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Preclinical studies on metal based anticancer drugs as enabled by integrated metallomics and metabolomics†

Luis Galvez,^{id a} Mate Rusz,^b Michaela Schwaiger-Haber,^{id acd} Yasin El Abiead,^{acd} Gerrit Hermann,^{ae} Ute Jungwirth,^{id f} Walter Berger,^{id gh} Bernhard K. Keppler,^{bg} Michael A. Jakupec,^{id bgh} and Gunda Koellensperger^{id *acd}

Resistance development is a major obstacle for platinum-based chemotherapy, with the anticancer drug oxaliplatin being no exception. Acquired resistance is often associated with altered drug accumulation. In this work we introduce a novel -omics workflow enabling the parallel study of platinum drug uptake and its distribution between nucleus/protein and small molecule fraction along with metabolic changes after different treatment time points. This integrated metallomics/metabolomics approach is facilitated by a tailored sample preparation workflow suitable for preclinical studies on adherent cancer cell models. Inductively coupled plasma mass spectrometry monitors the platinum drug, while the metabolomics tool-set is provided by hydrophilic interaction liquid chromatography combined with high-resolution Orbitrap mass spectrometry. The implemented method covers biochemical key pathways of cancer cell metabolism as shown by a panel of >130 metabolite standards. Furthermore, the addition of yeast-based ¹³C-enriched internal standards upon extraction enabled a novel targeted/untargeted analysis strategy. In this study we used our method to compare an oxaliplatin sensitive human colon cancer cell line (HCT116) and its corresponding resistant model. In the acquired oxaliplatin resistant cells distinct differences in oxaliplatin accumulation correlated with differences in metabolomic rearrangements. Using this multi-omics approach for platinum-treated samples facilitates the generation of novel hypotheses regarding the susceptibility and resistance towards oxaliplatin.

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Introduction

Already in the 1930s, Warburg and his contemporaries reported the concept of aerobic glycolysis in cancer. They highlighted the fundamental differences in the central metabolic pathways

between healthy and malignant tissues.¹ While for many years cancer research focused on genomic changes and oncogenes,^{2–4} links between metabolism and cancer only recently re-emerged as an exciting area of investigation.⁵ Indeed, dynamic changes of biological systems can be tracked by measuring the metabolome. Furthermore, molecular signatures are extremely powerful for hypothesis generation, offering novel insights, *e.g.*, in the crosstalk of tumor cells with the tumor microenvironment⁶ or in the drug mode of action.^{7,8} Metabolome profiling of drug-exposed cell cultures *in vitro* offers the unique opportunity to identify potential weaknesses in cellular drug responses, allowing correlations of biochemical pathways and/or genetic polymorphisms with drug susceptibility.^{3,9}

To date, only a few metabolomic studies exist in the field of metal-based anticancer agents, despite the fact that platinum-based therapies are among the most frequently clinically applied anticancer therapies.¹⁰ The amount of registered clinical studies involving metal-based anticancer drugs (novel compounds and combination therapies) is constantly high with increasing numbers over the last few years,^{11,12} such as successful combinations with immunotherapies in recent years.¹³ As for many drugs,

^a Institute of Analytical Chemistry, Faculty of Chemistry, University of Vienna, Waehringer Strasse 38, 1090 Vienna, Austria.
E-mail: gunda.koellensperger@univie.ac.at

^b Institute of Inorganic Chemistry, Faculty of Chemistry, University of Vienna, Althanstrasse 14 (UZA II), 1090 Vienna, Austria

^c Vienna Metabolomics Center (VIME), University of Vienna, Althanstrasse 14, 1090 Vienna, Austria

^d Research Network “Chemistry Meets Microbiology”, Althanstrasse 14, 1090 Vienna, Austria

^e ISOTopic Solutions, Waehringer Strasse 38, 1090 Vienna, Austria

^f Department of Pharmacy & Pharmacology, Centre for Therapeutic Innovation, University of Bath, Claverton Down, BA2 7AY, Bath, UK

^g Medical University of Vienna, Department of Medicine I, Institute of Cancer Research, Vienna, Austria

^h Research Cluster “Translational Cancer Therapy Research”, University of Vienna and Medical University of Vienna, Vienna, Austria

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including the clinically approved platinum compounds, it is not fully defined how the drug is taken up by the malignant tissues.^{14,15} A clear-cut mechanism remains to be elucidated even after years of clinical practice. Intrinsic and acquired platinum resistance are a major obstacle jeopardizing successful therapy.^{16–19} For the clinically approved platinum drugs, DNA is the established molecular target.^{11,15} However, the fact that only 1% of the platinum reaches the nucleus strongly suggests additional important cellular interactions.²⁰ Recently, oxaliplatin was found to kill cancer cells by inducing ribosome biogenesis stress rather than by engaging a DNA damage response.²¹

The few metabolomic studies investigating platinum drugs (1) address the role of metabolism in chemosensitivity of tumor cells towards platinum compounds,²² (2) investigate metabolomics as a predictive tool,^{23,24} (3) used metabolomics to discriminate isogenic sensitive and resistant cell types^{19,25,26} and (4) proposed metabolomics as a tool-set for early detection of nephrotoxicity.²⁷ By correlating biochemical pathways (measured by transcriptomics and metabolomics) from the NCI60 cell line panel with tumor cell chemosensitivity, it was found that pathways including the tricarboxylic acid (TCA) cycle, pyruvate metabolism, lipoprotein uptake and nucleotide synthesis (salvage pathways and *de novo* synthesis) were specific for sensitivity towards platinum compounds.^{28,29}

Overall metabolomic platforms and procedures are still not as mature as other -omic technologies.⁴ There is a need for new methods and technologies as analytical protocols have often to be adapted to the specific applications to try to cope with the intrinsic challenges of analysis such as metabolome coverage, analytical throughput and accuracy.³⁰ In this work we propose the combination of metabolomics and metallomics as a novel powerful tool-set in preclinical metallodrug research to address the metal uptake and cellular drug distribution within the same sample. This unique combination ultimately allows assessment of metabolome perturbations exerted by the metallodrugs and correlation of the corresponding biochemical pathways with drug accumulation and/or cytotoxicity. Complementary use of elemental inductively coupled plasma mass spectrometry (ICP-MS) and high-resolution molecular mass spectrometry (Orbitrap-MS) together with the developed sample preparation enabled the study of drug uptake, drug distribution between nucleus/protein and small molecule fraction and metabolic signatures upon drug exposure from one cell culture sample. Sample preparation in metabolomics is highly demanding^{25,31} and absolutely key when acquiring a snap-shot of the highly dynamic metabolome, particularly with regards to the handling time. Several preparation protocols have been established to simultaneously measure proteomics and metabolomics,^{32–34} but the combination of metal analysis and metabolomics has not been addressed so far. In the past, it has been shown that the choice of chromatography was key for the selectivity, throughput and metabolome coverage of the analysis.^{35,36} In this work we implemented hydrophilic interaction liquid chromatography (HILIC) for the retention of polar metabolites.^{37–45} Finally, ¹³C internal standardization based on yeast standards^{25,35,43,46,47} was employed at the extraction stage.

Together with high-resolution mass spectrometry this strategy allows (1) improvement of the identification task in untargeted metabolomics, an approach coined as credentialing,⁴⁸ and (2) merging of targeted quantification and untargeted analysis in one workflow.²⁵ With this method targeted relative quantification between different sample groups was facilitated without compromising untargeted data evaluation.²⁵ To test the novel metabolomics/metallomics strategy in a preclinical setting we investigated metabolic changes and drug accumulation in an oxaliplatin sensitive and resistant cell model over time.

Experimental

Reagents, chemicals and standards

The metabolite standards were purchased from Sigma-Aldrich or Fluka (Vienna, Austria) except for malic acid which was purchased from Merck (Vienna, Austria). A multistandard stock solution of 100 μM was prepared in water and used as a quality control (QC) of 10 μM . A fully ¹³C labeled yeast extract of *Pichia pastoris* (2 billion cells) from ISOTopic solutions e.U., (Vienna, Austria) was reconstituted in 2 mL of water and added in the same amount to the samples. The final dilution of the internal standard for the measurement was 1 : 10. As shown in previous studies,^{25,35,43,46,47} the yeast based material provided a ¹³C isotopic enrichment of >98.8% for primary metabolites resulting in a non-interfering isotopologue pattern with the natural compounds. The platinum standard ($1002 \pm 6 \mu\text{g mL}^{-1}$) was purchased from Inorganic Ventures (Christiansburg, Virginia, USA). Media and reagents for cell culture were purchased from Sigma-Aldrich (Vienna, Austria) and all materials such as dishes, plates and flasks were purchased from StarLab (Hamburg, Germany) unless indicated otherwise.

Cell culture and cytotoxicity tests

The human colon cancer line HCT116, acquired from ATCC (American Type Culture Collection, USA), and the oxaliplatin resistant subline (established as described elsewhere⁴⁹) were grown as adherent monolayer cultures in McCoy's 5A medium (Sigma-Aldrich) supplemented with 10% heat-inactivated fetal bovine serum (BioWest) and 4 mM L-glutamine (Sigma-Aldrich) without antibiotics at 37 °C (StarLab) under a humidified atmosphere containing 5% CO₂. HCT116 cells were seeded at a density of 5×10^3 viable cells per well into 96-well micro-culture plates (StarLab) 24 h prior to the treatment. Stock solutions of oxaliplatin were prepared in McCoy's 5A medium and diluted stepwise. Cells were incubated for 24 h with the indicated drug concentrations. Cell viability was measured using resazurin sodium salt (Sigma-Aldrich) (440 μM in PBS (Sigma-Aldrich)). After 4 h at 37 °C the fluorimetric measurement of the formed resorufin was performed with a Synergy HT reader (BioTek) (excitation wavelength at 530 nm, emission wavelength at 590 nm). The concentration–effect curves from three independent experiments were averaged. An average IC₅₀ value of $35 \pm 6 \mu\text{M}$ after 24 h of incubation ensured that a concentration of 5 μM oxaliplatin was adequate (sub-cytotoxic) for the following preparations (see Fig. S1 for the concentration–effect curves, ESI†).



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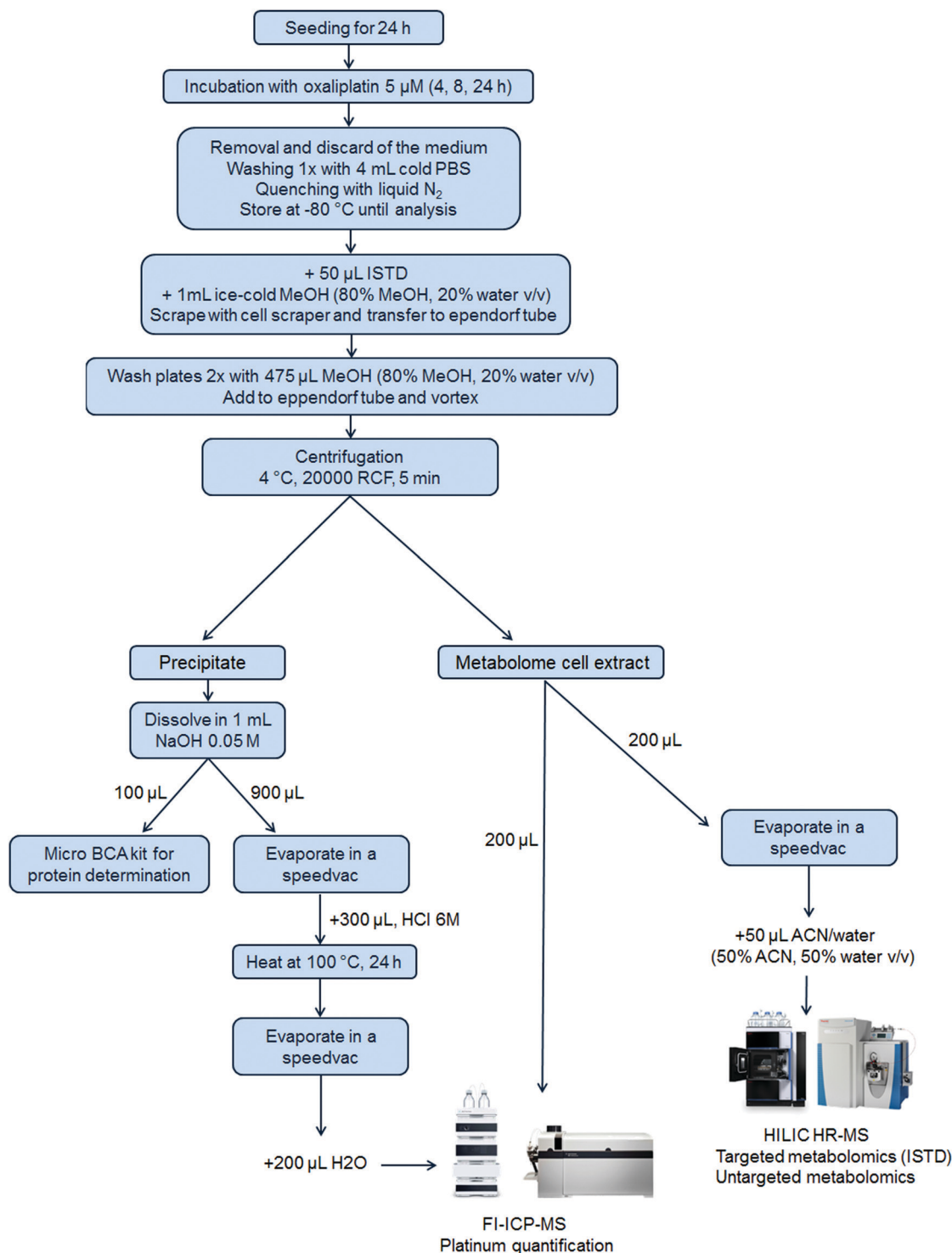


Fig. 1 A scheme of integrated metallomics/metabolomics – from sample preparation to analysis. The precipitate was employed for the protein determination and platinum quantification, the latter requiring protein hydrolysis before injection on the FI-ICP-MS system. In parallel to the analysis of the precipitate, two aliquots of the metabolome cell extract were analyzed: one was pre-concentrated by evaporation, re-suspended in ACN/water (1:1, v/v), and injected into the HILIC HR-MS system for metabolomic analysis whereas the other one was directly injected into the FI-ICP-MS system for platinum analysis.

experiment relates either relative or absolute concentration changes to cell number, protein amount or dry/wet weight.^{51,52} The same holds true for quantitative drug uptake studies. In platinum accumulation studies of adherent cell cultures, cells are

often trypsinized to consequently normalize the platinum content to total cell number. As trypsinization introduces significant alterations to the metabolome,^{31,42,53} protein content was used for normalization in this study. For this purpose, the protocol of a

ionization coverage, pH 4 was selected as an optimum separation condition. Detailed information on separated metabolites, retention times, ionization modes and separation of critical isomers is summarized in the ESI⁺ (Fig. S4, S5 and Tables S5–S7). Repeated injections of a quality control 10 μ M multi-metabolite standard over >25 hours revealed good technical repeatability (see Table S8, ESI⁺). Using the sub-2 μ m HILIC phase, most standard peaks revealed a full width at half maximum (FWHM) <10 s (see Table S9, ESI⁺). ¹³C enriched standards derived from the labeled yeast extract were added to the cancer cells during sample preparation with the aim of improving biological repeatability of sample preparation and subsequent HILIC analysis. This isotopically enriched biomass has been successfully used in numerous metabolomic studies addressing targeted absolute quantification^{35,43,46,47} and novel workflows merging targeted and untargeted analysis.^{25,55} It was shown that the addition of internal standard did not hamper the untargeted data evaluation, but enabled simultaneous absolute quantification of a targeted panel.²⁵ In this work, we implemented the internal standardization strategy for the first time with the aim of improving biological repeatability of relative quantification based on high-resolution mass spectrometry. Fig. 3a displays metabolites according to compound classes and numbers as found up-to-date in ¹³C-enriched *Pichia pastoris*.^{25,35,43,46,47,55} Fig. 3b shows the actual number of metabolites recovered in the cell extracts in targeted analysis using the here established protocols and available standards. Fig. 3c shows the number of metabolites recovered in yeast cell extracts

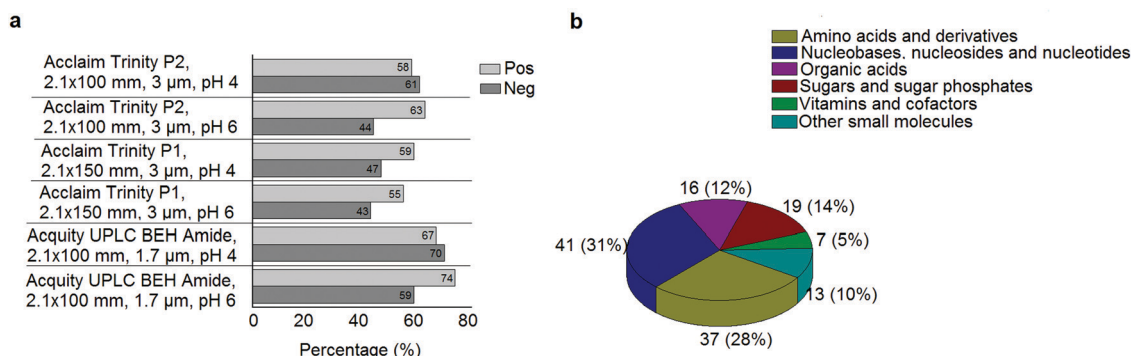


Fig. 2 (a) Percentage of metabolites found in a 10 μ M multicomponent standard with the different HILIC columns at pH 4 and pH 6 in positive and negative mode. When combining positive and negative mode, the UPLC BEH Amide column at pH 4 showed the highest coverage. (b) The number of metabolites and their classes (combining positive and negative mode) as found in a 10 μ M multicomponent standard of >130 metabolites with the UPLC BEH Amide column at pH 4.

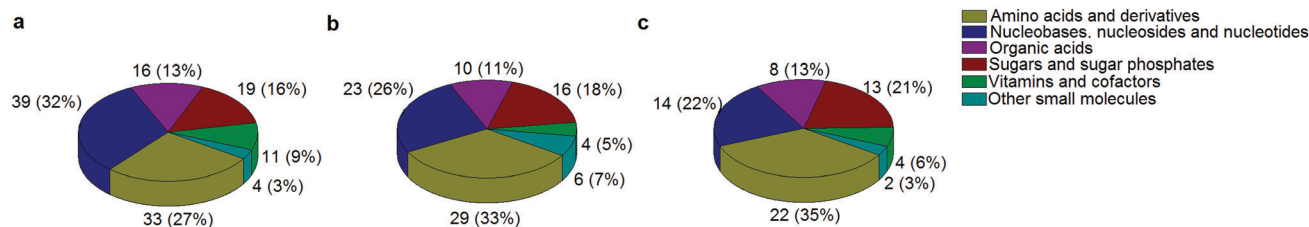


Fig. 3 The number of metabolites and their classes (combining a positive and negative mode) as found (a) up to date in ^{13}C -enriched *Pichia pastoris*,^{25,35,43,46,47,55} (b) in a sensitive control HCT116 cell extract measured with the UPLC BEH Amide column at pH 4 and (c) in ^{13}C -enriched *Pichia pastoris* added in sensitive control HCT116 prior to cell extraction and measured with the UPLC BEH Amide column at pH 4.

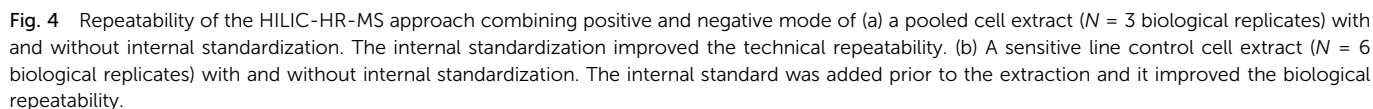


Fig. 5 shows the drug accumulation data obtained by ICP-MS based metallomics (LOD of $0.04 \mu\text{g L}^{-1}$ of Pt, 3σ criterion and RSDs of 1–24% and 16–45% for the precipitate and the metabolome cell extract respectively). While in the sensitive HCT116 cell line the precipitate concentration of platinum increased over time (to $\sim 10 \mu\text{g Pt per g protein}$), the metabolome cell extract remained rather constant ($\sim 15\text{--}18 \mu\text{g Pt per g protein}$). Within the first 4 h the platinum accumulation data were comparable for the sensitive and resistant cell models. Drug accumulation was reduced after 8 h of incubation, as previously shown.⁶² In contrast to the parental cell line, the resistant model showed constant low nucleus/protein concentration, while the metabolome cell extract was decreasing. Of note, to date there is no clear-cut uptake mechanism for oxaliplatin

established. Passive diffusion and transporter-mediated uptake mechanisms are discussed.^{63,64} The comparative drug accumulation data of Fig. 4, points towards predominant passive diffusion uptake for the first 4 hours. Differential active efflux transport mechanisms might be observed after 8 h of exposure between the parental and the resistant cell line. In fact, several studies linked overexpression of transporters to therapy outcome or resistance, however knowledge is still fragmentary.^{63,64} The influx transporters involve copper transporter (CTR) proteins and organic cation transporters (OCTs). The export of platinum drugs has been linked to efflux pumps such as ATP binding cassette (ABC) multidrug transporters, copper-transporting P-type adenosine triphosphatases (ATPases), and multidrug and toxin extrusion (MATE) proteins.⁶⁵

The metabolomics experiments revealed that the parental and resistant HCT-116 cell lines exhibited a distinctly different metabolotype from the start as evidenced by multivariate statistics (see heat-map and principal component analysis Fig. 6 and Fig. S6–S8, ESI†). Table 1 shows a list of significantly different metabolites after 24 hours of incubation. The list covers metabolites which were determined by targeted relative quantification (using ^{13}C internal standardization) together with metabolites discovered by untargeted data evaluation. Accordingly, their identity confirmation is based on the accurate mass, isotopologue pattern and spectral library match (MS2; mzCloud database), which is considered a level 2 structure confirmation.⁶⁶ Upon drug exposure, the sensitive cell models revealed a pronounced metabolic perturbation, while the resistant cells showed only subtle changes (see multivariate statistical evaluation Fig. S9–S12 (ESI†) and Table 1).

Scores Plot

PC1 (62.1 %)

PC2 (14.3 %)

Legend:

- Res_Ctrl (Red)
- Res_Ox (Green)
- Sens_Ctrl (Blue)
- Sens_Ox (Cyan)

and platinum chemosensitivity.²⁹ However, this study did not include oxaliplatin and is based on the correlation of untreated transcriptomics and the metabolomics data with the cell viability data. In contrast, our study includes simultaneous measurements of drug uptake and metabolomics. Parental HCT116 cells differ in glycolysis compared to the oxaliplatin resistant HCT116 cells. Pyruvate levels are higher in sensitive cells (Fig. S6, ESI[†]), and are strongly influenced upon drug incubation in this cell model (Fig. S9 and Table S10, ESI[†]). Additionally, the metabolotype of the oxaliplatin sensitive HCT116 compared to the resistant model revealed differences regarding the intermediates of the Krebs cycle (*i.e.*, fumarate, succinate and malate) confirming altered activity (Table 1 and Fig. S6, ESI[†]). All three metabolites are higher in sensitive cells compared to the resistant cells. Glutamate involved in glutaminolysis and purine synthesis *via* the folate cycle shows lower abundance in sensitive cells than resistant cells in the first 4 and 8 h. The low glutamate levels in sensitive cells are accompanied by low alpha-ketoglutarate (AKG) levels, the metabolite linking glutamate to the Krebs cycle. The biochemical basis for this increase of AKG in resistant cells might be explained by altered generation of carbon derived from amino acid catabolism and amino acid synthesis or by altered glutamine uptake from the media. Thus, our data suggest that the acquired resistance against oxaliplatin is accompanied by an overall altered energy metabolism. Moreover, the low glutamate level in sensitive cells is accompanied by the low cystathionine levels linked to glutathione biosynthesis (Fig. S6, ESI[†]). Glutathione decreases significantly during oxaliplatin incubation which can



Table 1 List of metabolites which showed significant differences ($p < 0.05$) in a HCT116 cell extract ($N = 6$ biological replicates) after incubation with oxaliplatin $5 \mu\text{M}$ for 24 h in targeted (internal standardization, Tukey's HSD test) and untargeted metabolomics (without internal standardization, MS2 library match, Benjamini–Hochberg correction). Column: UPLC BEH Amide pH 4 in positive and negative mode. The p value is the probability of obtaining an effect equal to or more extreme than the one observed considering the null hypothesis is true. The null hypothesis is said to be disproven if the effect observed is so important, and consequently the p value is so low, that either an exceptionally rare chance has occurred or the theory is not true.⁶⁷ On this table, the p value is expressed in logarithm base 10. The fold change (FC) value is the ratio between two quantities. On this table, FC is expressed in logarithm base 2

Compound	Polarity	Pathways	RT (min)	Resistant control vs. sensitive control		Sensitive control vs. resistant oxaliplatin		Resistant control vs. resistant oxaliplatin	
				–log 10 (p)	log 2 (FC)	–log 10 (p)	log 2 (FC)	–log 10 (p)	log 2 (FC)
				2.86	–0.38	3.26	0.44	—	—
Alanine ^d	Pos	Alanine, aspartate and glutamate metabolism Cysteine and methionine metabolism Taurine and hypotaurine metabolism Selenoamino acid metabolism	4.64	—	—	—	—	—	—
Alpha-ketoglutarate	Neg	Alanine, aspartate and glutamate metabolism TCA cycle D-Glutamine and D-glutamate metabolism Butanoate metabolism Histidine metabolism Lysine biosynthesis Ascorbate and aldarate metabolism Purine and pyrimidine metabolism	3.13	—	—	4.97	0.85	—	—
AMP ^a	Pos/Neg	Nitrogen metabolism Alanine, aspartate and glutamate metabolism Arginine and proline metabolism	5.62	—	—	3.66	1.34	—	—
Argininosuccinic acid	Pos	Alanine, aspartate and glutamate metabolism Alanine, aspartate and glutamate metabolism	6.83	6.12	–1.21	3.80	0.73	—	—
Asparagine	Neg	Nitrogen metabolism Alanine, aspartate and glutamate metabolism	5.47	4.16	–0.48	3.40	0.46	—	—
Aspartate	Neg	Alanine, aspartate and glutamate metabolism Glycine, serine and threonine metabolism Nitrogen metabolism Arginine and proline metabolism Cysteine and methionine metabolism Nicotinate and nicotinamide metabolism Histidine metabolism Lysine biosynthesis Pantothenate and CoA biosynthesis	5.99	4.53	–0.48	—	—	—	—
Carnitine	Pos	Beta-alanine metabolism Lysine degradation ABC transporters Fatty acid oxidation Glycine, serine and threonine metabolism Glycerophospholipid metabolism Nitrogen metabolism Cysteine and methionine metabolism Glycine, serine and threonine metabolism Phenylalanine, tyrosine and tryptophan biosynthesis Alanine, aspartate and glutamate metabolism TCA cycle	6.64	2.69	–0.29	2.96	0.35	—	—
Choline	Pos	—	2.01	3.58	–0.73	—	—	—	—
Cystathionine	Pos	—	6.64	6.81	0.73	—	—	—	—
Fructose-1,6-bisphosphate	Pos/Neg	—	7.35	—	—	3.15	1.31	2.78	1.11
Fumarate	Neg	—	3.15	6.56	–0.79	7.86	1.32	—	—
GDP	Pos	Arginine and proline metabolism Butanoate metabolism Nicotinate and nicotinamide metabolism Phenylalanine metabolism Tyrosine metabolism Purine and pyrimidine metabolism	7.62	—	—	2.31	0.45	—	—



Table 1 (continued)

Targeted										
Compound	Polarity	Pathways	RT (min)	Resistant control vs. sensitive control		Sensitive control vs. sensitive oxaliplatin		Resistant control vs. resistant oxaliplatin		
				−log 10 (p)	log 2 (FC)	−log 10 (p)	log 2 (FC)	−log 10 (p)	log 2 (FC)	
Glutamate	Pos/Neg	Arginine biosynthesis Alanine, aspartate and glutamate metabolism and proline metabolism Nitrogen metabolism D-Glutamine and D-glutamate metabolism Glutathione metabolism Histidine metabolism	5.55	—	—	4.82	0.53	—	—	
Glutamine	Pos/Neg	Arginine biosynthesis Alanine, aspartate and glutamate metabolism Purine metabolism Pyrimidine metabolism D-Glutamine and D-glutamate metabolism Nitrogen metabolism Arginine and proline metabolism Cysteine and methionine metabolism Glycolisis/gluconeogenesis Galactose metabolism Pentose and glucoronate interconversions	5.35 7.55 6.51	4.53	−0.53	3.03	0.42	—	—	
Glutathione oxidized Hexose phosphate ^a	Pos Pos/Neg			—	—	3.37 3.25	4.84 0.96	—	—	
Untargeted										
Compound	Polarity	Pathways	RT (min)	mZCloud results (match)	Resistant control vs. sensitive control		Sensitive control vs. sensitive oxaliplatin		Resistant control vs. resistant oxaliplatin	
					−log 10 (p)	log 2 (FC)	−log 10 (p)	log 2 (FC)	−log 10 (p)	log 2 (FC)
Arginine	Pos	Arginine and proline metabolism D-Arginine and D-ornithine metabolism	6.03	4 (81)	2.28	−0.53	—	—	—	—
Acetyl-carnitine	Pos	Fatty acid oxidation	2.47	4 (99)	5.01	−0.67	—	—	—	—
Acetyl-β-methylcholine	Pos	N/A	2.12	4 (92)	2.75	−0.32	—	—	—	—
N8-Acetylspermidine	Pos	N/A	5.16	3 (81)	—	—	6.09	−1.29	—	—
Acetylcholine	Pos	Glycerophospholipid metabolism	2.68	2 (98)	3.2	−0.48	—	—	—	—
Palmitoylcarnitine	Pos	Fatty acid oxidation Fatty acid metabolism	0.95	1 (96)	^b	−1.32	6.02	−1.11	—	—
4-Acetamidobutanoic acid	Pos	Arginine and proline metabolism	1.37	1 (99)	4.07	−0.78	—	—	—	—
Nicotinic acid adenine dinucleotide	Pos	Nicotinate and nicotinamide metabolism	7.03	1 (93)	3.71	0.52	4.74	0.75	—	—
Glutathione (reduced)	Neg	Cysteine and methionine metabolism Glutathione metabolism	5.97	3 (79)	2.57	0.44	2.62	0.49	—	—

^a The separation of the different isomers was not possible with this chromatographic method. If different peaks were partially separated, they were integrated as one single peak. ^b Only one biological replicate was detected in the resistant line.

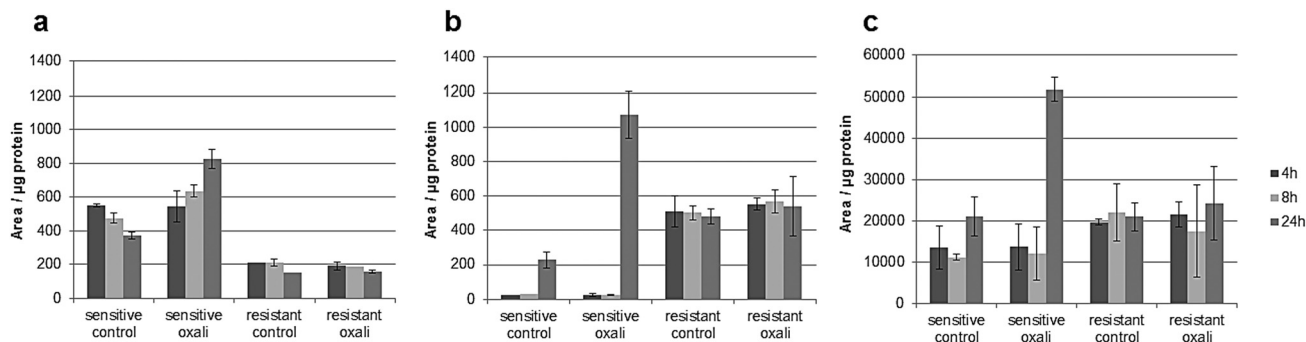


Fig. 7 Relative area normalized to the protein content upon incubation time with 5 μ M oxaliplatin in untargeted metabolomics in positive mode of (a) palmitoylcarnitine. Low values were observed for the resistant line whereas higher values were observed in the sensitive line which increased upon incubation time. (b) N1,N12-Diacetylspermine. No differences could be observed in the resistant line whereas high values were observed in the sensitive line upon incubation time. (c) N8-Acetylspermidine. No differences could be observed in the resistant line whereas high values were observed in the sensitive line upon incubation time. Column: UPLC BEH Amide at pH 4.

be inferred from the Pearson correlation data treatment addressing the differential impact of exposure time (see Tables S10–S13, ESI†) on metabolites and pathways. This same fact can be observed in Table 1 and Fig. S9 (ESI†). The involvement of glutathione in platinum drug efflux and its association to drug resistance has been discussed controversially in the past.⁷⁰ Whereas Mohn *et al.*⁷¹ did not observe any glutathione alteration upon oxaliplatin incubation in *in vitro* studies of the colorectal cancer line HCT-8, others have shown variations.¹⁷ Finally, Fig. 7 gives the comparative metabolomic data on palmitoyl-carnitine, N1,N12-diacetylspermine and N8-acetylspermidine discovered by non-targeted analysis (level 1 and 2 identification, based on spectral library match). The long chain acyl-carnitine is a key metabolite of fatty acid catabolism, more specifically of fatty acid oxidation.⁷² This pathway is an essential source of NADH, FADH₂, NADPH and ATP. Fatty acids are conjugated with carnitine for translocation into the mitochondria. Palmitoyl-carnitine has been reported to change the activity of several enzymes and transporters localized in the mitochondrial membrane and has been shown to stimulate caspase activity.^{73,74} Resistant cells showed consistently lower levels of palmitoyl-carnitine over 24 hours of incubation time, which were not affected by the drug uptake. In contrast, in sensitive cells, the levels decreased with time in the control samples while drug uptake resulted in the opposite trend (Fig. 7). There is growing interest in the role of fatty acid metabolism in cancer progression and metastasis,⁷⁵ but little is known about its role in platinum drug efficacy and resistance. Increased levels of fatty acid oxidation have been linked to apoptosis.⁷⁶ Already a decade ago, Riedel *et al.*⁷⁷ observed that fatty acid metabolism played a role in cisplatin-resistance. More recently, a positive correlation between fatty acid oxidation and malignant phenotypes including metastasis, therapeutic resistance to cisplatin and relapse was found.⁷⁸ Our data (see also Table 1) indicate that in the case of oxaliplatin not only the energy metabolism but also the fatty acid metabolism might be decisive for drug sensitivity. Hence, future studies should address the enzymes of the related pathways as potential drug targets reversing resistance. As shown by the metallomics approach, resistance was accompanied by differential drug uptake, which

could be explained by differential transport. Related to fatty acid metabolism (see Table 1), interestingly, it has been shown that the organic cation/carnitine transporter (OCTN1) plays a role in oxaliplatin accumulation, which is in agreement with the differential platinum uptake found in sensitive *versus* resistant cells. It was found that (OCTN1)-mediated uptake of oxaliplatin might contribute to its neuronal accumulation and treatment-limiting neurotoxicity.^{63,64} N8-Acetylspermidine and N1,N12-diacetylspermine are metabolites of polyamine catabolism. Interestingly, polyamine metabolites were discussed as potential biomarkers for colon cancer and oxidative damage (as ROS is produced by polyamine catabolism). Recently, it has become increasingly clear that polyamine catabolism can play a dominant role in drug response, apoptosis and response to stressful stimuli.⁷⁹ In the case of platinum drugs, polyamine catabolism was associated with renal toxicity.

Conclusion

In this preclinical study, colon cancer resistance towards oxaliplatin was studied for the first time by an integrated metallomics/metabolomics approach. Previous studies have mainly focused on cisplatin and little is known about oxaliplatin in the context of the metabolome. Our study compared treated and untreated samples of colon cancer cells allowing not only a static comparison of the altered metabolism in resistant *versus* sensitive cells, but also whether the treatment induces (or not) diverse metabolic perturbations in the different cells. We found that the oxaliplatin sensitive HCT116 cell line displayed a metabolic phenotype which differed most significantly in hallmarks of energy metabolism, sulfur metabolism, fatty acid metabolism and polyamine metabolites. From metallomics data, it could be inferred that the resistance in the HCT116 model was accompanied by a different drug transport mechanism. It could be speculated that the sensitive cells were less protected against oxaliplatin, since glutathione levels and other intermediates of the sulfur metabolism were lower than in the resistant cells. Furthermore, polyamine catabolism was significantly dysregulated upon



exposure to oxaliplatin which is known to increase the ROS burden to the cell.

In summary, the introduced methods revealed novel insights and provided valid tools for generating new hypotheses regarding resistance towards oxaliplatin. *E.g.*, future studies will investigate whether inhibition of fatty acid oxidation has an effect on drug sensitivity and resistance and could potentially serve for reversing platinum resistance.

Conflicts of interest

There are no conflicts to declare.

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