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An *in vitro* investigation of the induction of apoptosis and modulation of cell cycle events in human cancer cells by *bis*phenanthroline-coumarin-6,7-dioxacetatocopper(II) complex

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Abstract

The central objective of the current study was to investigate the potential in vitro anti-proliferative properties of the parent ligand, coumarin-dioxy-acetic acid (cdoaH₂), and its copper complex, copper-coumarin-dioxyacetic acetate-phenathroline ([Cu(cdoa)(phen)₂]) using four human-derived model cell lines, two neoplastic and two non-neoplastic. In addition, selected mechanistic studies were carried out using one of the neoplastic-derived model cell lines, Hep-G2. Results obtained show that the complex, rather than the ligand, could alter the proliferation of both human neoplastic renal (A-498) and hepatic (Hep-G2) cells. Furthermore, hepatic non-neoplastic cells (Chang) appeared to be less sensitive. However, this effect was not mirrored in nonneoplastic renal (HK-2) cells, a profile shared with cisplatin. The observed anti-proliferative effect appeared to be concentrationand time-dependant, and could be attributed to the complex, rather than any of the component parts, i.e. 1,10-phenanthroline, the coumarin ligand, or the simple metal salt. Furthermore, the complex was shown to decrease DNA synthesis, but did not intercalate with it. Based on IC₅₀ values, [Cu(cdoa)(phen)₂] was shown to be almost six times more potent than cisplatin. Moreover, there was no evidence to show that P-glycoprotein (P-gp)-mediated multi-drug resistance (MDR) was likely to play a role in decreasing the anti-proliferative activity of the complex. Cytological stains, analysis of genomic DNA, and biochemical assays [caspase-3 and -9 and cleaved poly(ADP-ribose)-polymerase protein], suggested that cell death could switch between apoptosis and necrosis, and this effect appeared to be concentration-dependent. Additionally, flow cytometric analysis showed that the complex functioned through an alteration in cell cycle progression. Taken together, [Cu(cdoa)(phen)₂] has been shown to be a more potent anti-proliferative agent than either the ligand or cisplatin, and is capable of altering key biochemical events leading to the execution of apoptotic and/or necrotic cell death, suggesting that it is worthy of further investigation. © 2007 Elsevier Ireland Ltd. All rights reserved.

Keywords: Apoptosis; Cell cycle progression; Copper-coumarin-phenanthroline complex; Caspase activity; PARP cleavage

1. Introduction

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There have been a number of reports highlighting the use of transition metal complexes as anticancer agents [1]. Probably the best known of these is cisplatin [*cis*-diamminedichloroplatinum(II)] which has been widely

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used in the treatment of a variety of cancers, especially testicular cancer, with a 70–90% cure rate. When combined with other drugs, it has successfully been used to treat brain, ovarian, bladder and breast cancer [2]. The clinical success of cisplatin is limited by its significant side effects, such as nausea, vomiting, severe nephrotoxicity and genotoxicity [2]. The use of cisplatin and related platinum complexes as anti-cancer agents has stimulated a search for other active transition metal complexes which are as, or more effective, but with lesser side effects.

Coumarins comprise a very large class of compounds found throughout the plant kingdom [3,4]. The bio-activity of coumarin and more complex related derivatives appears to be based on the coumarin nucleus [5–7]. Biological effects observed include antibacterial [8], anti-thrombotic and vasodilatory [9], anti-mutagenic [10], lipoxygenase and cyclooxygenase inhibition [11,12], and scavenging of reactive oxygen species, as well as anti-tumourigenic [13–19]. Since the late 1980s, a number of in vivo studies have investigated the possible use of coumarins in the treatment of malignant melanoma and renal cell carcinoma [20,21]. All of these studies have demonstrated a significant response rate following coumarin treatment alone or in combination therapy. The in vitro effects of coumarins on the growth of malignant melanoma and renal cell carcinoma-derived cell lines showed that coumarin and 7-hydroxycoumarin, along with several of their derivatives were potent cytotoxic and cytostatic agents [15,17–19]. Recent studies carried out in our laboratory compared the anti-proliferative capability of a series of natural and synthetic nitro- and hydroxylated-derivatives of coumarin, including 6-nitro-7-hydroxycoumarin and 7,8-dihydroxycoumarin, using both renal adenocarcinoma and malignant melanoma-derived cell lines. These compounds were shown to be potent cytotoxic agents, capable of killing cancer cells by modulation of key biochemical pathways such as mitogen-activated protein kinases [17-19].

Interest in metal–coumarin complexes has arisen from the search for novel lead compounds, along with the desire to improve the pharmacological profile of established anti-neoplastic agents. Kokotos et al. [22] synthesised a number of amino-coumarin–platinum(II) complexes and evaluated their *in vitro* anti-proliferative activity using a colonic carcinoma cell line (Caco-2). They screened a number of coumarins with an amino group at position six or seven and methyl groups at various positions around the coumarin nucleus. These researchers found that the most potent platinum–coumarin complex had functional groups attached at position six. More recently, Manalov et al. [23] investigated the *in vitro* cytotoxicity of a number of coumarin complexes with the rare earth metal, cerium, using both Burkitt lymphoma (P3HR1) and leukemic (THP-1) cell lines. These researchers found that complexation resulted in a 40% increase in cytotoxicity, compared to the metal-free ligand. Additionally, Manalov et al. [23] studied the effects of coumarin complexed to zirconium. Here again it was found that metal–coumarin complexes were more active than either the inorganic metal ion or the coumarin ligand on their own.

1,10-Phenanthroline (phen) and substituted derivatives, both in the metal-free state and as ligands co-ordinated to transition metals, disturb the functioning of a wide variety of biological systems [24]. Furthermore, when metal-free N,N'-chelating bases are found to be bioactive it is usually assumed that the sequestering of trace metals *in situ* is involved, and that the resulting metal complexes are the active species [25,26]. Previous work has shown that metal-phen complexes, namely [Cu(phen)₂(mal)]·2H₂O, [Mn(phen)₂(mal)]·2H₂O and [Ag₂(phen)₃(mal)]·2H₂O (malH₂ = malonic acid) inhibit growth of the fungal pathogen *Candida albicans* by around 95% in a concentration range of 1.25–5.0 µg/ml [27,28].

One of the most biologically active of the metal-phen complexes has been shown to be $[Cu(phen)_2]^{2+}$. This agent has been shown to promote hydroxyl radical formation from molecular oxygen by redox-cycling and could therefore be considered suitable for stimulating the production of reactive oxygen species. Transition metal cations such as Cu(II) and Fe(II) bind to negatively charged DNA and have been shown to play an important role in the local formation of •OH radicals [29,30]. One of the consequences of high copper levels in the body is an increase in the rate of radical formation leading to oxidative damage, which leads to a disruption of lipid bilayers due to oxidation and cleavage of vulnerable unsaturated fatty acid residues of phospholipids [31]. Alterations in protein function are also promoted through oxidation of thiol and possibly amino groups. Gene expression may also be altered due to oxidation of guanosine and adenosine residues in nucleic acids, or altered transcription factor/growth factor activities [31]. Tsang et al. [32] reported that incubation of a human hepatic cell line (Hep-G2) with $[Cu(phen)_2]^{2+}$ resulted in internucleosomal DNA fragmentation, a hallmark of apoptosis. Zhou et al. [33] also reported G₁-specific apoptosis in a liver carcinoma cell line (Bel-7402), caused by $[Cu(phen)_2]^{2+}$. Additionally, this complex was shown to up-regulate DNA-binding activity of p53, a pivotal molecule in the



Fig. 1. Structure of (A) [cdoaH₂] and (B) [Cu(cdoa)(phen)₂] used in this study.

regulation of cell progression, cell survival and apoptosis [34].

Based on the above, and given the anti-cancer properties of metal-based derivatives of both coumarin and phen, we decided to determine whether a complex composed of each of these component parts, namely $cdoaH_2$ and its copper complex, copper-coumarin-dioxyacetic acetate-phenathroline ([Cu(cdoa)(phen)₂] (Fig. 1) could decrease the *in vitro* proliferative activity of humanderived cancer cell lines. Therefore, the central objective of this study was to use a number of *in vitro*-based techniques to illustrate whether these agents could selectively kill cancer cells, and in doing so elucidate their molecular mechanism of action. In addition, comparative studies were carried out in order to highlight potential benefits, relative to one of the best known and most widely used metal-based anti-cancer drugs, cisplatin.

2. Materials and methods

2.1. Test compounds and reagents

Cisplatin, phen, $Cu(ClO_4)_2$ and dimethyl sulfoxide (DMSO) were purchased from Sigma–Aldrich, Ireland Ltd. and used as received. The preparation of the novel ligand cdoaH₂ and its copper complex ([Cu(cdoa)(phen)₂]) are described in full in another publication [35]. Structure and purity analysis was confirmed by thin layer chromatography, infrared analysis, ¹H and ¹³C NMR spectroscopy, along with elemental analysis. The X-ray crystal structure of the copper(II) complex showed that the copper complex had a trigonal bipyramidal geometry about the metal centre, with the copper atom bound to four nitrogen atoms of the two chelating phen ligands and a single oxygen from one of the carboxylate moieties of the $cdoa^{2-}$ ligands.

The chemiluminescence substrate Luminol, was purchased from Pierce Laboratories (UK), while the antibody specific to cleaved poly(ADP-ribose)polymerase (PARP) was purchased from New England Biolabs, and the DNA fragmentation kit was purchased from Calbiochem, UK. Jsb-1, the antibody specific for P-glycoprotein (P-gp) was purchased from Cappell, UK. All cell culture reagents and culture media were purchased from Euroclone, UK, unless otherwise stated.

2.2. Model cell lines

A-498 (human kidney adenocarcinoma), HK-2 (human proximal tubular), Chang (human hepatic) and Hep-G2 (human hepatocellular carcinoma) cells were purchased from the American Type Culture Collection, Manassas, USA. A-498, Chang and Hep-G2 cells were maintained in Eagles Minimum Essential Medium (EMEM) with Earle's Balanced Salt Solution, containing 1.5 g/L sodium bicarbonate, 2 mM L-glutamine, 0.1 mM non-essential amino acids, 1 mM sodium pyruvate, 100 U/ml penicillin, 100 µg/ml streptomycin and 10% (v/v) foetal bovine serum (FBS) (Sigma). HK-2 cells were maintained in Dulbecco's Modified Eagles Medium/Nutrient Hams F12 (50:50, v/v), supplemented with 2 mM L-glutamine, ITS (5 µg/ml bovine insulin, 5 µg/ml human transferrin, 5 ng/ml selenium), 36 ng/ml hydrocortisone, 4 pg/ml 3,3',5-tri-iodo-L-thyronine, and 10 ng/ml epidermal growth factor. All cell lines were grown at 37 °C in a humidified atmosphere with 5% CO₂, and were in the exponential phase of growth at the time of inclusion in assays.

Chinese hamster ovary cells (CHO-K1 and CH^RC5) were kindly provided by Dr. V. Ling, Ontario, Canada. CHO-K1 cells were maintained in Nutrient Hams F12, containing 2 mM L-glutamine, 100 U/ml penicillin, 100 μ g/ml streptomycin and 10% (v/v) FBS. CH^RC5 cells were maintained in EMEM, Alpha modification (without ribonucleosides and deoxynucleosides), containing 2 mM L-glutamine, 100 U/ml penicillin, 100 μ g/ml streptomycin and 10% (v/v) FBS. All cell lines were grown at 37 °C in a humidified atmosphere and in the presence of 5% CO₂.

2.3. Assessment of cytotoxicity using MTT assay

cdoaH₂, [Cu(cdoa)(phen)₂], phen, cisplatin and Cu(ClO₄)₂ were dissolved in DMSO, diluted in culture media and used to treat model cells over a range of drug concentrations for periods of 4, 24 and 96 h. The maximum percentage of DMSO present in any well was 0.05% (v/v). Cells were seeded in sterile 96 well flat-bottomed plates (Sarstedt) at a density of 5×10^4 cells/ml and grown in 5% CO₂ at 37 °C. A miniaturised viability assay using 3-(4,5-dimethylthiazol-2yl)-2,5-diphenyl-2H-tetrazolium bromide (MTT) was carried out according to the method described by Mosmann [36]. In metabolically active cells, MTT is reduced by the mitochondrial enzyme succinate dehydrogenase to form insoluble purple formazan crystals that are subsequently solubilised, and the optical density (OD) measured spectrophotometrically. Therefore, drug-treated cells were assayed by the addition of 20 µl of 5 mg/ml MTT in 0.1 M phosphate buffer saline (PBS), pH 7.4. Following incubation for 4 h at 37 °C, the overlying medium was aspirated with a syringe and 100 µl of DMSO was added to dissolve the formazan crystals. Plates were agitated at high speed to ensure complete dissolution of crystals and OD was measured at 550 nm using an Anthos HT-II microtitreplate reader. Viability was expressed as a percentage of solvent-treated control cells. This assay had five replicates per assay, and each experiment was carried out on at least three separate occasions. The IC₅₀ was calculated and defined as the drug concentration (µM) causing a 50% reduction in cellular viability.

2.4. Confirmation of MDR-1 phenotype

The pleotrophic drug-resistant cell line CH^RC5, has previously been shown to over-express the MDR-1 gene product, P-gp-170 and exhibit cross-resistance to structurally dissimilar drugs, while the P-gp-negative CHO-K1 cell lines fails to exhibit the MDR-1 phenotype [37]. To confirm these drug phenotypes, both CH^RC5 and CHO-K1 cells were assessed for chemosensitivity by exposure to a known anti-cancer drug, vinblastin. The viability of CHRC5 and CHO-K1 cell lines was assessed in parallel using a 96-well format with increasing concentration of vinblastin. Briefly, the cell density of both cell lines was adjusted to 5×10^4 cells/ml, and 100 µl of cell suspension was added per well to a 96-well plate (Falcon). Following overnight incubation, a concentrated stock solution of each test compound was prepared in DMSO was stored at -20 °C, thawed directly prior to the assay, and the required dilutions were prepared by

serial dilution in complete culture medium. The maximum concentration of DMSO present in all wells was 0.05% (v/v), a concentration which exhibited no effect on cell morphology or growth. Viability was determined using the MTT assay [36]. The relative degree of resistance for each cell line was determined by comparison of the IC₅₀ values [38].

2.5. DNA synthesis studies

DNA synthesis was determined using 5-bromo-2deoxyuridine (BrdU) colourimetric incorporation assay [39]. A-498 and Hep-G2 cells were seeded into 96 well plates and allowed to adhere overnight. $cdoaH_2$ and [Cu(cdoa)(phen)_2] was added and incubated for 96 h prior to the addition of BrdU (10 μ M per well). Plates were then incubated at 37 °C for 4 h and incorporation was quantified using ELISA (Roche). The significance of any reduction in DNA synthesis was determined using one-way ANOVA.

2.6. DNA binding studies

pGEM-3Z plasmid DNA was purified from Escherichia coli [strain JM 109 and previously cultured in LB broth (Oxoid), containing 50 µg/ml ampicillin] using a Qiagen isolation kit (Qiagen Ltd.). DNA purity and concentration was determined spectrophotometrically using A260/A280 spectrophotometric measurements. DNA concentration was adjusted to 1 µg/ml using 10 mM Tris-HCl, pH 7.5, containing 1 mM EDTA. Drug binding assays were carried out according to the method described by Lorcozio and Long [40]. Briefly, DNA was incubated for 2h at 37 °C, with doxorubicin employed as a positive control. Plasmid DNA was separated on a 1% (w/v) agarose gel in TBE (80 mM Tris-HCl, pH 8; 40 mM boric acid and 2 mM EDTA), and stained with ethidium bromide $(5 \mu g/ml \text{ in TBE})$. Bands were visualised by irradiation at 300 nm and photographed using a Pharmaciae 3D imaging system.

2.7. Morphological analysis

Preparations of Hep-G2 cells exposed to the complex for either 4 or 24 h and then stained with methylene blue and eosin [41]. Drug-treated cells were grown in Petridishes, washed once with PBS, once with PBS:methanol (1:1, v/v) and then fixed in 100% (v/v) methanol for 10 min. Following fixation, cell monolayers were rinsed with anhydrous methanol and stained with methylene blue and eosin for 2 min. Monolayers were then agitated for a further 2 min, destained by rinsing under a gentle stream of water and then finally rinsed with distilled water. Phase contrast microscopy was carried out using a Ceti Phase Contrast Microscope.

Cells were also stained using a dye specific for the detection of apoptotic cells, namely 4,6diamidino-2-phenylindole (DAPI). Briefly, a monolayer of drug-treated cells was washed in PBS and fixed with 4% (w/v) paraformaldehyde for 30 min at room temperature. These cells were then permeabilized with 0.2% (v/v) Triton X in PBS and incubated with 1 µg/ml of DAPI for 30 min. Cells were washed three times with PBS and viewed using a fluorescent microscope with 340/380 nm excitation filter at $60 \times$ magnification. Apoptotic cells were confirmed by identification of intensely stained, fragmented nuclei and condensed chromatin.

2.8. DNA fragmentation

Chromosomal DNA from drug-treated cells was extracted using the Suicide-trackTM DNA ladder isolation kit (Oncogene). Briefly, cells were cultured in 150 mm Petri-dishes and treated with complex at concentrations of 0, 7.5, 15 and 30 µM 24 h. Floating cells were collected by centrifuging, while adherent cells were harvested by scraping and then combined with collected floating cells. All cells were then centrifuged together and the resulting pellet, consisting of approximately 5×10^6 cells, was resuspended in 55 µl of lysis solution, followed by the addition of 20 µl of RNase A solution and incubated at 37 °C in a water bath for 1 h. Twentyfive microlitres of DNA isolation solution was added and tubes were incubated overnight at 50 °C. Five hundred microlitres of re-suspension buffer (10 mM Tris-HCl, pH 7.5, containing 1 mM EDTA) was then added to each sample. Intact and fragmented DNA was precipitated by the addition of 2 µl of Pellet-paintTM co-precipitant followed by 60 µl of 3 M sodium acetate, pH 5.2 and 662 µl of 2-propanol. Samples were mixed by inversion and then washed once in 70% (v/v) ethanol and once in 100% (v/v) ethanol. Finally, DNA samples were airdried and resuspended in 50 µl of resuspension buffer (10 mM Tris-HCl, pH 6.8) before analysis on 1.8% agarose gels. Positive controls consisted of 1×10^{6} HL-60 cells (Human leukaemia cells) treated with $0.5 \,\mu$ g/ml Actinomycin D for 24 h, both supplied by Oncogene.

2.9. Caspase activity assay

Activation of ICE-family proteases/caspases initiates apoptosis in mammalian cells [42]. Hep-G2 cells were incubated with complex at concentrations of 0, 7.5, 15 and 30 µM for 24 h. Both floating and attached cells were collected by centrifugation. Cells at a density of 1.5×10^6 cells/ml, were counted, washed with PBS and then re-suspended in chilled cell lysis buffer (supplied in the Caspase-3 colourimetric assay kit, Biovision, UK). Cells were incubated on ice for 10 min and then centrifuged for 1 min at $10,000 \times g$. The cytosolic fraction (supernatant) was collected into a fresh tube and 50 µl (2 mg/ml) of each protein sample was diluted with lysis buffer and added to 50 μ l of $\times 2$ reaction buffer containing, 10 mM DTT in a 96-well plate. Five microlitres of 4 mM DEVD-pNA substrate (200 µM) was added to each well and incubated at 37 °C for 1-2 h. OD was determined at 400 nm using an Anthos HT-II microtitreplate reader. The fold increase in caspase-3 and -9 activities was determined by comparing results to that obtained with un-induced control.

2.10. Immunoblot analysis for PARP cleavage

Test agent was dissolved in DMSO, diluted in culture media and used to treat model cells growing in 100 mm Petri-dishes. Cells were exposed to complex for 24 h at concentrations of 0, 15 or 30 µM. Both floating and attached cells were washed twice with icecold 0.1 M PBS, pH 7.4, harvested by scraping and centrifuged at $8000 \times g$ for 5 min. Whole cell extracts were prepared by re-suspension in lysis buffer [M-per lysing solution (Pierce, UK)], supplemented to contain 1 mM EDTA, 1 mM EGTA, 1 mM sodium vanadate, 1 mM phenylmethylsulfonylflouride (PMSF), 2 µg/ml leupeptin and 2 µg/ml aprotinin. After 15 min on ice, the mixture was clarified by centrifugation for 5 min at $10,000 \times g$ and the resultant supernatant collected. Forty micrograms of total protein lysates were resolved using electrophoresis on a 12% polyacrylamide gel (PAGE) and transferred to nitrocellulose membranes. The level of protein expression was determined using specific primary antibodies, followed by peroxidase-conjugated secondary antibodies, visualisation was achieved using a chemiluminescent substrate (Luminol) and exposure to X-ray film.

2.11. Cell cycle analysis

Hep-G2 cells were grown in 100 mm Petri-dishes and exposed to either solvent or complex at concentrations of 0, 4, 8 or 16 μ M for 24 h. Both floating and attached cells were collected by centrifugation, washed twice in ice-cold PBS, pH 7.4, harvested by trypsinisation and collected by centrifugation. The effect of treatment with the complex on cell cycle was determined using flow cytometric analysis according to the method of Nunez [43]. Briefly, cell suspensions were fixed and permeabilised by vigorous addition of nine volumes of ice-cold 70% (v/v) ethanol and stored at -20 °C for a minimum of 24 h, prior to analysis. Cells at a density of approximately 1×10^6 were re-suspended in 800 µl of propidium iodide staining solution (20 µg/ml propidium iodide and 200 µg/ml RNase A in PBS, pH 7.4) and incubated in the dark at room temperature for 30 min. The percentage of cells in sub-G₁, G₀/G₁, S and G₂/M phases of cell cycle was determined and analysed from at least three independent experiments using Cell QuestTM software (Becton Dickinson).

2.12. Statistical analysis

Statistical analyses were performed using the statistical software package Mini-tab[®]. Statistical evaluation of the untreated control cells along with drug- and solvent-treated cells was calculated using one-way ANOVA (analysis of variance). A probability of 0.05 or less was deemed statistically significant. The following notation was used throughout; *P < 0.05, **P < 0.01 and ***P < 0.001, relative to control.

3. Results

cdoaH₂ and [Cu(cdoa)(phen)₂] shown in Fig. 1, along with phen, cisplatin and $Cu(ClO_4)_2$ were initially incubated with four human-derived cell lines, two carcinoma (A-498 and Hep-G2) and two non-carcinoma (Chang and HK-2), and their cytotoxicity was determined using MTT (Figs. 2 and 3). Data obtained for both the ligand and the complex following 4, 24 and 96 h continuous incubation, was used to calculate IC50 values and are shown in Figs. 2-4, along with Table 1. All compounds displayed a concentration- and time-dependent anti-proliferative profile, and in all four cell lines, with the two neoplastic-derived cell lines, Hep-G2 and A-498, appearing to be most sensitive (Fig. 3). Also, based on IC₅₀ values it would appear that the complex was statistically more active than either the parent ligand or phen. Also, in order to establish that the anti-proliferative effect observed was due to the complex rather than the simple salt, it was decided to include Cu(ClO₄)₂ in the test protocol. Data presented in Table 1 suggests that $Cu(ClO_4)_2$ is not capable of displaying anti-profilerative effects blow 250 µM in any of the four model cell lines used here. In addition, we investigated the possibility that these agents could act as a potent anti-proliferative agent in neoplastic (Hep-G2 and A-498) rather than non-neoplastic-derived (Chang and HK-2) cell lines (Fig. 3). The results preTable 1

Compound	Hep-G2 (IC ₅₀ $(\mu M) \pm S.E.M.$)	CHANG (IC ₅₀ $(\mu M) \pm S.E.M.$)	A-498 (IC ₅₀ (μ M) ± S.E.M.)	HK-2 (IC ₅₀ $(\mu M) \pm S.E.M.$)
[cdoaH ₂]	>250	>250	>250	>250
[Cu(cdoa)(phen) ₂]·8.8H ₂ O	$2.5\pm1.4^*$	$14\pm2.2^*$	$2.5\pm0.9^*$	$3\pm1.1^*$
Cu(ClO ₄) ₂	>250	>250	>250	>250
Phen	4.5 ± 0.9	7 ± 1.2	5.5 ± 1.2	9 ± 1.5
Cisplatin	15.0 ± 2.65	45 ± 2.9	14.0 ± 2.3	18 ± 2.7

Anti-proliferative activity of test agents was determined using Hep-G2, Chang, A-498 and HK-2 cells, following 96 h continuous incubation and MTT assay

A graph of viability vs. drug concentration was used to calculate all IC₅₀ values (μ M), n = 5.

* Value is statistically distinct from that of the parent ligand at P < 0.05.

sented in Fig. 3 and Table 1 would suggest that Hep-G2 cells were significantly more sensitive than Chang, but this effect was not reflected in the non-neoplastic renal HK-2 cells. Thus, there is insufficient evidence to conclude that the complex can act in a cyto-selective manner i.e. sparing non-neoplastic cells. However, it is worth noting that the complex displayed a similar profile to that seen with cisplatin. Furthermore, the IC₅₀ values for the complex using A-498 and Hep-G2 cells, were shown to be between 5.6 and 6 times greater, respec-

tively, than those seen with ciaplatin. Taken together, the data presented would suggest that the complex was significantly more anti-proliferative than cisplatin, with a similar profile existing across all four model cell lines.

In order to provide information on the antiproliferative effect of the complex following relatively short exposure times, MTT-based viability assays were carried out at both 4 and 24 h. The IC₅₀ values calculated were shown to be 49 and 15 μ M, respectively for the most sensitive cell line, Hep-G2 (Fig. 4). Consequently,



Fig. 2. Dose–response curve for $[cdoaH_2]$, $[Cu(cdoa)(phen)_2]$ and phen using (A) Hep-G2 and (B) A-498 cells, following 96 h incubation, as assessed by MTT assay. In both cell lines, the complex produced the greatest concentration-dependent decrease in cellular proliferation, following 96 h incubation. Results are expressed as percentage viability of solvent-treated control cells. Bars indicate \pm S.E.M., n = 3.



Fig. 3. Dose–response curve for (A) [cdoaH₂] and (B) [Cu(cdoa)(phen)₂] using Hep-G2, Chang, A-498 and HK-2 cells following 96 h incubation, as assessed by MTT assay. In both cases, the complex produced the greatest concentration-dependent decrease in cellular proliferation. Results are expressed as percentage viability of solvent-treated control cells. Bars indicate \pm S.E.M., *n* = 3.

Table 2

 $\label{eq:constraint} Anti-proliferative activity and resistance factor used to confirm multi-drug resistance phenotype and demonstrating whether [Cu(cdoa)(phen)_2] was a substrate for P-gp$

Test agent	CHO-K1 CH ^R C5			
	IC_{50} ((M) ± S.E.M.	IC_{50} ((M) ± S.E.M.	Resistance factor	
[Cu(cdoa)(phen) ₂]	3.56 ± 0.47	6.83 ± 0.61	1.9	
Vinblastine	0.013 ± 0.005	0.48 ± 0.04	37	

The resistance factor was calculated by division of the IC_{50} for the CH^RC5 cell line by the IC_{50} for the CHO-K1 cell line. Results presented are representative of three independent experiments.

these concentrations and time points were included in subsequent mechanistic assays, unless otherwise stated.

It has been established that over-expression of P-gp is responsible for the "classical" type of MDR. This has been defined as the simultaneous resistance of a cell against a variety of structurally dissimilar cytotoxic drugs [44,45]. Using a cellular model of MDR-1, we confirmed the MDR phenotype by immunological detection of P-gp along with chemosensitivity testing using vinblastine. This method allows the MDR phenotype to be assessed by detection of the protein effector molecule and by comparison of the relative toxicities (IC_{50}) in the MDR-positive and -negative cell lines. Consequently, drugs that display less or equal effects in the MDRpositive cell line could be potential MDR substrates. Furthermore, comparison of the relative experimental toxicities allows calculation of a resistance factor. This factor was calculated by dividing the drug toxicity (IC₅₀ value) observed in the MDR-positive cells by the drug toxicity in the MDR-negative cells. In addition, the integrity of the two model cells lines was confirmed by Western



Blot Analysis. P-gp-170 was not detected in the MDR negative cells (CHOK1), while there was considerable P-gp expression in MDR positive cells (CH^RC5) (data not shown). In addition, the results presented in Table 2 show the cytotoxicity observed with vinblastine and the complex and indicate that the MDR phenotype of the CH^RC5 cells was retained, with vinblastine demonstrating a resistance factor of 37. This value is consistent with a previously published value of 40 [18]. In contrast, the data obtained for the complex illustrated a substantially lower

resistance factor, suggesting that it is not a potential



Fig. 4. Dose–response curves for $[Cu(cdoa)(phen)_2]$ using Hep-G2 cells following 4 and 24 h incubation, as assessed by MTT assay. This complex caused a concentration- and time-dependent decrease in cellular proliferation. Results are expressed as percentage viability of solvent-treated control cells. Bars indicate \pm S.E.M., n=3.

Fig. 5. The effects of $cdoaH_2$ and $[Cu(cdoa)(phen)_2]$ on DNA synthesis in both (A) A-498 and (B) on Hep-G2 cells was determined using BrdU assays. Both compounds produced a concentration-dependent decrease in DNA synthesis, and in both cell lines. Results are expressed as percentage viability of solvent-treated control cells. Bars indicate \pm S.E.M., n = 3.

MDR-1 substrate. In addition, greater cytotoxicity was observed in the MDR-positive cell line, rather than the MDR-negative cell line (Table 2). In an attempt to elucidate the events responsible for the observed reduction in cellular proliferation, the effect of both the complex and the ligand on DNA synthesis in both Hep-G2 and A-498 cells was determined using BrdU incorporation assays. Results obtained suggest that following a 96 h the complex rather than ligand, caused a concentrationdependent decrease in DNA synthesis (Fig. 5).

In order to explore the relationship between the observed anti-proliferative response and the possibility that DNA was a molecular target, intercalation studies were carried out using electrophoretic mobility shift assays. Treatment of pGEM-3Z plasmid DNA with complex at concentrations of 1, 10 and 200 μ M did not alter the migration of any of the three forms of DNA (super-coiled, linear and open-circular), unlike the positive control doxorubicin (Fig. 6). This indicates that [Cu(cdoa)(phen)₂] does not function through DNA intercalation.



Fig. 6. Electrophoretic mobility shift assays were used to determine the effects of $[Cu(cdoa)(phen)_2]$ on the migration of pGEM-3Z supercoiled plasmid DNA for 2 h at 37 °C. Results indicate that the complex did not inhibit the migration of super-coiled (SC), linear (L) or open circular (OC) forms of plasmid DNA, suggesting that it did not intercalate DNA. Lane 1 pGEM-3Z DNA (negative control); lane 2 positive control (pGEM-3Z DNA and doxorubicin, 10 μ M); lanes 3-5 pGEM-3Z DNA and complex (1, 10, and 200 μ M). Results presented are representative of three independent experiments.



Fig. 7. The effect of $[Cu(cdoa)(phen)_2]$ on the cellular morphology of Hep-G2 cells was assessed following 4 and 24 h incubation at concentrations of 0, 7.5, 15 and 30 μ M (panels A–D, respectively), and assessed by methylene blue and eosin, using phase contrast microscopy ($60 \times$ magnification). At 4 h and a concentration of 30 μ M (panel D), there was a thinning of the monolayer. Additionally, by 24 h, there was nuclear disintegration and vacuolation of the cytoplasm (15 and 30 μ M, panels C and D) cells become rounded with progressive nuclear shrinkage and disintegration. In contrast, treatment of cells with vehicle alone (panel A) appeared to have no visible effect, as cells retained the typical epithelial morphology associated with Hep-G2 cells.



Fig. 8. The effect of $[Cu(cdoa)(phen)_2]$ on the cellular morphology of Hep-G2 cells was assessed following 4 and 24 h incubation at concentrations of 0, 7.5, 15 and 30 μ M (panels A–D, respectively), and assessed by DAPI staining, using phase contrast microscopy (60× magnification). At 4 h, cells exposed to 7.5, 15 and 30 μ M resulted in nuclear shrinkage (panels B–D, respectively), while by 24 h, each concentration caused nuclei to became intensively stained and fragmented (panels B–D). In contrast, control cells (panel A) exposed to vehicle alone displayed no visible effects.

The cytological effects of treatment with the complex at concentrations of 0, 7.5, 15 and 30 μ M for either 4 or 24 h were determined using methylene blue and eosin (Fig. 7), along with DAPI staining (Fig. 8). The results presented in Fig. 7 clearly suggest that the complex as early as 4 h and a concentration of 30 µM (panel D) resulted in a visible thinning of the monolayer, with nuclear disintegration and vacuolation of the cytoplasm. Furthermore, following 24 h and again at concentrations of 15 and 30 μ M, cells become rounded with progressive nuclear shrinkage and disintegration, along with eventual detachment from the culture dish. These changes are generally considered to be characteristic of the induction of apoptotic and necrotic cell death. In contrast, treatment of cells with vehicle alone (Fig. 7A) appeared to have no visible effect, as cells retained the typical epithelial morphology associated with Hep-G2 cells.

The effect of the complex on DNA integrity was determined using DAPI. This stain is commonly used to visualise nuclear morphology and detect the presence of DNA condensation. Results presented in Fig. 8 show that following 4 h, cells exposed to 7.5, 15 and 30 μ M caused nuclear shrinkage (panels B–D, respectively). Furthermore, by 24 h, and at each of the test concentra-

tions, nuclei became intensively stained and the nuclear material fragmented (panels B–D). Taken together, these results may suggest the presence of both apoptotic and necrotic cell death.

Analysis of DNA from apoptotic cells by agarose electrophoresis is known to produce a characteristic DNA ladder that is widely regarded as a biochemical hallmark of apoptosis. Therefore, in order to confirm the results observed in both Figs. 7 and 8, genomic DNA was extracted from cells treated with complex and analysed. Consequently, both floating and attached cells were collected for analysis. The results presented in Fig. 9 illustrate that the complex was capable of fragmenting DNA. However, the exact nature of the fragmentation patter was unclear, as increasing concentration of complex caused band smearing. Thus, based on this result alone, there remains the possibility that the complex may cause both necrotic and apoptotic cell death.

Given the results obtained above, our next aim was to examine the involvement of two specific caspases, namely; caspases-3 and -9, which are known to play a major role in the execution of apoptotic cell death. Caspase-3 is known to be one of the main executioner/effector caspases which is activated by caspase-9



Fig. 9. Internucleosomal DNA cleavage of Hep-G2 cells treated with $[Cu(cdoa)(phen)_2]$ was determined following incubation (lanes 3–5 at concentrations of 7.5, 15 and 30 μ M) for 24 h. Both floating and attached cells were collected and analysed. Lane 1 consists of the positive control provided in the kit consisted of 1 × 10⁶ HL-60 cells (Human leukaemia cells) treated with 0.5 μ g/ml Actinomycin D for 24 h. Lane 2 consists of the negative control consisting of vehicle alone. Results presented are representative of three independent experiments.

[42]. The results presented in Fig. 10 shows the foldincrease in both caspase-3 and -9 activities following 24 h incubation with [Cu(cdoa)(phen)₂]. The results obtained suggest that the activity of caspase-3 was significantly increased following incubation with concentrations of 15 and 30 μ M, while caspase-9 was increased only at 30 μ M. Furthermore, the complex appeared to produce a greater response in caspase-3, relative to caspase-9 activity.

The results presented in Fig. 10 would suggest that cleavage of poly(ADP-ribose)-polymerase protein (PARP), is likely to occur as a consequence of caspase-3 activation. This theory was subsequently confirmed using Western Blot Analysis (Fig. 11), where the complex at test concentrations of 30 μ M, was shown to cause an increase in the amount of cleaved PARP. However, this increase was not seen at the lower concentration of 15 μ M. Taken together with the results from the caspase assays, it would indicate the complex at a concentration of 30 μ M, may cause induction of apoptotic cell death, through activation of caspases-3 and -9, with subsequent cleavage of PARP.

The results presented in Fig. 5 showed that the complex could bring about a significant and concentration-



Fig. 10. The effects of [Cu(cdoa)(phen)₂] on caspase-3 and -9 activities were determined in Hep-G2 cells following 24 h incubation at concentrations of 0, 7.5, 15 and 30 μ M. The fold-increase in caspases-3 and -9 activities was determined by comparison with that of the solvent control. Data obtained suggests that caspase-3 activity was significantly increased following incubation with concentrations of 15 and 30 μ M, while caspase-9 was increased only at 30 μ M. Results presented are representative of three independent experiments. Bars indicate \pm S.E.M. The asterisks indicate statistically significant differences to control: *P < 0.05 and **P < 0.01.

dependent decrease in DNA synthesis, suggesting that DNA synthesis appeared to be a significant event occurring in response to drug-treatment. Therefore, it was decided to investigate the effect of the complex on cell cycle events and examine the resultant histograms for



Fig. 11. The effect of $[Cu(cdoa)(phen)_2]$ at concentrations of 15 and 30 μ M (panel A, lanes 1 and 2) on the proteolytic cleavage of poly(ADP-ribose)polymerase (PARP) was determined in Hep-G2 cells, following 24 h incubation. Both floating and attached cells were collected and analysed. A band corresponding to cleaved PARP (85 kDa) was detected following drug-treatment at a concentration of 30 μ M (panel A, lane 1). The same lysates were probed for the presence of β -actin (45 kDa) as a normalisation control (panel B). Western Blots presented are representative of three independent experiments.



Fig. 12. The effect of $[Cu(cdoa)(phen)_2]$ at concentrations of 4, 8 and 16 μ M, on cell cycle progression was determined in Hep-G2 cells, following 24 h incubation. Results show a concentration-dependent disruption in phase progression (panel B), with the appearance of a sub-G₁ peak (panel A). Histograms presented are representative of three independent experiments.

evidence of apoptotic cell death. Hep-G2 cells were exposed to test agent (4, 8, and 16 μ M) for 24 h and the percentage of cells entering each phase of the cell cycle was determined. The results presented in Fig. 12B show a concentration-dependent decrease in the % of cells entering G₀/G₁ and G₂/M. In addition, the % of cells in S phase increased at the lower drug concentration (4 μ M) and subsequently decreased at the highest concentration studied (8 and 16 μ M). Examination of the resultant histograms (Fig. 12A) show that concentrations of 8 and 16 μ M lead to a dramatic increase in the sub-G₁ peak from 3.6% to 55.5%, respectively. Furthermore, a sub-G₁ peak is widely regarded as representing hypo-diploid cells and is generally considered to be a marker for the presence of apoptotic cell death.

4. Discussion

The primary objective of this study was to identify the anti-proliferative properties of the parent ligand, coumarin-dioxy-acetic acid ($cdoaH_2$) and its copper complex, copper-coumarin-dioxyacetic acetatephenathroline ([Cu(cdoa)(phen)₂]). We also attempted to determine whether this complex could selectively kill human neoplastic cells, leaving non-neoplastic cells viable. In addition, we sought to elucidate the molecular mechanism underlying the pharmacology of this complex. In order to highlight the potential advantage of this complex, comparative studies were carried out using one of the best known and most widely used metal-based anti-cancer drugs, cisplatin. Furthermore, this is the first study of its kind to determine the potential application of this complex as a novel anti-proliferative agent.

Initial anti-proliferative studies were carried out to determine the IC_{50} value for the ligand and the complex, along with the simple metal salt $Cu(ClO_4)_2$, phen and cisplatin, using four human-derived model cell lines, two derived from neoplatic origin and two of non-neoplastic origin. It was intended that this approach would allow us to determine whether the observed anti-proliferative effect was due to the entire copper–coumarin–phen complex, rather than the metal-free ligand, phen or the simple aquated copper metal ion. Additionally, it was hoped that this might also provide a means by which the potential cyto-selective nature of the complex could be identified. We considered a compound to be

cyto-selective if the IC_{50} value obtained for the nonneoplastic-derived cells was statistically greater from that obtained for cells of neoplastic origin. It was oblivious that a compound which could act in this manner could offer significant advantage in the successful treatment and management of cancer in man.

Initial anti-proliferative studies were carried out to determine the IC₅₀ value of test agents, using all four human-derived model cell lines following 96 h exposure. Results presented in Figs. 2 and 3 and Table 1, show that the complex had IC_{50} values significantly lower than that recorded for the metal-free ligand, phen or the free metal salt. Furthermore, the complex displayed both a concentration- and time-dependent anti-proliferative effect. Additionally, the complex appeared to be the most potent agent tested, as it had an IC_{50} value which was approximately 6 times more active than cisplatin, and in both Hep-G2 and A-498 cells. Also, the results obtained suggest that Hep-G2 cells were significantly more sensitive than Chang, but this effect was not seen with the non-neoplastic renal (HK-2) cells. Consequently, it would appear that like cisplatin, the complex is capable of reducing the proliferative capacity of cells, but not in a cyto-selective manner.

In the initial part of the study we showed that the complex could kill hepatic and renal neoplastic cells following 96 h incubation. However, this did not provide information on the cytotoxicity associated with this compound following relatively short exposure time points such as 4 and 24 h. Therefore, MTT-based viability assays were conducted at these earlier time-points and the IC₅₀ values again determined. The data obtained (Fig. 4) shows that even at these relatively short exposure times, the complex was capable of causing a potent antiproliferative effect, with IC₅₀ values of 49 and 15 μ M, for 4 and 24 h, respectively. Therefore, where possible these concentrations and time-points were used to probe observed anti-proliferative response, along with elucidating the molecular mechanism of action of the complex.

The morphology of treated cells was used to determine the extent and nature of cytological effects. Two different staining techniques were employed. Firstly, cells were stined with methylene blue and eosin in order to determine if gross morphological changes could be observed. The second stain used was DAPI. This stain is specific for visualisation for nuclear morphology and detection of DNA condensation. Results presented in Figs. 7 and 8 clearly show that the complex could induce changes which are consistent with the induction of both apoptotic and necrotic cell death. In addition, it would appear that the mode of cell death was dependent on both drug concentration and incubation time, as it would appear that higher doses and longer incubation times may be required to switch from apoptosis to necrosis.

In an attempt to provide evidence for the involvement of many of the biochemical processes which are central to controlling the underlying mechanisms, it was decided to study a number of the key features of cell death. Therefore, additional studies were carried out using genomic DNA isolated from cells treated with the complex. Cleavage of genomic DNA by endogenous endonucleases during apoptosis is an irreversible event that commits the cell to die [46]. The results presented in Fig. 9 show that by 24 h, Hep-G2 cells treated with the complex had activated the necessary endonucleases, such that endonucleolytic cleavage of DNA at internucleosomal linker sites had occurred. In addition, increasing complex concentration of complex appeared to cause band smearing, suggesting the possible induction of necrotic cell death.

It is now widely accepted that activation of the caspase cascade occurs upstream of DNA fragmentation [42,47]. This activation serves to induce the proteolytic cleavage of a wide range of substrates. Caspase-3 is known to cleave and inactivate the inhibitor of caspase-activated DNAase, which in turn causes the release of active endonucleases which translocate into the nucleus in order to activate internucleosomal DNA fragmentation, ultimately serving as a trigger for phagocytosis [42,48]. In addition, caspase-3 activation leads to increased cleavage of PARP, a known substrate of caspase-3 [48]. Proteolytic cleavage of native PARP (116 kDa) results in separation of the N-terminal binding domain (24 kDa) from its C-terminal catalytic domain (89 kDa) [49,50]. This is also an early critical event required for tumour cells that have been exposed to DNA-damaging agents and have committed to die by apoptosis. Therefore, we decide to investigate the involvement of both caspase-3 and -9 in mediating the mechanism of action of the complex (Fig. 10). Data obtained demonstrates that the complex could mediate the activity of both caspase-3 and -9, leading to PARP cleavage.

The ability of the complex to target DNA through an inhibition of synthesis was demonstrated and presented in Fig. 5. Additionally, we have shown (Fig. 6) that it was non-intercalative, but that it was capable of decreasing DNA synthesis (Fig. 5). Based on the findings presented here, we were confident that the effect on DNA synthesis was linked, not just to an anti-proliferative effect, but also to the machinery associated with cell division, and ultimately an ability to induce cell death. Consequently, Hep-G2 cells were exposed to test agent (4, 8 and 16 μ M) for 24 h and the percentage of cells entering each phase of the cell cycle was determined (Fig. 12). This finding sug-

gests that the complex caused a concentration-dependant decrease in the % of cells entering G_0/G_1 and G_2/M . These data indicate that the complex was capable of preventing cell cycle progression. It is now widely established that progression is a tightly ordered and regulated process involving multiple checkpoints. These checkpoints respond to a variety of growth signals, alterations in cell size and DNA integrity [51-53]. We postulate that the complex may act on these checkpoints, preventing further cell division and subsequently initiating death by apoptosis and/or necrosis. However, this theory has not yet been proven experimentally. It is worth noting that the test concentrations used in this part of the study were lower than those used before. These lower concentrations were chosen as a higher concentration of 30 µM lead to complete degradation of DNA, making it impossible to determine effects on cell cycle. This finding suggests that when cells were exposed to higher drug concentrations, they may undergo necrotic cell death, and by a mechanism which was caspase-dependant (Fig. 9). This theory may help explain the findings presented in Fig. 8, using DAPI staining, where cells display characteristics consistent with both apoptotic and necrotic cell death. Examination of the flow cytometric histograms (Fig. 11A) indicated the presence of a sub-G1 peak which increased with increasing concentration $(16 \,\mu M)$. However, a very similar concentration $(15 \,\mu\text{M})$ did not produce a statistically significant increase in caspase-9 activity and PARP cleavage (Figs. 10 and 11). Taken together, this would suggest that cell death my occur via either a caspase-independent or -dependent mechanism with concurrent blockage of cell cycle events. Recently, caspase-independent apoptosis has been observed in several cell types [54,55]. Researchers have shown that one of the proteins responsible for caspase-independent chromatin condensation is apoptosis-inducing factor (AIF) [56]. AIF is a 57 kDa flavoprotein which is confined to the mitochondrial inter-membrane space of healthy cells. However, upon exposure to lethal agents, AIF translocates from the mitochondria to the nucleus, via the cytosol. Although this protein may induce caspase-independent peripheral chromatin condensation and large-scale DNA fragmentation, the underlying molecular signalling mechanism remains to be identified. Consequently, the possibility remains that that the complex studied here may function through AIF.

In conclusion, the results from this study clearly indicate that [Cu(cdoa)(phen)₂], rather than the parent ligand [CdoaH₂], phen, or the simple salt, could act as a potent anti-proliferative agent. However, there is insufficient evidence to suggest that it could function in a cytoselective manner. Additionally, we have shown that this complex can induce morphological and biochemical features consistent with the induction of both apoptotic and necrotic cell death. However, concentration of the complex may be one of the main factors which causes a cell to switch between the two modes of death. Additional studies are currently underway by which both the number of apoptotic cells can be accurately quantified, and the role of regulatory proteins associated with cell division and death can be determined more fully. Furthermore, we intend to elucidate the inter-relationship between these regulatory proteins and those associated with signalling proteins, such as the mitogen-activated protein kinases which are known to control cellular proliferation, death and differentiation [57]. It is hoped that results from these studies will allow identification of additional molecular targets, which may further assist in the elucidation of the mechanism of action of this complex.

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