The role of mTOR inhibitors in the inhibition of growth and cortisol secretion in human adrenocortical carcinoma cells

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Abstract

Patients with adrenocortical carcinoma (ACC) need new treatment options. The aim of this study was to evaluate the effects of the mTOR inhibitors sirolimus and temsirolimus on human ACC cell growth and cortisol production. In H295, HAC15, and SW13 cells, we have evaluated mTOR, IGF2, and IGF1 receptor expressions; the effects of sirolimus and temsirolimus on cell growth; and the effects of sirolimus on apoptosis, cell cycle, and cortisol production. Moreover, the effects of sirolimus on basal and IGF2-stimulated H295 cell colony growth and on basal and IGF1-stimulated phospho-AKT, phospho-S6K1, and phospho-ERK in H295 and SW13 were studied. Finally, we have evaluated the effects of combination treatment of sirolimus with an IGF2-neutralizing antibody. We have found that H295 and HAC15 expressed IGF2 at a >1800-fold higher level than SW13. mTOR inhibitors suppressed cell growth in a dose-/time-dependent manner in all cell lines. SW13 were the most sensitive to these effects. Sirolimus inhibited H295 colony surviving fraction and size. These effects were not antagonized by IGF2, suggesting the involvement of other autocrine regulators of mTOR pathways. In H295, sirolimus activated escape pathways. The blocking of endogenously produced IGF2 increased the antiproliferative effects of sirolimus on H295. Cortisol production by H295 and HAC15 was inhibited by sirolimus. The current study demonstrates that mTOR inhibitors inhibit the proliferation and cortisol production in ACC cells. Different ACC cells have different sensitivity to the mTOR inhibitors. mTOR could be a target for the treatment of human ACCs, but variable responses might be expected. In selected cases of ACC, the combined targeting of mTOR and IGF2 could have greater effects than mTOR inhibitors alone.

Endocrine-Related Cancer (2012) 19 351–364

Introduction

Adrenocortical carcinomas (ACC) are uncommon malignancies with an incidence of 1–2 new cases/million per year (Allolio & Fassnacht 2006, Fassnacht et al. 2011). ACCs are highly aggressive tumors, associated with a 5-year survival ranging between 37 and 47%, for which novel treatment options are required (Allolio & Fassnacht 2006, Baudin et al. 2011, Fassnacht et al. 2011).

The insulin-like growth factor (IGF) system is a major actor in the pathogenesis of ACC and is presently considered an attractive target for new treatments in these cancers (Libe & Bertherat 2005, Almeida et al. 2008, Barlaskar et al. 2009).

mTOR is a protein kinase of the phosphatidylinositol 3-kinase (PI3K)/AKT signaling pathway, functions as a gatekeeper of cell growth, metabolism, and proliferation, receiving signals from sensors of cell stress,
intracellular nutrient levels, and several growth factor receptors including IGFs and vascular endothelial growth factors (Wan & Helman 2007, Hanna et al. 2008, Konings et al. 2009). mTOR exists as part of two complexes: mTORC1 and mTORC2, respectively, sensitive or insensitive to rapamycin (sirolimus) (Guertin & Sabatini 2007). The binding of growth factors to their receptor leads to the phosphorylation and activation of AKT, which elicits many downstream signaling events including the activation of mTOR as part of the mTORC1 complex. Activation of the mTORC1 complex leads to the phosphorylation and activation of downstream effectors of the pathway: the protein 70 ribosomal protein S6 kinase-1 (S6K1 (RPS6KB1)) and eukaryotic translation initiation factor 4E binding proteins (4EBP1 (EIF4EBP1)) (Guertin & Sabatini 2007). Both S6K1 and 4EBP1 are regulators of mRNA translation and stimulate the synthesis of several proteins involved in cell proliferation (Guertin & Sabatini 2007).

Alterations in the mTOR pathway have been found in many human tumors, regardless of deregulation of IGF system (Wan & Helman 2007, LoPiccolo et al. 2008, Konings et al. 2009). Therefore, the mTOR pathway is considered a target for antineoplastic therapy in several malignancies, and it has very recently been proposed as target for ACC treatment (De Martino et al. 2010, Doghman et al. 2010). mTOR inhibitors may exert their antitumor effects directly by inhibiting cell growth and proliferation and indirectly by inhibiting tumor angiogenesis (Guertin & Sabatini 2007, LoPiccolo et al. 2008).

Presently, many clinical trials are investigating the effects of compounds inhibiting mTORC1 activity (traditional mTOR inhibitors), such as sirolimus, temsirolimus, and everolimus, alone or in combination with other compounds, in several types of malignancy (Wan & Helman 2007, LoPiccolo et al. 2008, Konings et al. 2009, Liu et al. 2009).

The role and function of mTOR and its pathway in ACC have not been clarified yet (De Martino et al. 2010). Recently, Doghman et al. (2010) showed that mTOR is activated in childhood ACCs and that everolimus is able to inhibit in vitro cell proliferation in ACC cell lines and growth of ACC xenografts in immunodeficient mice.

The aim of this study was to i) evaluate the expression of mTOR, IGF2, and IGF1 receptor (IGF1R) in different human ACC cell lines; ii) test the in vitro effects of the mTOR inhibitors sirolimus and temsirolimus on ACC cell lines in order to understand the mechanism of mTOR inhibitor-induced cell growth inhibition; iii) explore the role of the IGF2 autocrine loop in the effects of mTOR inhibitors; and iv) evaluate the effect of mTOR inhibitors on cortisol secretion.

Materials and methods

Study methodology

In this study, we characterized the expression of the mTOR and IGF2 in three different human ACC cell lines: NCI-H295R (H295), HAC15, and SW13. In H295 and SW13, we also evaluated the expression of IGF1R. In all these cell lines, we tested the dose- and time-dependent effects of sirolimus and temsirolimus on cell growth and the effects of sirolimus on induction of apoptosis and cell cycle. In H295, we tested the effects of sirolimus in the presence and absence of IGF2 stimulation on colony formation and determined the effect of blocking of endogenously produced IGF2 by an IGF2-specific neutralizing antibody on sirolimus-induced cell growth inhibition. In H295 and SW13, we explored the effects of sirolimus on basal and IGF1-induced AKT, ERK1/2, and S6K1 phosphorylation. In the hormonally active ACC cells (H295 and HAC15), the effect of sirolimus on cortisol production was evaluated.

Cell lines and culture conditions

The hormonally active human ACC cell line H295, its clone HAC15, and the hormonally inactive ACC cell line SW13 were obtained from the American Type Culture Collection (Manassas, VA, USA), from Dr W Rainey (as gift), and from ECACC (Salisbury, Wiltshire, UK) respectively (Wang & Rainey 2012).

The cells were cultured in 75 cm² culture flasks at 37 °C in a humidified incubator at 5% CO₂. For all cell lines, the culture medium consisted of DMEM/F12K medium, supplemented with 5% FCS, penicillin (1 × 10⁵ U/l), and l-glutamine (2 mmol/l). Cells were harvested with trypsin (0.05%)-EDTA (0.53 mM) and resuspended in culture medium. Cell viability always exceeded 95%. Media and supplements were obtained from Invitrogen.

Drugs and reagents

mTOR inhibitors sirolimus and temsirolimus were purchased from LC Laboratories, Inc. (Woburn, MA, USA). They were dissolved in dimethylsulfoxide (DMSO) as concentrated (10⁻³ M) stock solutions (stored at −20 °C) and diluted in DMSO before use. IGF1 and IGF2 were purchased from Sigma–Aldrich and from Biosource (Tilburg, The Netherlands).
respectively; both IGFs were diluted in 0.01 M acetic acid solution as concentrated (10⁻⁵ M) stock solutions (stored at −20 °C) and diluted in medium before use.

Anti-IGF2-neutralizing antibody (m610 human monoclonal antibody to IGF2) was kindly provided by Drs Dimiter Dimitrov and Yang Feng (Feng et al. 2006).

Quantitative RT-PCR
The expression of mTOR and IGF2 mRNA in human ACC cells was evaluated by quantitative RT-PCR.

From human ACC cell lines, total RNA was isolated using a commercially available kit (High Pure RNA Tissue kit; Roche). cDNA was synthesized using 500 ng total RNA in a Super Reverse Transcriptase (RT) buffer (HT Biotechnology Ltd., Cambridge, UK), together with 40 nmol of each deoxynucleotide triphosphate, 15 ng oligo-dT primer, 20 U RNase inhibitor, and 4 U AMV/Super RT (HT Biotechnology) in a final volume of 40 μl. This mixture was incubated for 1 h at 94 °C and then five times diluted in bidist. A quantitative PCR was performed by TaqMan Gold nuclease assay (Perkin Elmer Corporation, Foster City, CA, USA) and the ABI-PRISM-7900 sequence Detection System (Perkin Elmer, Groningen, The Netherlands) for real-time amplifications, according to the manufacturer’s protocol. The assay was performed using 7.5 μl TaqMan Universal PCR Master Mix (Applied Biosystems, Alphen a/d Ryn, The Netherlands), primers and probes amount as reported in supplementary materials 1 and 5 ml cDNA template, in a total reaction volume of 12.5 μl. After an initial heating at 50 °C for 2 min and 95 °C for 10 min, samples were subjected to 40 cycles of denaturation at 95 °C for 15 s and annealing for 1 min at 60 °C. The primers and probes were purchased from Sigma–Aldrich. The sequence of the primers and probes used are reported in supplementary material 1. Samples were normalized against the expression of the housekeeping gene hypoxanthine phosphoribosyltransferase 1 (HPRT (HPRT1)). PCR efficiencies (E) were calculated for the primer–probe combinations used (supplementary material 1) (Rasmussen 2001). The relative expression of genes was calculated using the comparative threshold method, 2⁻ΔΔCt (Schmittgen & Livak 2008), after efficiency correction (Pfaffl 2001) of target and reference gene transcripts (HPRT).

Immunohistochemistry: AgarCyto cell block
The expression of mTOR and IGF2 proteins in human ACC cell lines was evaluated by immunohistochemistry using AgarCyto cell blocks. H295, HAC15, and SW13 cell pellets were fixed in 4% formaldehyde solution in PBS, embedded in 2% agarose and afterward in paraffin (Kerstens et al. 2000). AgarCyto cell blocks were cut in 5 μm sections, deparaffinized, and dehydrated. Antigen retrieval was performed by microwave treatment in Tris–EDTA buffer (pH 9.0). The slides were cooled for 1 h at +4 °C and later incubated for 1 h at room temperature (RT) with the anti-mTOR primary antibodies or overnight at +4 °C with the anti-IGF2 primary antibodies. The slides incubated with anti-IGF2 antibodies were subsequently washed and incubated for 30 min at RT with Poly-Rabbit anti-Goat IgG. The slides were further washed and incubated for 30 min at RT with Poly-AP-Goat anti-Mouse/Rabbit IgG. After washing, staining was visualized by 30 min incubation in new fuchsin solution. Slides were counterstained with hematoxylin and coverslipped. The antibody and the controls used are listed in supplementary material 2.

Immunocytochemistry: chamber slides
Cells were plated on poly-L-lysine-coated culture chamber slides (NUNC A/S, Roskilde, Denmark). After 48 h, medium was removed and cells were fixed with 4% paraformaldehyde and 0.2% picric acid in phosphate buffer, pH 6.9, for 40 min at RT. After washing, the cells were treated for 3 min with 50% methanol and for 3 min with 100% methanol. After another washing, the cells were treated with a 3% H₂O₂–PBS solution for 15 min at RT in the dark to quench endogenous peroxidase. After washing, the cells were incubated for 1 h at RT with an IGF1R monoclonal antibody (supplementary material 2). Finally, the cells were incubated for 30 min at RT with HRP/anti-Rabbit/Mouse (Dako Detection System). Bound antibodies were visualized by incubation with freshly prepared DAB (Dako Detection System). Slides were counterstained with hematoxylin and coverslipped. For negative controls, the primary antibody was omitted.

Cell proliferation assay
Measurement of total DNA content
Cells were plated in 1 ml medium in 24-well plates at the density necessary to obtain a 65–70% cell confluence in the control groups at the end of the experiment. Twenty-four hours later, sirolimus or temsirolimus were added to wells in quadruplicate. The concentrations of compounds tested in H295 and HAC15 ranged between 10⁻⁹ and 10⁻⁵ M. In the SW13, a maximal effect of compounds was observed already at 10⁻⁸ M. Therefore, we tested concentrations of compounds ranged between 10⁻¹² and 10⁻⁸ M.
Controls were vehicle treated. The cells inoculated for 6 and 9 days were refreshed every 3 days by adding fresh compounds. After 24 h, 3, 6, and 9 days of treatment, the cells were harvested for DNA measurement, as a measure of cell number. Measurement of total DNA content was previously described in detail (Hofland et al. 1990).

**Cell proliferation reagent WST-1 (WST)**

In H295 cells, the effect of IGF2-specific neutralizing antibody on sirolimus-induced inhibition of cell proliferation was determined by WST-1 assay (Cell Proliferation Reagent WST-1 (Roche)) according to the protocol provided by the manufacturer. Cells were plated in 100 µl medium + 5% FCS (standard medium) in 96-well plates (20 000 cells/well). After 24 h, the medium was changed with medium +1% FCS and the following reagents were added: vehicle, sirolimus (10⁻⁹ M), anti-IGF2 (4×10⁻⁸ M), and sirolimus + anti-IGF2. After 72 h, cell proliferation was measured by WST-1 assay. The experiment was repeated twice, and each experiment was performed in quadruplicate.

**DNA fragmentation assay**

DNA fragmentation assay was used to determine the effects of the compounds on apoptosis. The cells were plated in 24-well plates and treated as described earlier for the cell proliferation assay. After 24 h and 3 days of incubation, DNA fragmentation was determined using a commercially available ELISA kit (Roche Diagnostic GmbH). The standard protocol supplied by the manufacturer was used. The same plates were also analyzed for the measurement of total DNA content. The amount of DNA fragmentation (apoptosis) was corrected for the total DNA content in each well.

**Cortisol secretion assay**

In H295 and HAC15, we evaluated the effects of sirolimus on cortisol production. The cells were plated in 24-well plates and treated for 6 days as described earlier for the cell proliferation assay. We tested the effects of the sirolimus on cortisol production in concentrations corresponding to the EC₅₀ on cell proliferation after 6 days of treatment. The culture supernatants from experiment performed in H295 and HAC15 cells were collected and stored at −20 °C until determination of the cortisol concentration.

The cortisol concentration was determined by a nonisotopic, automated chemiluminescence immunoassay system (Siemens Medical Solutions Diagnostics, Breda, The Netherlands). Cortisol levels were expressed as percentage of control and were corrected for the total DNA content in each well, thereby reflecting cortisol production per cell.

**Cell cycle analysis**

Cells were plated in 12-well plates at the density necessary to obtain a 65–70% cell confluence in the control groups at the end of the experiment. Twenty-four hours later, sirolimus was added to wells in triplicate. In each cell line, the effects of sirolimus on cell cycle were tested in concentrations corresponding to the EC₅₀ on cell proliferation after 6 days of treatment. In addition, the effects of the compounds at concentrations of 10⁻⁶ M in H295 and HAC15 and 10⁻⁸ M in SW13 were tested. Control groups were vehicle treated. We evaluated the effects of the compounds on cell cycle after 24 h of treatment in SW13 and in H295 and HAC15 cell lines after 72 h of treatment according to the different growth rates of these cells. Following treatment, cells were harvested by gentle trypsinization, washed with ice-cold PBS, and collected by centrifugation. Cells were resuspended in 200 µl PBS and fixed in 70% ice-cold ethanol, followed by an overnight incubation at −20 °C. After centrifugation, the cells were washed once with PBS and incubated for 30 min at 37 °C in PBS containing 40 µg/ml propidium iodide (Sigma–Aldrich) and 10 µg/ml DNase-free RNase (Sigma–Aldrich). For each tube, 20 000 cells were immediately measured on a FACScalibur flow cytometer (Becton Dickinson, Erembodegem, Belgium) and analyzed using CellQuest Pro Software.

**Colony-forming assay**

Cells were plated in poly-γ-lysine (10 µg/ml; Sigma–Aldrich)-coated 12-well plates (2500 cells/well) and cultured in complete medium for 3 weeks.

Cells were allowed to attach for 24 h before to be treated with the vehicle, sirolimus (5×10⁻⁹ M), IGF2 (10⁻⁸ M), or the combination of the two compounds. The experiment has been performed two times in triplicate. Cells were treated continuously and medium plus the compounds were refreshed every 3 or 4 days. After 3 weeks, the formed colonies were fixed with 100% ethanol and stained with hematoxylin to allow calculation of the average colony-forming efficiency. Colonies containing more than 50 cells were automatically counted with a Multi Image Light Cabinet from Alpha Innotech Corporation (Cell Biosciences, San Leandro, CA, USA).

Plating efficiency was defined as the mean number of colonies formed divided by the number of plated cells for control cultures expose to the vehicle express.
as percentage. The surviving fraction (SF) was calculated as \((\text{mean number of colonies}) / (\text{number of plated cells} \times \text{plating efficiency})\) (Franken et al. 2006).

**Protein extraction**

H295 and SW13 cells were plated in 3 ml medium in six-well plates at the density required to obtain 65–70% cell confluence at the end of the experiment. Seventy-two hours later, cells were starved for 12 h and then incubated for 1 h with sirolimus or vehicle. The final concentrations of sirolimus tested were \(10^{-6}\) M and \(5 \times 10^{-9}\) M in H295 and \(10^{-8}\) and \(10^{-10}\) M in SW13. Thirty minutes before collection of cells, IGF1 (\(10^{-8}\) M) was added to selected wells. Cells were washed with ice-cold PBS. Whole-cell lysates were prepared by adding 200 µl ice-cold RIPA lysis buffer (Pierce Biotechnology, Inc., Rockford, IL, USA) with the addition of 1% Halt Phosphatase Inhibitor Cocktail (Pierce Biotechnology, Inc.) to each well. After 15 min of incubation on ice (mixing every 5 min), the samples were spun down at \(-80\,\text{°C}\). The supernatants were stored at \(-80\,\text{°C}\).

The total amount of proteins was calculated with dye-binding assay (Bio-Rad Protein Assay), using BSA as standard curve and a spectrophotometer set to 595 nm as reader.

**Western blotting**

Total protein solution (30 µg) diluted in a water solution containing 20% SDS sample buffer was denatured (5 min in a bath at 95 °C) and separated by electrophoresis on 10% SDS–PAGE gel and transferred to a nitrocellulose membrane. The membranes were first incubated for 2 h with blocking buffer (0.1% Tween 20–PBS/5% BSA for membranes for AKT measurement and 0.1% Tween 20–PBS/3% nonfat dry milk for the remaining membranes) and subsequently incubated overnight at 4 °C with the primary antibody (supplementary material 3). After 1 h of washing in 0.1% Tween 20–PBS, the membranes were incubated for 1 h with the secondary antibody at room temperature, followed by 1 h wash in 0.1% Tween 20–PBS. Starting from the incubation with the secondary antibodies, the membranes were preserved in dark condition. Immunodetection was performed using the Odyssey infrared imaging system (LI-COR Biosciences, Cambridge, UK). The optical density of the appropriately sized bands was measured using the Odyssey molecular imaging software (LI-COR Biosciences). The relative expression of total AKT, total S6K, or total ERK was calculated as a ratio to the expression of actin. The relative expression of phospho-AKT, phospho-S6K, or phospho-ERK was calculated as a ratio to total AKT, S6K, or ERK respectively.

**Statistical analysis**

All the experiments were carried out at least three times, with the exception of colony-forming assay and the WB that were performed twice. The repeated experiments gave comparable results. For the statistical analysis, statistical software of SPSS (SPSS 15.0; SPSS, Inc., Chicago, IL, USA) and GraphPad Prism 5.0 (GraphPad Software, San Diego, CA, USA) were used.

We used nonparametric tests to evaluate the differences among groups (Mann–Whitney and Kruskal–Wallis tests).

The comparative statistical evaluations among treatment groups were performed by ANOVA followed by a multiple comparative test (Newman–Keuls or Dunnett’s test).

**Results**

**Expression of mTOR IGF2 and IGF1R in ACC cell lines**

The \(IGF2\) mRNA levels in H295 and HAC15 (H295 = 59.3 ± 31; HAC15 = 50.6 ± 9; ration over HPRT, mean ± s.d.) cells were more than 1800-fold higher (\(P < 0.001\)) than in SW13 in which \(IGF2\) mRNA was just detectable (0.03 ± 0.03; mean ± s.d.), whereas the mRNA expression levels of mTOR were comparable between the cell lines (H295 = 0.12 ± 0.05; HAC15 = 0.12 ± 0.08; SW13 = 0.14 ± 0.06). The higher expression levels of IGF2 in H295 and HAC15 compared with SW13 were also confirmed at protein level by immunostaining (Fig. 1). In addition, the mTOR immunostaining showed a strong positivity in all cell lines (Fig. 1). A positive immunoreactivity for IGF1R was shown in both H295 and SW13 cell lines (Fig. 2).

**Effects of mTOR inhibitors on cell growth and apoptosis in ACC cell lines**

In ACC cell lines, sirolimus and temsirolimus significantly suppressed the cell growth in a dose- and time-dependent manner (Fig. 3 shows the effects in H295 and SW13; effects in HAC15 are shown in supplementary Fig. 1).
In H295, both compounds were able to significantly inhibit the cell growth with a comparable potency after 9 days of treatment (EC50: 4.8×10⁻⁹ vs 1.9×10⁻⁸ M). The effects of sirolimus ranged between 61.7% inhibition (P<0.001) at the maximal dose (10⁻⁵ M) and 16.7% (P<0.01) at the minimal dose tested (10⁻⁹ M). The effects of temsirolimus ranged between 57.1% inhibition (P<0.001) at the maximal

![Figure 1](image1.png) **Figure 1** Immunocytochemical detection of mTOR (middle panel) and IGF2 (right panel) in human ACC cell lines. Left panel shows the absence of staining in the negative controls. Magnification, ×100.

![Figure 2](image2.png) **Figure 2** Immunocytochemical detection of IGF1R (right panel) in the human ACC cell lines H295 and SW13. Left panel shows the absence of staining in the negative controls. Magnification, ×200.
dose ($10^{-5}$ M) and 16% ($P<0.05$) at the minimal dose tested ($10^{-9}$ M).

In HAC15, both compounds were able to significantly inhibit the cell growth with a comparable potency after 9 days of treatment ($EC_{50}$: $1.4\times10^{-8}$ vs $4.3\times10^{-7}$ M). The effects of sirolimus ranged between 79.9% inhibition ($P<0.001$) at the maximal dose ($10^{-5}$ M) and 24.4% ($P<0.05$) at the minimal dose tested ($10^{-9}$ M). The effects of temsirolimus ranged between 81% inhibition ($P<0.001$) at the maximal dose ($10^{-5}$ M) and 24.6% ($P<0.05$) at the minimal dose tested ($10^{-9}$ M).

Nine days of treatment with sirolimus (Fig. 3C) and temsirolimus $10^{-10}$ M were already able to significantly inhibit the cell growth of SW13 cells. Sirolimus was significantly more potent than temsirolimus in terms of $EC_{50}$ ($EC_{50}$: $3.3\times10^{-11}$ vs $1.7\times10^{-10}$ M; $P=0.02$) but not with respect to the maximal and the minimal effective concentration of the two compounds. The effects of sirolimus ranged between 91.7% inhibition ($P<0.001$) at the maximal dose ($10^{-8}$ M) and 49.3% ($P<0.05$) at the dose of $10^{-10}$ M. The effects of temsirolimus were ranged between 91.5% inhibition ($P<0.001$) at the maximal dose ($10^{-8}$ M) and 34.9% ($P<0.05$) at the dose of $10^{-10}$ M.

In H295, sirolimus was able to significantly induce DNA fragmentation only at the highest dose used ($10^{-5}$ M) (Fig. 4). Sirolimus ($10^{-5}$ M) was able to induce apoptosis also in HAC15. These effects were

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**Figure 3** Dose-/time-dependent effect of sirolimus (S; panels A and C) and temsirolimus (T, panels B and D) treatment on cell proliferation, expressed as DNA content/well after 24 h (closed square), 3 days (closed triangle), 6 days (closed down triangle), and 9 days (closed diamond) treatment in H295 (left panels) and SW13 (right panels) cells. Data are expressed as the percentage of control and represent the mean±s.e. Control is set as 100%.
more pronounced after 24 h than after 3 days of treatment. At the doses tested (10^{-8} to 10^{-12} M), 24 h and 3 days of treatment, sirolimus was not able to significantly induce apoptosis in SW13 (not shown).

Effects of sirolimus on cortisol secretion in ACC cell lines

Sirolimus induced a significant inhibition of cortisol secretion in H295 and HAC15. These effects were still present after the correction for the estimated cell number in each well, suggesting a direct effect of sirolimus on hormonal secretion in ACC cells (Fig. 5). Cortisol secretion was inhibited by 21.7% in the H295 sirolimus (5 \times 10^{-9} M)-treated cells (P < 0.01) (Fig. 5A) and by 41.3% in sirolimus (10^{-8} M)-treated HAC15 cells (P < 0.001) (Fig. 5B).

Effects of sirolimus on cell cycle progression and colony formation in ACC cell lines

To explore the mechanisms involved in mTOR inhibitor-induced inhibition of cell proliferation, we performed FACS analysis and colony-forming assay. At FACS analysis, sirolimus (10^{-8} M) induced a significant G1-phase arrest in H295 and HAC15 (Table 1). In SW13, we observed a significant G1-phase arrest by sirolimus at 10^{-8} and 10^{-10} M (Table 1). This effect at the highest concentration of compound used was accompanied by a decrease in S-phase and G2-phase (Table 1).

The plating efficiency for H295 in colony forming was 8.6%. Three weeks of treatment with sirolimus 5 \times 10^{-9} M significantly inhibited the formation and growth of colonies as measured by a reduced SF (69.9% vs control; P < 0.001) and average colony size (56.6%; P < 0.001) (Fig. 6). IGF2 10^{-8} M was able to significantly increase the colony growth by increasing their size (62.7%; P < 0.001) and the SF (29%; P < 0.05). At the condition tested, the effects of sirolimus on SF and colony size were not reverted by the coadministration of IGF2. Similar results were also obtained when we repeated the experiment using IGF2 5 \times 10^{-8} M (results not shown).

Effects of sirolimus on the IGF-activated intracellular pathways in ACC cells

To further understand the mechanisms responsible for the effects of the mTOR inhibitor in ACC cell lines, we studied the effects of sirolimus and/or IGF1 on some key intracellular components of the IGF pathway in H295 and SW13 (Fig. 7). Thirty minutes of IGF1 (10^{-8} M) stimulation significantly increased the phosphorylation of S6K1 and AKT in both cell lines. IGF1 stimulation increased the phosphorylation of ERK1/2 in H295. H295 cells treated with sirolimus 10^{-6} and 5 \times 10^{-9} M had significantly lower phospho/total S6K1 than control and IGF1-stimulated cells, as expected by a successful inhibition of the mTORC1 complex activity. Sirolimus (10^{-8} and 10^{-10} M) reduces phospho/total S6K1 also in SW13, but this reduction resulted statistically significant only when compared with the IGF1-stimulated cells and not when compared with the control (12 h starved cells). In both cell lines, the sirolimus-induced inhibition of S6K1 phosphorylation was not reverted by the IGF1 stimulation. In H295, the treatment with sirolimus was associated with an increased AKT phosphorylation and this AKT stimulation was enhanced by the IGF1 stimulation. In SW13, the treatment with sirolimus alone did not increase the AKT phosphorylation. However, an increased phospho/total AKT was observed in all IGF1-stimulated cells, despite the sirolimus treatment. In SW13, the ERK1/2 phosphorylation was not affected by the IGF1 and/or sirolimus treatment.
with sirolimus combined with anti-IGF2 Abs was able to almost totally block H295 cell proliferation (90% inhibition compared with controls). Sirolimus or anti-IGF2 antibody alone induced an inhibition in H295 cell proliferation of 64 and 42% respectively (Fig. 8).

Discussion

In this study, we describe the expression of mTOR, IGF2, and IGF1R and the in vitro antiproliferative and antisecretive effects of the mTOR inhibitors in the currently available human ACC cell lines. All ACC cell lines expressed comparable mRNA and protein mTOR levels. Both H295 and SW13 showed a significant IGF1R protein expression. Conversely, the expression levels of IGF2 were considerably higher in H295 and its clone HAC15 than those in SW13. These results show that mTOR is expressed in human ACC cell lines and its expression appears to be unrelated to IGF1R expression or IGF2 overexpression.

The mTOR inhibitors caused a significant inhibition of cell growth in vitro and sirolimus induced a significant reduction of hormonal production in the hormonally active cells, independent of the effect on cell growth. Sirolimus appeared to be more potent than temsirolimus in inhibiting cell proliferation in SW13. Temsirolimus acts as direct inhibitor of mTOR, but in vivo temsirolimus is also converted in sirolimus (Atkins et al. 2004). After having proven that temsirolimus inhibits the in vitro cell growth in ACC cell lines also in a direct way, we continued the experiments using sirolimus only. Cell cycle arrest appeared the predominant mechanism responsible for the observed antiproliferative effects of sirolimus, as already reported in other cancer cell lines (Huang & Houghton 2002).

In H295 and SW13, IGF1 stimulation has been correlated with increased AKT phosphorylation (Cantini et al. 2008, Barlaskar et al. 2009). In this study, we describe an IGF1-induced AKT and S6K1 phosphorylation in both ACC cell lines confirming the role of the AKT/mTOR pathway as intracellular mediator of the IGF signaling in ACCs. Moreover, we prove that long-term exposure to IGF2 promotes colony growth in H295 and these effects are antagonized by mTOR inhibitors. It has been reported that everolimus can produce antivascular effects in in vivo model ACCs (Doghman et al. 2010). Therefore, mTOR plays a role as intracellular mediator of the autocrine/paracrine loops considered to be involved in the pathogenesis of ACCs (Volante et al. 2008, De Martino et al. 2010).

In this study, we found that the different ACC cell lines display a differential sensitivity to the antigrowth
effects of the mTOR inhibitors. The antiproliferative effects of the drugs were observed at concentrations of sirolimus and temsirolimus that can be reached in vivo in humans (Atkins et al. 2004). Moreover, cell growth inhibition at these concentrations was considerably higher in SW13 than in H295 (and its clone HAC15). Many factors can contribute to this difference. SW13 cells differ from H295 because they harbor TP53 mutation (Forbes et al. 2008); they are less differentiated, they do not overproduce IGF2 and steroids, and they present a higher growth rate. Cells with TP53 mutation have been suggested to be more sensitive to mTOR inhibitors (Kurmasheva et al. 2006, Liu et al. 2009). The absence of the IGF2 overproduction can contribute to the higher sensitivity of SW13 cells compared with other two cell lines. The overstimulation of the growth factor receptors can determine the overactivation of the mTOR pathway upstream to mTOR (i.e. increased phosphorylation of AKT), or can overactivate other pro-growth pathways such as the RAS/RAF/MEK/ERK pathway (i.e. increased phosphorylation of ERK1/2), determining resistance or escape to the effects of traditional mTOR inhibitors (Easton et al. 2006, Wan et al. 2007, Zitzmann et al. 2007, Liu et al. 2009). We performed all our experiments using the same culture medium in all cell lines. In such a setting, the endogenous production of growth factor by the cells may determine differential sensitivity to mTOR inhibitors. The proliferation of H295 is stimulated by an autocrine/paracrine IGF2/IGF1R loop (Logie et al. 1999). The overactivation of this loop can negatively influence the sensitivity of H295 to the mTOR inhibitors. This hypothesis is supported by the results obtained in western blotting (WB), the experiments using anti-IGF2 neutralizing Abs and the colony-forming experiments. Using WB, we demonstrated that the effects of sirolimus on the IGF-activated intracellular pathways are different in H295 and SW13 cells. At the condition tested, IGF1 induced the activation of the AKT/mTOR pathway in both cell lines and ERK activation only in H295. Sirolimus suppressed the mTORC1 activity in both cell lines. However, in H295, but not in SW13, the inhibition of mTORC1 activity was associated with a significantly increased phosphorylation of AKT.

Table 1 Effects of sirolimus on cell cycle distribution in mean ± s.d. in human adrenocortical cancer cell lines (H295, HAC15, and SW13)

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<th>Phase sub G0</th>
<th>Phase G0/1</th>
<th>Phase S</th>
<th>Phase G2/M</th>
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<tr>
<td>H295 Control</td>
<td>2.9 ± 0.6</td>
<td>55.8 ± 5.1</td>
<td>12.4 ± 2.8</td>
<td>27.8 ± 3.7</td>
</tr>
<tr>
<td>Sirolimus 10⁻⁶ M&lt;sup&gt;a&lt;/sup&gt;</td>
<td>2.8 ± 0.7</td>
<td>59.4 ± 3.8*</td>
<td>11.3 ± 2.9</td>
<td>26.4 ± 3.8</td>
</tr>
<tr>
<td>Sirolimus 5×10⁻⁹ M&lt;sup&gt;b&lt;/sup&gt;</td>
<td>3.9 ± 1.8</td>
<td>55.9 ± 4</td>
<td>11.6 ± 1.4</td>
<td>28.6 ± 4.2</td>
</tr>
<tr>
<td>HAC15 Control</td>
<td>7.8 ± 2.9</td>
<td>60.7 ± 1.5</td>
<td>15.7 ± 0.9</td>
<td>15.8 ± 3.4</td>
</tr>
<tr>
<td>Sirolimus 10⁻⁶ M&lt;sup&gt;a&lt;/sup&gt;</td>
<td>6.8 ± 1.5</td>
<td>63.8 ± 2.3*</td>
<td>14.2 ± 1.6</td>
<td>15.3 ± 2</td>
</tr>
<tr>
<td>Sirolimus 10⁻⁸ M&lt;sup&gt;a&lt;/sup&gt;</td>
<td>8 ± 2.2</td>
<td>61.6 ± 1.9</td>
<td>15.6 ± 1.3</td>
<td>14.8 ± 1.2</td>
</tr>
<tr>
<td>SW13 Control</td>
<td>1.8 ± 0.3</td>
<td>56.7 ± 5</td>
<td>15.9 ± 0.9</td>
<td>25.7 ± 5.2</td>
</tr>
<tr>
<td>Sirolimus 10⁻⁶ M&lt;sup&gt;b&lt;/sup&gt;</td>
<td>1.9 ± 0.6</td>
<td>72.9 ± 5.7*</td>
<td>11.2 ± 2.4†</td>
<td>14 ± 3.6†</td>
</tr>
<tr>
<td>Sirolimus 10⁻¹⁰ M&lt;sup&gt;b&lt;/sup&gt;</td>
<td>1.8 ± 0.3</td>
<td>67 ± 6.2†</td>
<td>14.4 ± 1.7</td>
<td>16.8 ± 4.7†</td>
</tr>
</tbody>
</table>

<sup>a</sup>P<0.05 vs control; <sup>b</sup>P<0.001 vs control.
<sup>a</sup>Cell cycle distribution measured after 72 h of incubation.
<sup>b</sup>Cell cycle distribution measured after 24 h of incubation.

Figure 6 Effects of 3-week treatment with IGF2 (10⁻⁸ M) and/or sirolimus (5×10⁻⁹ M) on colony formation and growth of the human ACC cell line H295. Left panel: IGF2 stimulates H295 cell proliferation by increasing the average size of colonies (A) as well as the surviving fraction (B). Both these effects are efficiently antagonized by the coadministration of sirolimus. Data are expressed as percentage of control and represent the mean ± s.d. Control is set as 100%. The right panel (C) shows a representative photograph of the wells containing treated and untreated cells as used to perform colony-forming experiments. ***P<0.001 vs control.
Supporting an overactivation of the mTOR pathway upstream to mTORC1 in H295, likely representing an escape pathway. This activation could result by the IGF2 endogenous production that persistently stimulates the IGF1R (autocrine IGF loop) even in starved H295 cells. The effects of sirolimus on AKT were even enhanced by IGF1 administration, which also induced ERK stimulation in the sirolimus-treated H295, despite the fact that both basal and IGF1 S6K phosphorylation was fully blocked by sirolimus. These results show that in H295 cells treated with sirolimus, IGF can stimulate two pathways potentially associated with traditional mTOR inhibitors treatment escape: AKT and ERK pathways (Kurmasheva et al. 2006, Liu et al. 2009). To further provide evidence that in H295, the endogenous overproduction of IGF2 has a negative interference with the effects of mTOR inhibitors, we explored the effects of sirolimus alone or in the presence of anti-IGF2 neutralizing antibodies (at concentration predicted to effectively neutralize the endogenous IGF2 production). These experiments demonstrated for the first time that IGF2 neutralization increases the antiproliferative effects of mTOR inhibitors in an ACC model. This raises the question whether the cotreatment of traditional mTOR inhibitors and IGF1R antagonists should be considered for patients with ACCs known to have a strong IGF autocrine loop.

In colony-forming assay, H295 cells were more sensitive to sirolimus than observed with the DNA measurement. Possible mechanisms that could explain this higher sensitivity include the disruption of the growth factor paracrine/autocrine loops; the selection of ‘aggressive clones’, and the mTORC2 complex inhibition. In colony-forming experiments, the cell density is very low leading to the disruption of growth factor paracrine/autocrine loops and reducing the growth factor-induced activation of escape pathways. However, in the colony experiments, IGF2 (used at a dose comparable to the concentration reached in the medium of H295 in DNA-measurement experiments) stimulated cell proliferation but did not revert the effects of sirolimus, suggesting that IGF2 is not the only autocrine/paracrine regulator of the mTOR pathway activity in H295. By disrupting the autocrine/paracrine loops, we forced the cells to grow in a less favorable condition and this could lead to the selection of ‘more aggressive clones’. H295 cells showed a low plating efficacy, suggesting that only a small percentage of cells are able to adapt and grow under these conditions. These cells could be less dependent by the autocrine/paracrine loops, less sensitive to the IGF2, and consequently less exposed to the growth factor-induced activation of the escape pathways.
pathways. This hypothesis could also contribute to explain the observed incapability of the IGF2 to revert the sirolimus-induced inhibition on H295 colony growth. Three weeks of continuous treatment of H295 cells with sirolimus induced a significant reduction of the cell-SF compared with controls. These results can suggest that longtime treatment with mTOR inhibitor does not only block the cell growth but also induce cell death. Traditional mTOR inhibitors such as sirolimus and temsirolimus have the mTORC1 complex as target. The presence of activated mTORC2 can stimulate the AKT activation representing a potential mechanism of escape to the effects of traditional mTOR inhibitors for cancer cells. However, it has been suggested that long-term treatment with traditional mTOR inhibitors can also indirectly inhibit the TORC2 complex by sequestering mTOR as part of the TORC1 complex (Loewith et al., 2002, Hanna et al., 2008). This double block is considered as one of the potential mechanisms of mTOR inhibitor-induced tumor cell death (Liu et al., 2009). Moreover, mTORC2, as well as mTORC1, is activated by growth factors. Therefore, in colony experiments, the disruption of the autocrine/paracrine loops may also contribute to the mTORC2 inhibition (Sarbassov et al., 2005, Sabatini 2006). This raises the question whether the use of drugs simultaneously blocking mTORC1 and mTORC2 or PI3K could have a place in the treatment of selected patients with ACCs.

For the first time, we show an antisecretive effect (inhibition of cortisol production) of mTOR inhibitors in ACC cell lines. The mechanisms responsible for this effect still need to be clarified. mTOR inhibitors are already used in the clinical setting and no signs or symptoms of hypoadrenalism have been described (Hudes et al., 2007). Therefore, it is probable that mTOR inhibitors are not able to suppress the physiological adrenal steroid production. The IGFs are able to stimulate adrenal steroid production. It is thus possible that mTOR could play a role as intracellular mediator of the effects of IGFs and that mTOR inhibition could antagonize this prosecretive effect of IGFs in ACC cells.

Conclusions, translational aspects, and future directions

The results of the current study suggest that ACCs may be considered for treatment with traditional mTOR inhibitors. The effects of these compounds in vitro at concentration potentially reachable in vivo are predominantly cytostatic, although it is shown that longtime treatment with traditional mTOR inhibitors (in conditions disrupting the autocrine loops) can lead to cell death. Additional clinical benefit in patients with hypersecretive ACCs could be an inhibitory effect of these compounds on cortisol secretion. However, several factors such as cell type, cell differentiation, the presence of an autocrine growth factor loop, as well as the cell environment could largely influence the sensitivity of ACCs to these drugs. These differences point out the importance to investigate the presence of biomarkers predictive of potential clinical benefit and to eventually proceed in the clinical investigation of these compounds only in selected patients with higher chance to respond to this treatment. This study also suggest to investigate the role of TP53 mutations, cell differentiation, proliferative index, the presence of activated autocrine loops as potential marker predictive of mTOR inhibitor effects in ACCs, and the activation of AKT and ERK during the treatment as potential markers of escape. Finally, it is suspected that in some cases of ACCs, combined treatment with mTOR inhibitors and other compounds should be considered to overcome possible mechanisms of resistance to mTOR inhibitors used as monotherapy.

Particularly, the effects of treatment targeting the IGF2 autocrine loop, in combination with mTOR inhibitors, warrant further investigation in ACC.

Declaration of interest

The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

Funding

This research did not receive any specific grant from any funding agency in the public, commercial, or not-for-profit sector.

Acknowledgements

Dr Dimiter Dimitrov and Dr Yang Feng kindly provided the anti-IGF2 antibody. Fadime Dogan and Claudia Pivonello kindly contributed to develop the protocol of the western blotting.

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Received in final form 27 February 2012
Accepted 12 February 2012
Made available online as an Accepted Preprint 14 February 2012