textsuperscript{36} UMC-11 cells expressed ABCC2 (MRP2) and ABCC3 (MRP3) at higher levels than the drug-sensitive H835 cell line. MRPs appear to mediate glutathione (GSH) homeostasis and the efflux of oxidized GSH derivatives (eg, glutathione disulfide, S-nitrosoglutathione, and glutathione-metal complexes) and other glutathione S-conjugates.\textsuperscript{37} Among the many processes, apoptosis, cell proliferation, and differentiation are influenced by GSH transporters. MRP gene expression was detected in almost all lung cancer cell lines, including carcinoids and normal lung tissue.\textsuperscript{36} Furthermore, ABCG1 and ABCD1 are involved in the transport of lipids. In conclusion, MDR in UMC-11 cells seems to be partially effectuated by the classical ABC drug efflux pumps.

UMC-11 cells exhibited higher expression of ATP1B1 encoding the Na\textsuperscript{+}/K\textsuperscript{+}-ATPase that exchanges three intracellular sodium for two extracellular potassium ions and is upregulated by cyclic adenosine monophosphate (cAMP). It serves as a signal transducer, regulates cell adhesion, and its aberrant expression and activity are implicated in the development and progression of different cancers.\textsuperscript{38} Inhibition of this pump by cardiac glycosides reduces tumor metastasis, which
is possibly due to the sensitization to anoikis. Altered ion gradients were also proposed as a potential cause of resistance to chemotherapy. Furthermore, inhibition of Na+/K+-ATPase markedly reduces intracellular cisplatin accumulation. A hemisynthetic cardenolide shows high anticancer activity in cells expressing diverse forms of MDR, which is either conferred by inherent overexpression of selected drug transporter proteins or induced by a range of chemotherapeutic agents. Ion transport by Na+/K+-ATPase is modulated by a regulatory subunit belonging to the FXYD protein family. UMC-11 cells showed high levels of FXYD2 and FXYD3 constituting the Na+/K+-ATPase γ-subunit and an ion pump regulator, highly expressed in breast cancers and responsible for cancer cell proliferation, respectively. The other ion pumps overexpressed in UMC-11 cells namely ATP2A2, B1, and C2 are responsible for the maintenance of cytoplasmic Ca2+ homeostasis.

Growth factors and their cognate receptors do not confer chemoresistance, but since they determine the proliferation rate, they constitute interesting targets for chemotherapy. The EGF/EGFR and ERBB3 growth factor system, as found overexpressed in UMC-11 cells, comprises a range of receptors and mitogenic factors including TGFα and others. The coexpressed factors TGFβ1 and β2 are involved in the regulation of many physiological processes like cell growth, cell differentiation, and extracellular matrix production among others. Moreover, TGFβ may function as tumor suppressor or promotor depending on the type, differentiation state, and physiological characteristics of target cells. The ErbB ligand epiregulin, found in UMC-11 cells, is highly expressed in non-small cell lung carcinoma (NSCLC) and correlates with nodal metastasis and a shorter duration of survival. The related and coexpressed EGFR/TGFR ligand, amphiregulin, was found to predict NSCLC resistance to gefitinib and to suppress apoptosis by sequestration of BAX in the cytoplasm. EGFR and activated EGFR (p-EGFR) were expressed in both well-differentiated gastrointestinal carcinoids and pancreatic endocrine tumors in primary and metastatic specimens with a poor prognosis. The role of EGFR was studied in pulmonary typical and atypical carcinoid tumors. Analysis showed that approximately half of typical carcinoids and one-third of atypical carcinoids produce EGFR, and all of the tumors exhibit moderate to intense staining for ErbB3 and ErbB4 but lack expression of ErbB2. High expression of the chaperone Hsp90 stabilizes oncogenic kinases and mutant EGFR driving proliferation of lung cancer cells. It was recently demonstrated that mutant EGFR is a Hsp90 target. In addition, SPRY1 seems to be operative in the regulation of EGFR signaling. Another growth factor system frequently overexpressed in cancers is represented by the IGFs. IGF2 and a number of associated regulatory IGF-binding proteins (IGFBP1, 3, 5, 6, and IGFBP1/2) were elevated in UMC-11 cells. Expression of IGFBP2 along with low amounts of IGFBP1 was found in all carcinoid samples in association with varying occurrences of IGF1R, IGF2R, and IGFBP6. CALCB was reported to play an important role in the proliferation of various types of epithelial and endothelial cells. In an in vitro study, calcitonin-gene related peptide increased the proliferation of A549 alveolar epithelial cells in a dose-dependent and time-dependent manner. IL-8 is a chemokine and angiogenic factor that also functions as an autocrine growth factor in several human cancers. In lung cancer, all NSCLC cell lines produced IL-8, in contrast to low levels of IL-8 in SCLC cell lines despite expression of the IL-8 receptors CXCR1 and CXCR2. FGF12 is a FGF-homologous factor, which interacts with the intracellular kinase scaffold protein islet brain-2 and voltage-gated sodium channels. UMC-11 cells produce AGT that may influence tumor growth and metastasis in a tissue-specific and tumor-specific manner. In contrast, SST released by UMC-11 cells counteracts signaling of many other growth factors that contribute to proliferation, such as prolactin, IGF, TGFα and β, platelet-derived growth factor, EGF, and vascular endothelial growth factor (VEGF).

Because carcinoids resemble neuroendocrine tumors, the high expression of neuropeptides comprising VIP, NTS, VGF, and NPW by UMC-11 cells is expected to contribute significantly to autocrine growth stimulation. VIP causes increased proliferation of human breast and lung cancer cells in vitro. It binds to cancer cells with high affinity and increases cAMP and gene expression of c-fos, c-jun, c-myc, and VEGF. SCLC, which is a neuroendocrine cancer, produces and secretes gastrin releasing peptide (GRP), NTS, and adrenomedullin (AM) as autocrine growth factors. Most of these neuropeptides are detectable in serum samples of carcinoid patients. GRP, NTS, and AM bind to G-protein-coupled receptors triggering increased phosphatidylinositol (PI) turnover or elevation of cAMP in SCLC cells. Addition of GRP, NTS, or AM to SCLC cells causes altered expression of nuclear oncogenes like c-fos and stimulation of growth. Analysis of peptides secreted by the large-cell neuroendocrine carcinoma cell line revealed 2 fragments that were demonstrated to be parts of VGF, which is usually expressed in nerve cells or neuroendocrine cells. Reverse transcription–polymerase chain reaction of lung cancer cell lines showed that VGF mRNA was expressed only in neuroendocrine carcinoma-derived cells. Neuropeptide
B (NPB) and NPW are the endogenous ligands of the 2 G protein-coupled receptors GPR7 and GPR8 and activate protein kinase A and protein kinase C (PKC) signaling. NPB and NPW were reported to stimulate tyrosine kinase and MAPK activities, mediating the proliferative and anti-apoptotic effects of NPB and NPW.

Cell type–specific differences exist among the various signal transduction pathways, comprising cAMP, hydrolysis of PI mobilization of intracellular calcium, and tyrosine phosphorylation, and, moreover, different receptors for the same trigger may be linked to different signal transduction pathways. Basically, the mitogenic signal of neuropeptides is transmitted into the cell via specific receptors that couple to heterotrimeric G proteins. Subsequent activation of phospholipase C-β influences the activation of PKC and the elevation of intracellular calcium. The antiproliferative effect of the Ca2+-channel blocker verapamil was investigated in vitro on 3 human lung cancer cell lines. Verapamil inhibited cell proliferation in the neuroendocrine cancer cell line H727 in the nM range. STIM2 overexpressed in UMC-11 cells functioned as an important second messenger of growth signals in these resistant carcinoid cells. In conclusion, UMC-11 cells seem to rely on EGF-related, IGF-related, and neuropeptide growth factors for stimulation of proliferation, and this multitude of autocrine and paracrine loops is expected to impede antiproliferative therapy by kinase inhibitors.

Overexpression of a large number of S100 Ca2+-binding proteins in UMC-11 cells pointed to their important functions in cell biology and possibly drug resistance of carcinoids. Intracellular Ca2+ seems to be permanently elevated in UMC-11 cells in response to continuous stimulation by growth factors. Downregulation of proapoptotic genes such as serine/threonine kinase 17a and BNIP3 in association with S100P was reported to be linked to oxaliplatin resistance in the THC8307/L-OHP colon cancer cell line, and 8.7-fold overexpression of S100 protein family members was reported to be associated with oxaliplatin resistance in ovarian cancer cells. Furthermore, human ALDH7A1 expression in Chinese hamster ovary (CHO) and GRX were elevated in pancreatic ductal carcinoma tissues compared with pancreatic cystadenocarcinoma or normal pancreatic tissue. Likewise, genetic polymorphisms of GSTP1 and GSTA1 are also linked with increased overall survival in patients with different malignancies. Levels of thioredoxin (TRX) and GRX were elevated in pancreatic ductal carcinoma tissues compared with pancreatic cystadenocarcinoma or normal pancreatic tissue. Furthermore, cisplatin-resistant subclones of HeLa cells had higher expression of TRX and GRX compared with the parental cells.

AHR encodes a ligand-activated transcription factor binding to the xenobiotic response element-containing promoter region that is involved in the regulation of biological responses to planar aromatic hydrocarbons. This receptor has been shown to regulate levels of xenobiotic-metabolizing enzymes like CYP, of which CYP26B1 and 2B6 were comparatively overexpressed in UMC-11 cells. Human ALDH7A1 protects against hyperosmotic stress through generation of osmolytes and metabolism of toxic aldehydes. Human ALDH7A1 expression in Chinese hamster ovary cells attenuated osmotic stress-induced apoptosis caused by increased extracellular concentrations of sucrose or sodium chloride. AKRs are phase I drug-metabolizing enzymes for a variety of carbonyl-containing drugs and are implicated in cancer chemotherapeutic drug resistance. They are
stress-regulated genes and play a pivotal role in the cellular response to osmotic, electrophilic, and oxidative stress. The 10 known human AKR enzymes can turnover a range of substrates, including drugs, carcinogens, and reactive aldehydes. AKRs like AKR7A3 are soluble NAD(P)H oxidoreductases that primarily reduce aldehydes and ketones to primary and secondary alcohols, respectively.81

Eukaryotic topo I, a DNA unwinding enzyme, is essential for several cellular functions and is the target of camptothecin derivatives like irinotecan and topotecan. However, regulation of topo I activity was not known for a long time. In an effort to identify potential regulators of topo I activity, at least 2 antisense transcripts coded by TOP1 pseudogenes were described.82 Although the function of these TOP1 antisense transcripts has remained unknown, recent studies of naturally occurring antisense RNA demonstrated a number of potential regulatory roles. Downregulation of topo I in carcinoids would increase resistance to camptothecin derivatives.

Conclusion
Multidrug-resistant UMC-11 cells seem to use classical drug transporters, such as P-gp and MRP, drug conjugation and metabolism systems, and possibly new mechanisms, such as suppression of apoptosis by S100 proteins and metabolization systems, and possibly new mechanisms, such as suppression of apoptosis by S100 proteins and thereby their cellular responses to osmotic, electrophilic, and oxidative stress. The genome-wide search for drug resistance-associated genes described here provides new evidence for possible targets to circumvent the chemoresistant phenotype of carcinoids. Functional involvement of the candidate genes found needs to be verified by experiments deleting the corresponding transcripts, and, furthermore, it remains to be investigated how far these results apply to other neuroendocrine tumors.83

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References


