

Metabolomic profiles delineate potential roles for gadolinium chloride in the proliferation or inhibition of Hela cells

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Abstract Lanthanides (Lns) compounds have been reported to possess contrary effects on cell activity, i.e., promoting cell cycle progression and cell growth by lower concentration treatment, but suppressing cell proliferation and inducing cell apoptosis at higher dosing. However, the cellular processes during the intervention and the possible underlying mechanisms are still not well clarified. Using a combination of high-throughput liquid chromatography (LC) with mass spectrometry (MS), we have investigated the metabolomic profiles of Hela cells following gadolinium chloride (GdCl_3) treatment in time- and concentration- dependent manners. A total of 48 metabolites released by Hela cells are identified to be differentially expressed ($P < 0.05$) in different states. Metabolic pathways analyses reveal that the differential metabolites are mainly characterized by increased lipid and amino acid metabolisms and by

decreased lipid, amino acid, and carbohydrate metabolisms for cells treated with GdCl_3 at lower and higher concentrations, respectively. Notably, in the higher level GdCl_3 case, the down-expressions of metabolites are predominantly in the glycolytic and the redox pathways. The above results, obtained by using a metabolomic strategy for the first time, disclose that different cell signaling pathways are activated by GdCl_3 treatment with different concentrations, leading to inhibitory or promotional effect on Hela cells.

Keywords Gadolinium chloride · Hela cells · Metabolomic profiling · Liquid chromatography-mass spectrometry · Cell growth

Introduction

Lns (rare earth metals) have a variety of physical or chemical properties, and have been widely investigated and applied in agriculture and medicine since twenty century (Ni 2002; Fricker 2006). As a member of Lns family, gadolinium (Gd) shows particularly multi-biological effects on organisms and attracts more and more interests of biochemists and clinicians. For example, clinically, chelates of gadolinium such as gadolinium diethylenetriamine pentaacetic acid (Gd-DTPA) are used as contrast agents in magnetic resonance imaging (MRI) (Shellock and

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Spinazzi 2008; Li et al. 2008). In medicine, gadolinium texaphyrin complex (MGd) is currently subjected to phase III clinical trials for the treatment of brain metastases of nonsmall cell lung cancer (Fricker 2006). Moreover, a wide variety of physiological changes brought about by gadolinium salts are reported. Gadolinium salts are known to inhibit the function of the mononuclear phagocytic system, and have an anticoagulant effect by inhibiting clotting reactions that require calcium (Lee et al. 2004; Liao et al. 2009). The effects of gadolinium salts on the proliferation and apoptosis of some normal and cancer cells have also been studied extensively (Sato et al. 1998; Liu et al. 2006; Fu et al. 2009; Zhang et al. 2009), and these effects related to cell proliferation and apoptosis depend on the concentrations or the types of cells being studied. This suggests that Gd-based treatments have potentials in medical applications in effective therapy of some diseases like cardiac disorders and cancers, and growing interest in the study on the mechanisms of Gd-induced biological effect on cell growth has been aroused. Up to date, the possible molecules and cellular pathways responsible for the promotion and apoptosis of cells induced by Gd-based treatments have been investigated, and the roles of some proteins and cellular processes have been revealed. But the underlying mechanisms are still far from being well elucidated as many more molecules and different cellular pathways are likely involved.

Metabolomics is a “omics” strategy that allows the simultaneous assessment of substrate fluxes within and among different pathways of metabolites under various physiological conditions (Weckwerth 2003; Robertson et al. 2007; Saito and Matsuda 2010). As well known, metabolomic analysis, in contrast to genomics and proteomics that examine the global genes and proteins expression, represents the unbiased distal read-out of the cellular states enabling the generation of meaningful conclusion from the integrative effect of gene expression and protein function. Multiple technologies have been currently used to profile metabolites of the samples in metabolomic researches, including high pressure liquid chromatography (HPLC), nuclear magnetic resonance (NMR) and mass spectrometry (CE/MS, GC/MS, and LC/MS) (Lenz and Wilson 2007; Issaq et al. 2009). Mass spectrometry-based profile, being high

throughput, robust, and sensitive, could allow for simultaneous identification of known metabolites as well as characterization of unknown compounds (Bedair and Sumner 2008; Griffiths and Wang 2009). This would meet the challenge for relative insensitivity or for examination of a limited number of metabolites existed for other methods, and has become increasingly popular for metabolomic profiling survey.

In the present study, we have studied the profile change in metabolites released by Hela cells following the treatment with various concentrations of GdCl_3 using a high-throughput metabolomic strategy coupling LC to both linear ion trap LTQ Orbitrap and IT TOF MS. This method with enhanced mass resolution, mass accuracy, and detection sensitivity, would allow to investigate the role of metabolites and relevant metabolic processes in different states. Previous study has demonstrated that GdCl_3 could inhibit or promote proliferation of several types of cancer cells lines including Hela cells, depending on the concentrations applied (Liu et al. 2006; Zhang et al. 2009). However, the underlying mechanism involved is poorly understood. Additionally, HeLa cell line was found to be more sensitive to Lns than some other cancer cell lines (Shen et al. 2009a). Understanding of Gd-induced cell growth promotion or inhibition would be valuable for development of Lns-based drugs for therapeutic intervention as well as avoiding negative effects. We profiled total 48 metabolites with significant alterations during the cellular responses to the treatment. In combination with multivariate data analysis, we revealed that GdCl_3 -promoted cell proliferation and progression were characterized by elevated lipid and amino acid metabolisms, indicating an increased utilization of these metabolic intermediates for biosynthetic or energetic purposes. With regard to cells undergone the growth inhibition, down-regulations of lipid, amino acid, and carbohydrate metabolisms, especially down-regulations of metabolites related to the glycolytic and redox pathways were observed. Herein, the study demonstrates that metabolomic information could provide a detailed view of the molecular profiling, and the networks analysis showed that different cell signaling pathways could be triggered by GdCl_3 treatment.

Materials and methods

Materials

RPMI 1640 medium was purchased from Gibco (Grand Island, NY, USA). Fetal bovine serum (FBS) was obtained from Hyclone (Logan, UT, USA). Trypsin, trypan blue, standard chemical compounds including haloperidol, diclofenac, verapamil hydrochloride, reserpine, and 3-(4,5-Dimethylthiazoyl-2-yl)-2,5-diphenyltetrazolium bromide (MTT) were from Sigma–Aldrich (St. Louis, MO, USA). Methanol (CH₃OH), chloroform (CHCl₃), formic acid (FA), acetonitrile (ACN), and ammonium hydroxide (LC grade) were from Fluka (Buchs & Steinheim, Germany). Penicillin and streptomycin were from Merck (Whitehouse Station, NJ, USA). Other analytical grade chemicals used were from domestic sources. All buffers are prepared with Milli-Q deionized water. GdCl₃ solution was prepared by dissolving gadolinium oxide in HCl, evaporating the solution to remove acid, and diluting to different concentrations (0.00075, 0.001, 0.005, 0.01, 0.05, 0.1, 0.5, 1, 1.5, and 2 mM, respectively) to be used in the experiments. Hela, a human cervical carcinoma cell line, was obtained from Shanghai Institute of Biochemistry and Cell Biology, Chinese Academy of Sciences (China).

Cell culture

Hela cells was cultured as previously described (Su et al. 2009). Cells were seeded onto 96-well plates (100 mm²) at a density of 1×10^6 cells/dish and then incubated for 24 h. GdCl₃ treatment was performed by incubating the cells in RPMI 1640 containing 0.5% FBS for 24 and 48 h, respectively, with various concentrations of GdCl₃ as stated above. Cell viability was determined using the MTT assay, and trypan blue exclusion. In separate experiments for metabolomic profiling analysis, cells were cultured in the flasks (75 cm²) with GdCl₃ at final concentrations of 0.00075, 0.1, and 2 mM, respectively. Culture media were collected at 24 h after exposure to GdCl₃ and extracted using Bligh–Dyer technique as described (Miccheli et al. 1988) and modified by us. Briefly, 1 ml of medium was mixed with 3 ml of cold CH₃OH:CHCl₃ (2:1), vortexed for 10 min on ice, followed by centrifugation (Eppendorf, AG, Germany)

at 1,4000×g for 15 min at 4°C. The residue was re-extracted with 2 ml of mixed CH₃OH:CHCl₃:H₂O (2:1:1) treated as mentioned above to remove any precipitated proteins. The combined upper (aqueous) phase was evaporated in a SPD1010 speed-vac concentrator (Thermo-Fisher, Milford, MA, USA), re-suspended in 150 µl of water, and then ultrafiltered through a 1,000 Da cut-off filter membrane on a centrifugal filter device (Millipore, Billerica, MA, USA). The extract was lyophilized and reconstructed with mobile phase. All samples were stored at –80°C until use.

MTT assay

The MTT assay was used to evaluate the effect of tested concentrations of GdCl₃ on cell growth, as described previously (Situ and Wu 1996). Briefly, 100 µl of a 5 mg/ml MTT stock solution was added to each well of 96-well plate at the end of the treatment time, incubated for 4 h at 37°C. The insoluble formazan product was dissolved in 100 µl of DMSO and the incubation continued for another 30 min at 37°C. Cell growth was assayed by measuring the absorbance of each well at 490 nm using a microplate reader (Tecan, Sunrise, Switzerland) following the equation: Cell growth (%) = (A₄₉₀ (sample) × 100%/A₄₉₀ (control) × 100%. Results were expressed as the percentage of the control for cell growth evaluation, with experiments being carried out in triplicate. Cell proliferation as assessed by MTT assay was directly compared to the results from trypan blue exclusion assay, in which cells were counted in triplicate under the optical microscope. All results were presented as the mean ± the standard deviation (SD) for independent experiments, and statistical significance between groups was based on two sided paired Student's *t* test. *P* < 0.05 was considered as statistically significant.

Liquid chromatography/Mass spectroscopy

Extracts of the metabolites were separated by Liquid chromatography (LC) before Mass spectroscopy (MS) analysis to reduce the sample complexity and thereby enhance the detection sensitivity. To obtain higher separation performance, reversed-phase liquid chromatography (RPLC) and hydrophilic interaction chromatography (HILIC LC) online coupled to MS

detection were utilized to cover a larger part of the metabolome. For RPLC separation, a 300 μm inner diameter C_{18} precolumn (LC Packings, San Francisco, CA) was used, where the pre-concentrated and clean-up sample was washed and eluted into a connected *nano*-column (100 mm \times 75 μm ID, New Objective Inc., Woburn, MA) filled with 3 μm C_{18} stationary phase. Equal injection volume (50 μl) for the extracts was used and flow rate was 300 nl/min. The gradients for mobile phase (A: 5% ACN/0.1% FA, and B: 100% ACN/0.1% FA) were 5 min at 100% A, 15 min at 5–45% A, and 35 min at 45–95% A, followed by 100% A for another 5 min. For HILIC LC analysis, capillary column XB-NH₂-150 \times 2.1 mm with 3 μm particle size (Welch Materials Inc., USA) was used. The gradient and recondition back to the starting condition were done as described above, but mobile solvents were added by 10 mM ammonium acetate (pH 9.1, adjusted with NH₄OH).

Both the IT-TOF (Shimadzu Biotech., Kyoto, Japan) and LTQ-Obitrap (Thermo Electron Corp., USA) MS were applied for monitoring metabolomic patterns. The eluents for LC experiments were electrosprayed into a mass spectrometer for MS analysis and the scan was set for acquisition of both positive and negative ions. Standardizations containing five internal standards in injection solvent were used to assure both chromatographic consistency and internal mass calibrations. Full scan mass spectra were acquired from 50 to 1,000 Da in mass acquisition, followed by MS/MS derived from collision-induced dissociation (CID). For ensuring the reproducibility, three replicate LC–MS measurements were run for each sample, and then the results were exported for further process.

Data processing and metabolomic analysis

Mass spectra data was processed with Xcalibur version 3.2 (Thermo Electron Corp.) and LCMS Solution version 3.10 (Shimadzu Corp.) softwares. Chromatograms were deconvoluted and monoisotopic ion peaks were extracted. XCMS software available from (<http://masspec.scripps.edu/xcms/documentation.php>) was used to perform background suppression, baseline correction, and data smoothing using default setting. The peaks were aligned and integrated between chromatograms for

each ion detected. For metabolites assignment, the Human Metabolome Database (HMDB) (<http://www.hmdb.ca/>), METLIN metabolite database (<http://metlin.scripps.edu/>), and Kyoto Encyclopedia of Genes and Genomes (KEGG) ligand database (<http://www.genome.jp/kegg/ligand/>) were used to determine potentially matching human metabolites consistent with measured accurate masses, elemental compositions, and MS/MS product ions.

To assess the association of significant change in metabolites levels, one-way analysis of variance (ANOVA) and two-tailed *t* test was performed to test for differences in two-sample comparisons or between groups. All mass peak heights were normalized to the peak heights of internal standards (first by summing the total ion current to 10,000) for samples, which is necessary to overcome errors due to the sample loading and the instrument response variation. Measures were run per metabolite on those groups that had detectable expression in at least 20% of the samples. Variations in expression were calculated between data sets (with significance $P < 0.05$ for matched value). The data averaged over the replicate measurements in each sample group was used.

Clustering of class-specific metabolomic patterns was performed using cluster (Eisen et al. 1998) and visualized as heat maps using tree view (Saldanha 2004). Unsupervised hierarchical clustering of samples was accomplished with the use of the log₂ transformed and normalized data. Pearson's correlation was used for the similarity metric. In hierarchical clustering, the data were expressed as two-dimensional heat maps of metabolomic signatures using Java TreeView software.

The metabolites that were differentially expressed were mapped to the KEGG biochemical pathways. Mapping of the metabolites to the metabolic pathways used the compound IDs against the IDs as specified in KEGG, followed by search of the relevant pathways and the anabolic and catabolic enzymes for metabolites with variable expressions.

Results

Effect of GdCl₃ on Hela cell growth

The effects of GdCl₃ on the growth of Hela cells were evaluated by MTT assay, and the results showed that

the status of cell proliferation exhibited a clearly different pattern after incubating in different concentrations of GdCl_3 for the different time points. As seen in Fig. 1, the increase in cell growth was observed at lower concentrations of GdCl_3 (≤ 0.5 mM) while the decrease in the growth was found at higher concentrations (≥ 1 mM) after both 24 and 48 h as compared to the control. The highest percentage for cell proliferation-promoting was $22.4 \pm 1.27\%$ at the concentration of 0.01 mM while the highest percentage for growth suppression was $26.4 \pm 1.03\%$ at the concentration of 2 mM for 24 h treatment. In addition, effect of GdCl_3 on cell growth was observed after 48 h of culture. The inhibitory effect was observed at concentrations larger than 1 mM, and the maximum value achieved $64.0 \pm 2.68\%$ of the control on incubation with higher concentration of 2 mM, which was over twofold than that of 24 h treatment at the same concentration. In contrast, the promotional effect was still observed for 48 h with concentrations less than

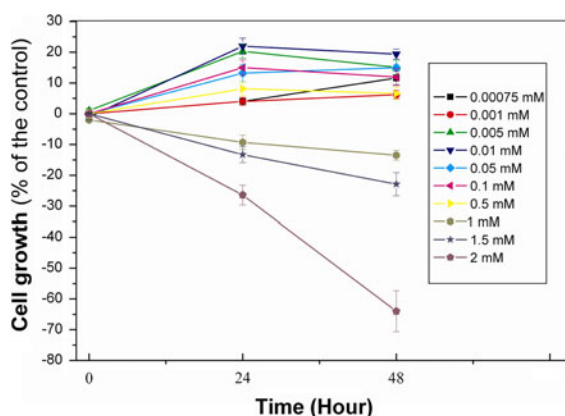


Fig. 1 Effect of GdCl_3 on cell growth as determined by MTT assay. HeLa cells were treated with various concentrations of GdCl_3 as indicated in “Materials and methods” for 24 and 48 h, respectively, and cells exposed to 0.5% FBS medium only at various time points were used as the controls. The results demonstrated that low concentration of GdCl_3 stimulated the cell growth, while relative high concentration of GdCl_3 inhibited the growth. Additionally, on incubation with GdCl_3 for 48 h, low concentration of GdCl_3 (0.00075–0.5 mM) did not markedly increased the cell growth compared to that for 24 h treatment, but high concentration of GdCl_3 (concentrations ≥ 1 mM) significantly decreased cell growth. Data were mean \pm standard deviations of triplicate independent determinations. Cell growth was expressed as the percentage of the control

0.5 mM, but the increase in cell growth was not obvious compared to the 24 h treatment.

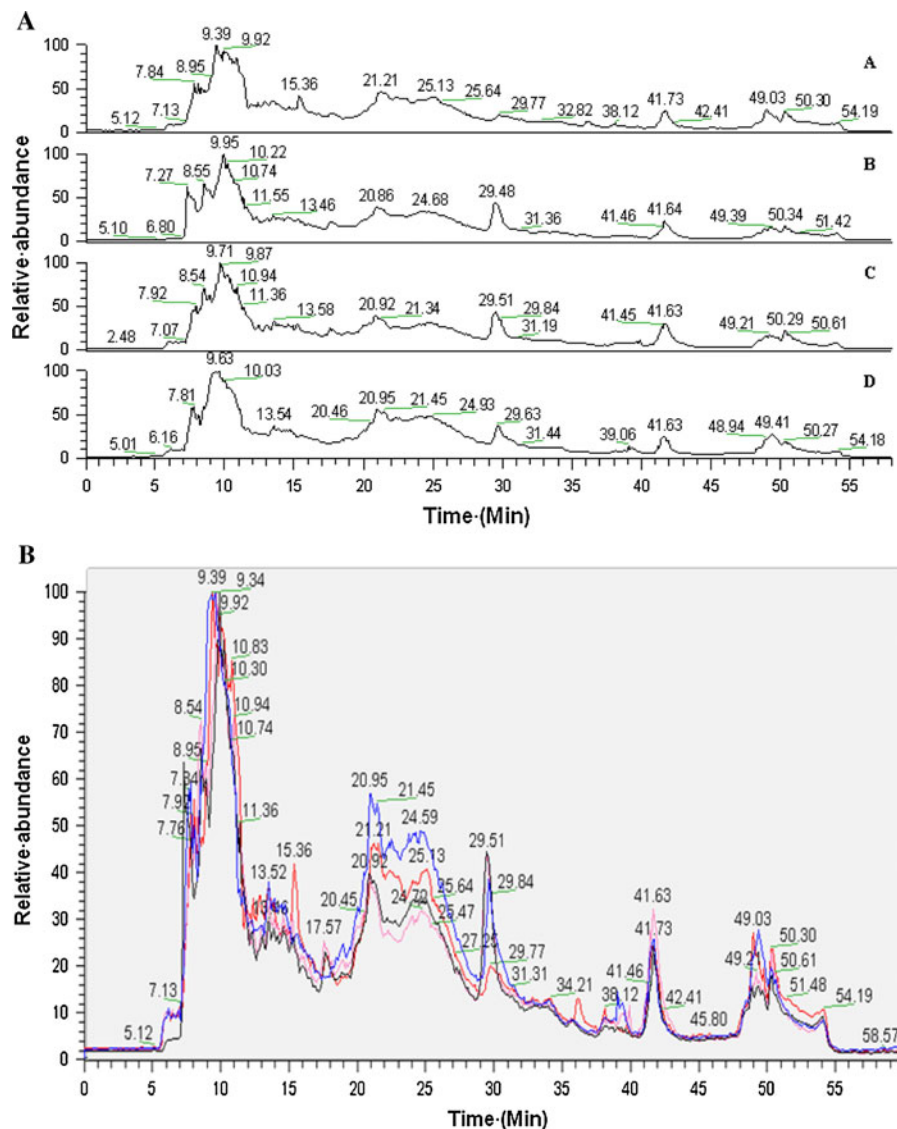
The above results were in good agreement with those obtained by parallel cell counting assay using Trypan Blue exclusion. Morphological feature under phase-inversed microscope also showed the cell growth significantly differed under different GdCl_3 treatments. Thus, it can be seen that GdCl_3 treatment had either inhibitory or promotional effects on the growth of HeLa cells, in concentration- and time-dependent manners.

Extracellular metabolites following GdCl_3 treatment

Both lipophilic and hydrophilic LC were utilized for *online* up-front separation to acquire a more comprehensive metabolomic profiling. Figure 2a showed a representative total ion chromatogram (TIC) spectra of *nano*-LC-LTQ Orbitrap for the samples after exposure to GdCl_3 , and an overlaid pattern of the spectra was shown in Fig. 2b. The results exhibited a significant change in metabolic expression profiles following exposure for 24 h at different concentrations. To reduce between-sample variation and to ensure the reproducibility, three replicate analyses (including biological and technique replicate for each sample) were run. Comparisons across the three measurements (Fig. 3) were evaluated and average correlation coefficients R^2 between two consecutive LC-MS experiments under the identical conditions was greater than 0.95, indicating the reproducibility and reliability of the sample runs in independent replicates.

Metabolite assignments were obtained with accurate mass, elemental composition (mass accuracy <10 ppm), and MS-MS fragmentation against the databases. To obtain altered individual “features” observed in various response states, the variables of peak heights were compared (calculated from replicates measures) from the samples with or without GdCl_3 treatment. Combined with Multivariate Data Analysis, total 48 metabolites (with $P < 0.05$) were differentially expressed (up or down-regulated, at least twofold variable compared to the control). Listed in Table 1 was the differentially expressed metabolites. Figure 4 displayed an example of extracted ion chromatogram (EIC) of the metabolic intermediate Lysophospholipid following the treatment with

Fig. 2 Representative TIC metabolomic pattern of cells different states using *nano*-LC/LTQ-Obitrapp MS. Figure 3a, a–d represented profiles of control, 0.00075 mM, 0.1 mM, and 2 mM of GdCl_3 respectively, for 24 h treatment. Three replicate analyses were run for each sample. Figure 3b, overlaid pattern of TIC from Fig. 3a, comparison between the samples showed that overall changes in profile were observed following exposure to various concentrations of GdCl_3



various GdCl_3 concentrations. The up-expressions of the metabolite were observed after treatment with lower GdCl_3 concentrations (≤ 0.1 mM). These metabolites, as listed Table 1, were further mapped to their respective pathways in KEGG, and a detailed information on the metabolite characteristics (such as functional roles, and cellular localization etc.) was contained in Table 2. Hierarchical clustering was used to visualize the relationship of detected changes for metabolites within and between the groups under higher or lower GdCl_3 concentrations (Fig. 5). From the overview of identifications of up- or down-regulated metabolites and pathways as specified by KEGG, the differentially expressed metabolites could be

grouped into several functional categories, such as lipid metabolism, carbohydrate metabolism, redox homeostasis, and amino acid metabolism etc. The metabolites differentially expressed might represent key regulators for influencing the growth, survival, or progression of Hela cells induced by GdCl_3 .

Discussion

Global metabolomics as a part of systems biology could allow simultaneous detection of large number of metabolites, and be a useful complement to other “omics” such as transcriptomics or proteomics for

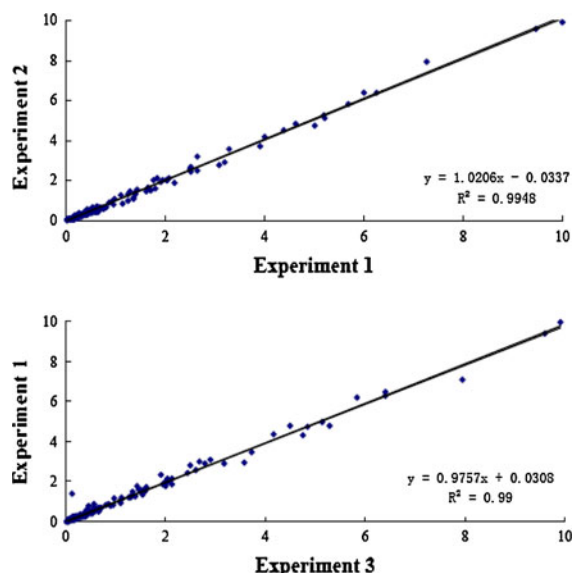


Fig. 3 Reproducibility analysis between consecutive LC-MS runs. Three replicate LC-MS analyses were run for each sample. Each spot represents a pairwise of metabolite with its relative percentage in the sample from the first and second analysis shown on the *x*-axis and the *y*-axis, respectively

characterization of molecules and relevant pathways at given stages for cells, tissues, and organisms. In this work, we utilized the high-throughput LC/MS strategy to investigate the cells extracellular metabolites following GdCl_3 incubation at either relatively lower or higher concentrations. The overall changes were observed and a total of 48 metabolites were identified as being changed. These perturbed metabolites, as analyzed by KEGG, could be grouped into several functional categories and involved in different signaling pathways. The involvement of the metabolites implicated the important roles they would play in GdCl_3 -induced cell growth promotion and inhibition.

A number of lipid-related metabolites were found to be differentially expressed, which were characterized by their generally higher expressions when being treated at lower concentrations while lower expressions at higher concentration of GdCl_3 . There were some of the metabolites for fatty acid metabolism and energy source, such as lauroyl-CoA, lysoPE, malonyl-carnitine, and phosphatidylinositol (PI) etc., that were highly expressed for the faster-growing cells. Some of these are involved in such as fatty acid elongation and transport, and some are phospholipids associated with energy production and cell signaling. For example,

lauroyl-CoA and malonyl-carnitine are related to the fatty acid elongation, transport, or energy demand (Ushikubo et al. 1996). Phosphatidylinositol is also involved in energy production and is important for signal transduction (Gardocki et al. 2005; Skwarek and Boulianne 2009). These metabolites were up-regulated at lower concentration GdCl_3 treatment, suggesting that lipid metabolism for biosynthesis or energetic purpose is active for proliferating cells. Whereas some of the metabolites related to lipid metabolism were down-regulated at higher concentration treatment, suggesting a lower activity for lipid metabolic pathway in viability inhibited cells. Cells under proliferative condition utilize more active substrates to participate physiological processes and to satisfy energy demands than cells under inhibited condition. The enrichments of the intermediates might reflect rapid lipid metabolism turnover for dividing cells, through the use of the metabolites as precursor for synthesis of nucleic acids, proteins, and lipids required for cell proliferation. The variable expression of the lipid-related metabolites demonstrated that GdCl_3 could exert different effects on the cells at various concentrations.

Changes in relation to carbohydrate and sugar utilization pathway were observed following incubation of GdCl_3 at either lower or higher concentrations. Observably, some of the metabolites related to carbohydrate metabolism were down-expressed after higher concentration GdCl_3 treatment. Moreover, a majority of the metabolites belonging to glycolysis for carbohydrate metabolism and ATP synthesis, such as trehalose 6-phosphate, 2-phosphoglyceric acid, and dihydroxyacetone phosphate (DHAP) etc., was detected down-regulated following higher concentration incubation, suggesting a regulatory role of GdCl_3 in the metabolic pathway. 2-phosphoglyceric acid, for example, can serve as the substrate in glycolysis through catalyzing the intermediate into phosphoenolpyruvate (PEP) by enolase, which could convert glucose to pyruvate. DHAP, produced from the dehydrogenation of L-glycerol-3-phosphate catalyzed by glycerol 3-phosphate dehydrogenase (GAPDH), is part of the entry of glycerol into the anaerobic glycolytic pathway (Romano and Conway 1996). The observed lower expressions of the metabolites involved in the glycolytic pathway suggested that GdCl_3 functions in controlling cell growth by regulating the expressions of these metabolites. It has been proven that in tumor cells there are some protein

Table 1 Differentially expressed metabolites following GdCl₃ treatment for 24 h in concentration-depended manner

Metabolite ID ^a	Molecule formula	GdCl ₃ concentration ^c (mM)		
		0.00075	0.10	2.0
Lipids metabolism ^b				
Lauroyl-CoA	C ₃₃ H ₅₈ N ₇ O ₁₇ P ₃ S	+	+	–
Malonylcarnitine	C ₁₀ H ₁₇ NO ₆	+		–
LysoPE	C ₂₉ H ₆₀ NO ₇ P	+	+	
PI ^c	C ₄₁ H ₇₅ O ₁₃ P	+	+	
12a-Hydroxy-3-oxocholadienic acid	C ₂₄ H ₃₄ O ₄		+	
5b-Cholestane-3a,7a,12a,23S,25-pentol	C ₂₇ H ₄₇ O ₅	+		
12-Ketodeoxycholic acid	C ₂₄ H ₃₈ O ₄	–		–
Carbohydrates metabolism				
Trehalose 6-phosphate	C ₁₂ H ₂₃ O ₁₄ P			–
2-Phosphoglyceric acid	C ₃ H ₇ O ₇ P	–		–
DHAP(10:0)	C ₁₃ H ₂₅ O ₇ P			–
N-Acetyl-b-glucosaminyamine	C ₈ H ₁₆ N ₂ O ₅			–
N-Acetylneuraminic acid	C ₁₁ H ₁₉ NO ₉			+
Cotinineglucuronide	C ₁₆ H ₂₀ N ₂ O ₇	–		–
5-Methylthioribose 1-phosphate	C ₆ H ₁₃ O ₇ PS			
2-(acetylamino)-1,5-anhydro-2-deoxy-3-O-b-D-galactopyranosyl-D-arabino-Hex-1-enitol	C ₁₄ H ₂₃ NO ₁₀			–
1-Phosphatidyl-D-myo-inositol	C ₁₁ H ₁₉ O ₁₃ P			–
Peptides and amino Acids metabolism				
L-beta-aspartyl-L-alanine	C ₇ H ₁₂ N ₂ O ₅	+		
L-alpha-glutamyl-L-hydroxyproline	C ₁₀ H ₁₆ N ₂ O ₆	–	–	–
Aminomalonic acid	C ₃ H ₅ NO ₄			
Ornithine	C ₅ H ₁₂ N ₂ O ₂	+		–
Citrulline	C ₆ H ₁₃ N ₃ O ₃			
Spermidine	C ₇ H ₁₉ N ₃	+		
L-Arginine ^c	C ₆ H ₁₄ N ₄ O ₂	+		–
Dimethyl-L-arginine	C ₈ H ₁₈ N ₄ O ₂			–
Hydroxyproline	C ₅ H ₉ NO ₃			+
2-Oxo-4-methylthiobutanoic acid	C ₅ H ₈ O ₃ S			–
L-Cystine	C ₆ H ₁₂ N ₂ O ₄ S ₂			–
Ophthalmic acid	C ₁₁ H ₁₉ N ₃ O ₆			–
Glutamylphenylalanine	C ₁₄ H ₁₈ N ₂ O ₅			–
L-Isoleucine	C ₆ H ₁₃ NO ₂			
Succinylacetone	C ₇ H ₁₀ O ₄			
Nucleic acids metabolism				
Deoxycytidine	C ₉ H ₁₃ N ₃ O ₄			–
Phosphoribosyl formamidocarboxamide	C ₁₀ H ₁₅ N ₄ O ₉ P	–		
SAICAR	C ₁₃ H ₁₉ N ₄ O ₁₂ P	+		
Xanthylic acid	C ₁₀ H ₁₃ N ₄ O ₉ P	+		
6-Methyladenine	C ₆ H ₇ N ₅	+		–
1,7-Dimethylguanosine	C ₁₂ H ₁₇ N ₅ O ₅			–

Table 1 continued

Metabolite ID ^a	Molecule formula	GdCl ₃ concentration ^c (mM)		
		0.00075	0.10	2.0
Vitamins and hormones				
Niacinamide	C ₆ H ₆ N ₂ O	–		
<i>N</i> -Methylnicotinamide	C ₇ H ₈ N ₂ O			–
Thiamine	C ₁₂ H ₁₇ N ₄ OS			–
7-Hydroxy-6-methyl-8-ribityl lumazine	C ₁₂ H ₁₆ N ₄ O ₇			–
3-Chlorotyrosine	C ₉ H ₁₀ ClNO ₃			–
8-iso-15-keto-PGE2	C ₂₀ H ₃₀ O ₅	–		
Others				
Uroporphyrinogen III ^c	C ₄₀ H ₄₄ N ₄ O ₁₆	–	–	–
Coproporphyrin III ^c	C ₃₆ H ₃₈ N ₄ O ₈			–
Portulacaxanthin II	C ₁₈ H ₁₈ N ₂ O ₇			–
10-formyldihydrofolate	C ₂₀ H ₂₁ N ₇ O ₇			–
5-Formiminotetrahydrofolic acid	C ₂₀ H ₂₄ N ₈ O ₆			+
Perillyl alcohol	C ₁₀ H ₁₆ O			

^a Metabolites based on searching against Human Metabolome database (HMDB), METLIN, and Kyoto Encyclopedia of Genes and Genomes (KEGG) ligand database

^b Functional category and metabolic pathway were classified as described under “Materials and methods”

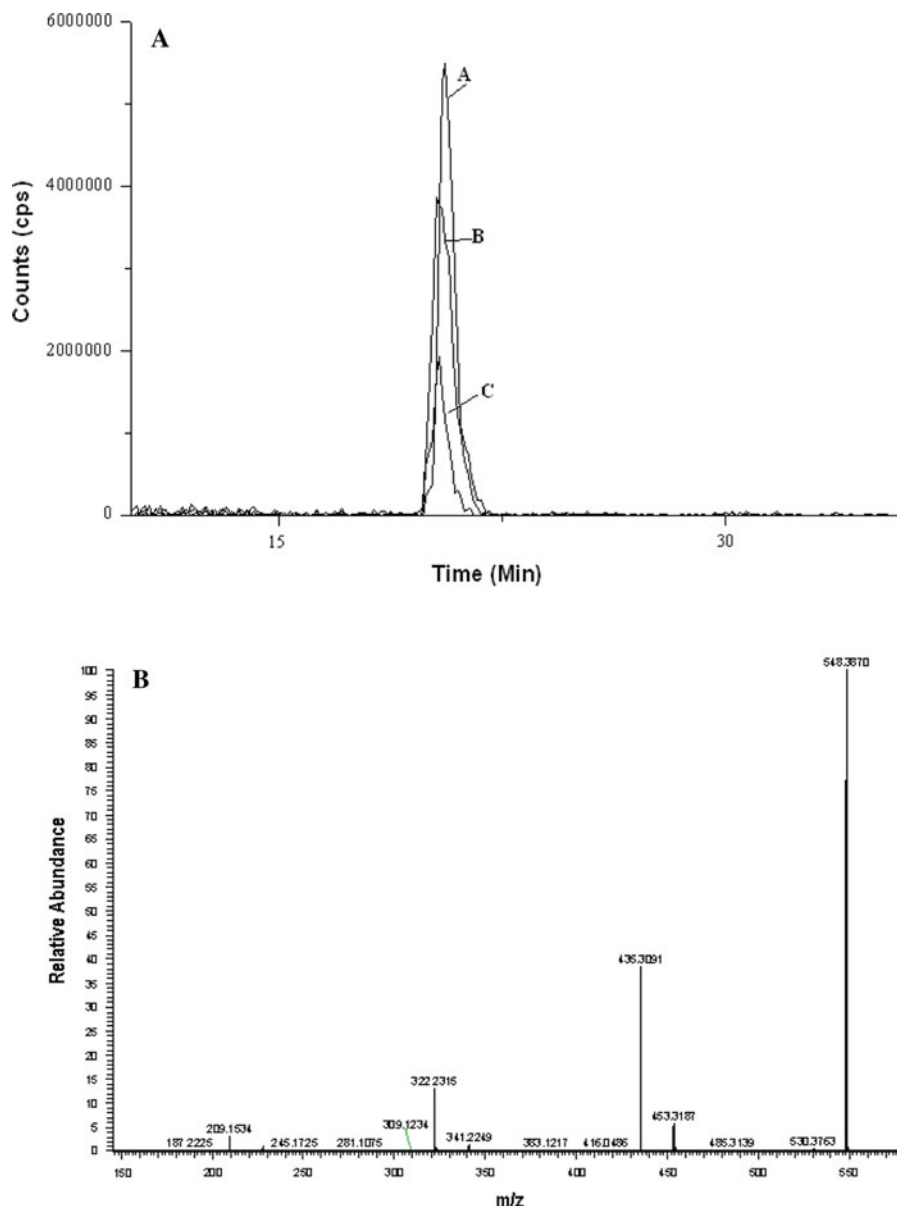
^c ‘+’ and ‘–’: fold equal or more than two in GdCl₃-treated groups versus the control. Evaluated by the peak areas of all features reported by XCMS to detect changes between the two groups. Average data of three replicate experiments was used

enzymes associated with glycolysis, such as different dehydrogenase, enolase, and aldolases etc., are generally overexpressed (Ding et al. 2004; Dos Santos et al. 2004), allowing malignant cells to proliferate and aggress under oxygen deficiency for cells respiration. The development of glycolytic regulation in tumor and proliferating cells is an important strategy for cell growth inhibition since increased glycolysis is frequently seen in cancer cells (Xu et al. 2005). Our data demonstrated that GdCl₃ could exhibit the inhibitory effect on cell growth through the pathway related to glycolysis. Furthermore, the variable expressions of the metabolites for glycolytic metabolism indicated that GdCl₃ exhibited inhibitory effect through effective intervention of the relevant glycolytic enzymes. It was reported that La³⁺, one of rare-earth element series, could interact with GAPDH of which the activity can be regulated by Ca²⁺/Calmodulin (CaM) (Xu et al. 2008). Based on the present results and chemical similarity of Lns series, one might speculate that the target of glycolytic enzymes might be one of the biochemical action of GdCl₃, which initiate signaling cascades and play crucial role in regulating cell growth. This might provide a new

clue to understand the biological influence of GdCl₃ on cell activity. Further functional investigation of the GdCl₃-mediated targets would lead to a deeper understanding of the role of GdCl₃ in the inhibition of tumor cell proliferation and developing attractive target sites for cancer therapeutics.

Several metabolites that are involved in amino acids metabolic pathway also revealed the increase or decrease in expressions after the treatment. For example, some intermediates involved in arginine, serine, and threonine metabolism displayed the increase in expressions following lower concentration incubation, while those in arginine, and proline or aspartate metabolism pathways showed decreased expressions after higher concentration treatment. The expressions of these peptides or amino acids metabolism-associated metabolites were determined to increase or decrease following the lower or higher concentration treatment, indicating the association of these several metabolites in the inhibitory or promotional effect on Hela cells induced by GdCl₃. Moreover, it was interesting to note that some in the glutathione or redox metabolic pathway, such as 2-oxo-4-methylthiobutanoic acid, spermidine, and

Fig. 4 Typical extracted ion chromatogram (EIC) for metabolite (lysoPE) from the extracts of the different status. **a** direct integration of the EICs. The symbols A–C displayed in the EIC corresponded to GdCl_3 concentrations of 0.1 mM, 0.00075 mM, and the control, respectively. **b** MS–MS spectrum of the metabolite. The metabolite was considered as differentially expressed with increased or decreased expression (more than twofold, P values <0.05). cps, counts/s



ophthalmic acid etc., were detected with decreased levels after higher concentration treatment, suggesting that the redox pathway plays a key role in GdCl_3 -induced cell growth inhibition. Growing evidence demonstrates that there is a relationship between redox homeostasis/antioxidative system and cell proliferation. Previous studies indicated that glutathione could play a role in maintaining cell redox state and have protective effect against oxidative stress damage (Schafer and Buettner 2001; Vertuani

et al. 2004). Reactive oxygen species, such as hydroxyl radical, and hydrogen peroxide etc., generated during metabolism, would lead to cell oxidative injury, and the expressions of some antioxidants such as glutathione and antioxidant enzymes like thiol-transferase could reduce or eliminate the freeradicals (Fang et al. 2002). A number of metabolites involved in glutathione pathway and metabolites such as citrullin and arginine with antioxidant capacity showed changed profile, indicating an important role

Table 2 Detailed information about biochemical properties, localization and pathways of differential metabolites

Metabolites	Metabolic pathways ^a	Cellular location ^b	LogP/hydrophobicity ^c
Lauroyl-CoA	Lipid biosynthesis, fatty acid transport, fatty acid elongation in mitochondria	Cytoplasm; peroxisome	N/1.35
Malonylcarnitine	Fatty acid transport, energy production	Membrane	N/−1.98
LysoPE(0:0/24:0)	Phospholipids, Lipids	Membrane	N/6.79
PI(16:0/16:2(9Z,12Z))	Lipids, phospholipids, membrane component, energy source, cell signaling		N/6.59
12a-Hydroxy-3-oxocholadienic acid	Cholesterols and derivatives, fat solubilization		N/4.3
5b-Cholestane-3a,7a,12a,23S,25-pentol	Steroids and steroid derivatives, hormones, membrane component	Membrane, cytoplasm	N/4.2
12-Ketodeoxycholic acid	Fat solubilization and waste products		N/5.1
Trehalose-6-phosphate	Disaccharide phosphates, starch and sucrose metabolism	Cytoplasm ^b	N/−2.42
2-Phosphoglyceric acid	Glycerophosphates, glycolysis	Cytoplasm	N/−3
DHAP(10:0)	Derivative of dihydroxyacetone phosphate glycolysis metabolic pathway		N/2.0
N-Acetyl-b-glucosaminyllamine	Carbohydrates	Cytoplasm ^b	N/−2.52
N-Acetylneuraminic acid	Carbohydrates, nucleotide sugar and amino sugar metabolism	Cytoplasm, lysosome, nucleus	N/−2.78
Cotinineglucuronide	Carbohydrates and carbohydrate conjugates	Cytoplasm ^b	N/−1.57
5-Methylthioribose 1-phosphate	Sugar phosphates, cysteine and methionine metabolism		N/−3.2
1-Phosphatidyl-D-myo-inositol	Sugar phosphates, sugar phosphates; inositol phosphate metabolism		N/−1.66
L-beta-aspartyl-L-alanine	Proteolytic breakdown product of larger proteins		N/3.42
L-alpha-glutamyl-L-hydroxyproline	Dipeptides, breakdown product of collagen		N/−3.49
Aminomalonic acid	Amino acids		N/−3.5
Ornithine	Arginine and proline metabolism; glycine, serine and threonine metabolism	Cytoplasm ^b , extracellular, mitochondria	−4.22/−3.64
Citrulline	Alanine and aspartate metabolism, arginine and proline metabolism	Cytoplasm ^b , mitochondria	−3.19/−3.27
Spermidine	Arginine and proline metabolism, glutathione metabolism		−0.66/−0.62
L-Arginine	Essential amino acids, alanine and aspartate metabolism, aminoacyl-tRNA biosynthesis	Cytoplasm, extracellular, mitochondria	−4.20/−3.6
Dimethyl-L-arginine	Protein synthesis, amino acid biosynthesis	Cytoplasm ^b	N/−3.15
Hydroxyproline	Arginine and proline metabolism	Cytoplasm, endoplasmic reticulum, mitochondria	−3.17/−3.31
2-Oxo-4-methylthiobutanoic acid	Cysteine and methionine metabolism, glucosinolate biosynthesis	Cytoplasm	N/−0.07
L-Cystine	Amino acids, cysteine and methionine metabolism, ABC transporters	Cytoplasm; extracellular	−5.08/−5.5
Ophthalmic acid	Peptides, analogue of glutathione		N/−3.11
Glutamylphenylalanine	Peptides, gamma-glutamyl derivative	Cytoplasm	N/−4.4
L-Isoleucine	Essential amino acids, aminoacyl-tRNA biosynthesis,	Cytoplasm, extracellular, mitochondria	−1.70/−1.73

Table 2 continued

Metabolites	Metabolic pathways ^a	Cellular location ^b	LogP/ hydrophobicity ^c
Succinylacetone	Valine, leucine and isoleucine biosynthesis	Cytoplasm ^b	N/−0.18
Acetyl- <i>N</i> -formyl-methoxykynurenamine	Tyrosine metabolism		−0.158/0.50
Deoxycytidine	Tryptophan metabolism	Extracellular, lysosome, mitochondria, nucleus	N/−1.83
Phosphoribosyl formamidocarboxamide	Purine metabolism, pyrimidine metabolism, pyrimidine metabolism	Cytoplasm ^b	N/−1.82
SAICAR	Biosynthesis from histidine and purine	Cytoplasm	N/−1.95
Xanthylic acid	Biosynthesis of purine nucleotides		−0.18/−0.20
6-Methyladenine	Energy currency, DNA/RNA synthesis, enzyme cofactors, purine metabolism	Cytoplasm	N/−1.77
1,7-Dimethylguanosin	Purines and purine derivatives, nucleosides and nucleoside conjugates		−0.37/−0.45
Niacinamide	Methylated nucleosides	Cytoplasm, extracellular	0.00/−0.21
<i>N</i> -Methylnicotinamide	Component of Nicotinate and nicotinamide metabolism	Cytoplasm ^b	N/−2.11
Thiamine	Essential vitamins	Cytoplasm, membrane, extracellular, mitochondria	N−2.12
7-Hydroxy-6-methyl-8-ribityl lumazine	Riboflavin metabolism, hormones		N/−1.65
3-Chlorotyrosine	Myeloperoxidase-catalyzed oxidation product	Cytoplasm ^b	N/2.5
Uroporphyrinogen III	Porphyrin metabolism	Cytoplasm	N/0.67
Coproporphyrin III	Porphyrin metabolism	Cytoplasm; mitochondria	N/2.53
Portulacaxanthin II	Betaxanthin biosynthesis		N/1.75
10-formyldihydrofolate	One carbon pool by folate	Cytoplasm ^b	N/−1.83
5-Formiminotetrahydrofolic acid	Folate compound	Cytoplasm; extracellular; lysosome; mitochondria	N/−1.26
Perillyl alcohol	Biosynthesis from ornithine, lysine and nicotinic acid	Cytoplasm; extracellular	3.17/2.50

^a Metabolic pathways derived from KEGG ligand database

^b Predicted from LogP

^c Calculated using ALOGPS software (<http://www.vclab.org/lab/alogs/>)

for these metabolites in the antioxidant system for high dose GdCl₃-treated Hela cells. This suggested that functional control of cellular redox and oxidative defense system pathway might be an important strategy or machinery exhibited by GdCl₃. MGd, a gadolinium texaphyrin complex, is regarded as an proapoptotic agent by mediating cellular redox reaction, and is currently subjected to phase III clinical trial for cancer therapy (Hashemy et al. 2006; Fricker 2006). The drug could interfere with the activities of some enzymes such as thioredoxin peroxidases (peroxiredoxins) with redox-active residues, and mediate catalyzed reaction of reducing metabolites

such as glutathione, which induce oxidative stress and subsequent apoptosis in tumor cells. Additionally, recent proteomic studies of Hela cell apoptosis induced by Lns salts (such as Yb³⁺ and Gd³⁺) revealed that some proteins related to redox state and stress resistance, including peroxiedoxin 6, glutathione peroxidase, superoxide dismutase 1, and heat shock proteins, were observed decreased at high concentration (Li et al. 2009; Shen et al. 2009b), which was in agreement with our metabolomic results and demonstrated that the redox and oxidative defense were involved in lanthanide ions-induced cell apoptosis. However, considering that there is a

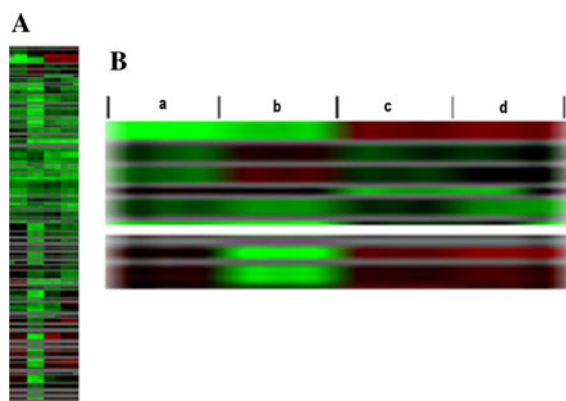


Fig. 5 Heat map representation of unsupervised hierarchical clustering of the sample data. **a** Truncated two-dimensional features of metabolites in given status. The difference in the shade of color represented the difference in expressions of the metabolites. Three technical replicates for each biological group were shown (by three columns). **b** Magnified comparison map of **a**. *a–d* respectively represented the different states as described above

similarity/dissimilarity between MGd complex and Gd salts due to common/unique chemical properties, the biological effects on cell growth and the mechanisms of action between them might behave differently. Further understanding the action of Gd complexes and Gd salts would be important for developing Gd-based compounds as drugs and for rational design of new compounds in therapeutic application. The next step is to establish in vivo experiment to verify the results obtained from in vitro cell culture. The favorable cellular response of the treatment demonstrated by in vivo study will be valuable for development of effective therapies by the intervention of targeted biomolecules in treatment of cancers. More studies warrants to be performed and are currently undergone.

Calcium (Ca^{2+}), acting as a ubiquitous second messenger of eukaryotic cells, participates in a large number of signal transduction and regulate cell proliferation, apoptosis, or differentiation (Carafoli 2002). Also Ca^{2+} is believed to play a pivotal role in carcinogenesis and progression (Joseph et al. 2001). Lns ion based on their similarity to Ca^{2+} in ionic radius could replace activating centers of metals such as K^+ , Ca^{2+} , Cu^{2+} , or Mg^{2+} , especially Ca^{2+} , which modulate Ca^{2+} -depended enzymatic activities and signal transduction required for cell growth regulation. In our results, as mentioned above, it was found that GdCl_3 affected the key enzymes of glycolytic

metabolism which require Ca^{2+} -depended CaM regulation. It was reasonable to postulate that Gd^{3+} at a higher concentration could induce Ca^{2+} channel inhibition. As reported, blocking Ca^{2+} entry by Ln ions contributed to the inhibition of cell proliferation of human colon carcinoma cells (Weiss et al. 2001). The biochemical interaction with Ca^{2+} channel by inhibiting the fluxes of intracellular Ca^{2+} might be one of the mechanic action that Gd^{3+} exerted the inhibitory effect on Hela cells. On the other hand, how does Gd^{3+} promote the growth of cells via Ca^{2+} channel or Ca^{2+} -depended signal transduction at lower concentration? Although little information about this is available up to now, induction of cell proliferation by low concentration Ca^{2+} was reported previously (Dai et al. 2008). Based on the chemical/biological similarity of Ln^{3+} to Ca^{2+} , it might be possible that Ln^{3+} functions in cell biological processes, directly or indirectly, through participating in signal transduction mediated by Ca^{2+} (Wang and Yang 2009). For example, Gd^{3+} might interact with Ca^{2+} -depended membrane receptors, such as integrins, G protein-coupled receptor (GPCR), and Ca^{2+} channel, which are potential targets of Ln^{3+} . As a matter of fact, a low concentration of Gd^{3+} can activate membrane receptors on cell surface and initiate downstream signals (Tateyama and Kubo 2006). However, further study is still needed to understand the role of Gd-mediated cell growth proliferation and inhibition.

Those that are associated with nucleic acids metabolism, such as DNA/RNA biosynthesis, purine metabolism, and energy currency etc., were also observed to be regulated following incubation with lower or higher concentrations, suggesting that the metabolites in nucleic acid metabolism were involved in the response to GdCl_3 exposure. Results revealed some intermediates such as xanthylic acid, and 6-methyladenine etc., were detected with enhanced expressions following the treatment with lower concentration, whereas 6-methyladenine and 1,7-Dimethylguanosine were significantly under-expressed following the treatment with higher concentration. A high 1,7-Dimethylguanosine (a methylated nucleoside) activity appears to be possibly related with aberrant increase of tRNA methylases activity within tumor tissues (Niwa et al. 1998). Other interesting observations were the differently regulated metabolites involved in other metabolic processes that were essential for cell growth and

development. The altered expressions of the metabolic processes-associated metabolites might reflect the essence and indispensability of these biologically active molecules for cell activity interfered by GdCl_3 . And involvement of the metabolites in the metabolic pathways might provide potential markers for development of the therapies to inhibit cell malignant proliferation.

In the present work, we have investigated the extracellular metabolomic profile changes of Hela-cell model following conditioned GdCl_3 treatments at the system level. A total of 48 metabolites were found to be up or down-expressed ($P < 0.05$) in response to the treatment. The metabolites differentially expressed were involved in different metabolic pathways, such as lipid metabolism, glycolytic pathway, and redox metabolic pathway etc., suggesting that these metabolites altered in the expressions might play a role in GdCl_3 -mediated cell growth proliferation and inhibition. The observations demonstrated that the untargeted metabolomics could provide a detailed view of a molecular profile, and give some new insights into growth promotion or inhibition of Hela cells regulated by GdCl_3 . Such results would extend our understanding of the mechanism of tumor cells growth activity perturbed by GdCl_3 , which in turn could propel the rational exploration and design of Gd-based drugs for development of the treatment of cancers in pharmacological intervention.

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