

Maria Dung Cao

# MR metabolic characterization of locally advanced breast cancer

– treatment effects and prognosis

Thesis for the degree of Philosophiae Doctor

Trondheim, March 2012

Norwegian University of Science and Technology  
Faculty of Medicine  
Department of Circulation and Medical Imaging



**NTNU – Trondheim**  
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## Sammendrag

Brystkreft er den hyppigste kreftsykdommen blant kvinner. Lokalavansert brystkreft utgjør omtrent 10% av alle brystkrefttilfeller og omfatter en heterogen pasientgruppe med ulike prognoser. Pasienter med lokalavansert brystkreft får ofte kjemoterapi før kirurgisk fjerning av tumor, såkalt neoadjuvant kjemoterapi, for å redusere størrelsen på tumoren. Det er stor variasjon i behandlingsrespons for denne pasientgruppen, og det er derfor behov for å utvikle målrettet og individualisert behandling, samt metoder for oppfølging av behandlingsrespons.

Metabolomics er en systematisk analyse av småmolekylære forbindelser (metabolitter) i biologiske prøver. Den metabolske profilen til brystkreftvev er vist å korrelere med viktige kliniske parametere, for eksempel tumorgrad, hormonreseptorstatus og lymfeknutespredning. Magnetisk resonans (MR) spektroskopi er en metode som kan gi en detaljert beskrivelse av metabolittprofilen i vevet. En fordel med denne metoden er at vevsprøven er intakt etter analysen slik at den samme vevsprøven kan analyseres videre med andre metoder, for eksempel immunohistokjemi, genuttrykk- eller proteinanalyse.

En sentral gruppe metabolitter innenfor brystkreftforskning er kolinforbindelser. Disse metabolittene er viktig for celledeling, signaloverføring, lipidmetabolisme og cellens membranstruktur. Laktat er en annen viktig metabolitt som inngår i energimetabolismen. I dette arbeidet ble vevsprøver fra pasienter med lokalavansert brystkreft analysert ved bruk av MR spektroskopi for prediksjon av behandlingsrespons og overlevelse. I tillegg undersøkte vi rollen til glycerophosphodiester phosphodiesterase (GDPD) i regulering av kolinforbindelser.

## Sammendrag

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Alle pasienter hadde en effekt av behandlingen som ble gitt, og nesten alle fikk en reduksjon i tumorstørrelse etter behandling. Resultatene viste ingen metabolske forskjeller mellom pasienter med klinisk god eller dårlig behandlingsrespons. Resultatene viser derimot at de metabolske forandringene som skjer under neoadjuvant kjemoterapi er forskjellig i pasienter som overlever mer enn fem år og de som dør før fem år. Høyere nivå av laktat, glycine og kolinforbindelser etter behandling var forbundet med dårlig prognose. Analysene av GDPD5 tyder på at enzymet er involvert i reguleringen av kolinmetabolismen, men dets rolle for bruk i målrettet terapi er fortsatt uklart og nye studier må til for å undersøke dette.

MR metabolomics kan brukes til å undersøke metabolske forandringer under neoadjuvant kjemoterapi behandling og kan identifisere viktige metabolitter for prediksjon av overlevelse hos pasienter med lokalavansert brystkreft.

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*Maria Dung Cao*

Trondheim, December 2011

## Summary

Breast cancer is the most frequent cancer disease among women globally. Locally advanced breast cancer (LABC) constitutes a heterogeneous group of patients with variable prognosis. Today's treatment decision is predominately based on clinical assessment, histopathological evaluation, and hormone receptor and lymph node status. So far, these data are not sufficient for designing a proper personalized treatment or accurately predicting treatment response and survival. Molecular characterization of tumors may help stratifying patients for individualized treatment, thereby achieving better prognosis.

Magnetic resonance (MR) metabolomics analyses assess the downstream products of gene and protein expressions, i.e. the metabolites, and have shown to provide both predictive and prognostic information for several types of cancers. Proton high resolution magic angle spinning ( $^1\text{H}$  HR MAS) MR spectroscopy is a non-destructive and high-throughput technique that provides highly resolved MR spectra from biological tissue. Recently, altered cell metabolism is suggested as a new emerging hallmark of cancer. Choline phospholipid metabolism is involved in cell signaling, lipid metabolism, and the structural integrity of the cell membrane. Several MRS studies have suggested the total choline-containing metabolite (tCho) level as an *in vivo* biomarker for diagnosis and treatment evaluation of breast cancer. Reprogramming of energy metabolism and activation of tumor hypoxic response are commonly observed in cancers, and can be characterized by high lactate production.

In this thesis, multivariate data analyses and metabolite quantification of  $^1\text{H}$  HR MAS MRS data were performed to investigate the potential of metabolomics for prediction of clinical response and long-term survival in LABC patients receiving neoadjuvant

## Summary

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chemotherapy (NAC). In addition, the role of glycerophosphodiester phosphodiesterase (GDPD) in choline phospholipid metabolism of human breast cancer was investigated.

All patients had a metabolic response to NAC and almost all patients had a reduction in tumor size. Our results show no clear differences in metabolic responses to NAC between patients with partial response and stable disease and no significant multivariate models for prediction of clinical response by MR metabolomics data. In general, all patients experienced a decrease in tCho levels. It is possible that a cohort including also patients with progressive disease would reveal clearer differences in the metabolite profiles between the clinical response groups. This thesis demonstrates that MR metabolomics contain prognostic information that is associated with survival status of LABC patients. Increase in lactate levels as a response to NAC was associated with low survival rates ( $< 5$  years), while decreased glycine and choline phospholipid metabolites were associated with long-term survival ( $\geq 5$  years). The observed metabolite profiles consisting of higher levels of lactate, glycine, and tCho post-treatment were predictive of low breast cancer survival rates.

GDPD5 gene expression was correlated with choline phospholipid metabolite levels and with CHKA and PLD1 gene expressions suggesting GDPD5 to have a role in regulation of choline phospholipid metabolism in human breast cancer. However, more studies are needed to investigate the relationship between GDPD5 and tumor malignancy, and also estrogen receptor status, for use as target in breast cancer treatment.

In conclusion, monitoring metabolic responses to NAC by MR metabolomics may have the potential to assist the prediction of survival and help identify new targets for therapeutic treatment of breast cancer.



## Symbols and abbreviations

$\mu$	magnetic moment
$^1\text{H HR MAS}$	proton high-resolution magic angle spinning
AJCC	American Joint Committee on Cancer
AQ	acquisition time
ATCC	American Type Culture Collection
ATP	adenosine triphosphate
$B_0$	external magnetic field
BRCA	breast cancer susceptibility gene
CDP-choline	cytidine diphosphate choline
CHKA	choline kinase alpha
Cho	free choline
CHT-1	choline transporter-1
CPMG	Carr-Purcell-Meiboom-Gill
CR	complete response
CT	computerized tomography
ct	threshold cycle
CTP	phosphocholine cytidyltransferase
CV	cross-validation
EGFR	epidermal growth factor receptor
ER	estrogen receptor
ERETIC	electronic reference to access in vivo concentration
FBS	fetal bovine serum
FEC	5-fluorouracil, epirubicin and cyclophosphamide
FID	free-induction decay
GA	genetic algorithm
GDPD5	glycerophosphodiester phosphodiesterase domain containing 5
GPC	glycerophosphocholine
GPC-PDE	glycerophosphocholine phosphodiesterase
HER2	human epidermal growth factor receptor 2
HES	hematoxylin-eosin-saffron
HiF-1	hypoxia inducible factor-1
HR	high-resolution
HRP	horseradish peroxidase

## Symbols and abbreviations

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I	spin quantum number
IBC	inflammatory breast cancer
IDC	invasive ductal carcinoma
ILC	invasive lobular carcinoma
LABC	locally advanced breast cancer
LDH	lactate dehydrogenase
LV	latent variable
LYSO-PLA1	lysophospholipase A1
MAS	magic angle spinning
MCT	monocarboxylate transporters
MRI	magnetic resonance imaging
MRS	magnetic resonance spectroscopy
NAC	neoadjuvant chemotherapy
NBCG	Norwegian Breast Cancer Group
NPP6	nucleotide pyrophosphatases/phosphodiesterases 6
OCT2	organic cation transporter-2
PBS	phosphate buffered saline
PC	phosphocholine
PC	principal component
PCA	principal component analysis
pCR	pathological complete response
PD	progressive disease
PgR	progesterone receptor
PLA2	phospholipase A2
PLC	PtdCho-specific phospholipase C
PLD	PtdCho-specific phospholipase D
PLS-DA	partial least squares discriminant analysis
ppm	parts-per million
PR	partial response
PtdCho	phosphatidylcholine
PULCON	pulse length based concentration determination
pw	pulse width
qRT-PCR	quantitative real-time PCR
RECIST	Response Evaluation Criteria on Solid Tumors
RF	radio frequency
RIN	RNA integrity number
ROC	receiver operating characteristic
S/N	signal-to-noise ratio
SD	stable disease
SDS-PAGE	sodium dodecyl sulfate–polyacrylamide gel electrophoresis
T <sub>1</sub>	longitudinal relaxation time
T <sub>2</sub>	transversal relaxation time

## Symbols and abbreviations

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tCho	choline-containing metabolites
TE	echo time
TMS	tetramethylsilane
TNM	extend of tumor (T), degree of spread to lymph nodes (N), distant metastasis (M)
TR	repetition time
TSP	trimethylsilyl propionic acid
UICC	Union for International Cancer Control
VEGF	vascular endothelial growth factor
VIP	variable importance in the projection
WHO	World Health Organization
$\omega_r$	spin-rate

## List of papers

Paper I

**Predicting long-term survival and treatment response in breast cancer patients receiving neoadjuvant chemotherapy by MR metabolic profiling**

Maria D. Cao, Beathe Sitter, Tone F. Bathen, Anna Bofin, Per E. Lønning, Steinar Lundgren and Ingrid S. Gribbestad

*NMR Biomed.* 2012 Feb;25(2):369-78.

Paper II

**Prognostic value of metabolic response in breast cancer patients receiving neoadjuvant chemotherapy**

Maria D. Cao\*, Guro F. Giskeødegård\*, Tone F. Bathen, Beathe Sitter, Anna Bofin, Per E. Lønning, Steinar Lundgren and Ingrid S. Gribbestad (\*shared first authorship)

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Paper III

**Glycerophosphodiester phosphodiesterase domain containing 5 (GDPD5) expression correlates with malignant choline phospholipid metabolite profiles in human breast cancer**

Maria D. Cao, Mailin Doepkens, Balaji Krishnamachary, Farhad Vesuna, Mayur M. Gadiya, Per E. Lønning, Zaver M. Bhujwalla, Ingrid S. Gribbestad and Kristine Glunde

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## 1 Introduction

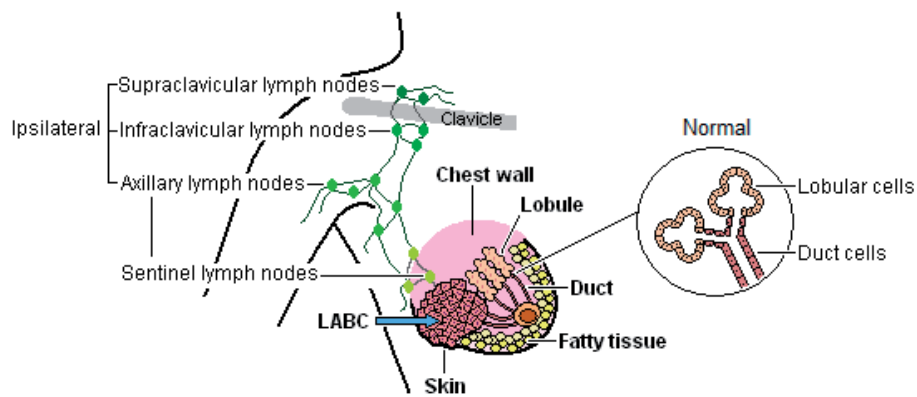
### 1.1 Breast cancer

Breast cancer is the most frequent cancer disease among women globally with approximately 1.6 million new cases diagnosed in 2010 [1]. Despite improvements in early detection and treatment, breast cancer is still one of the leading causes of cancer-related death among women globally with an estimated 425 000 deaths in 2010 [1]. In Norway, 2745 newly diagnosed breast cancer cases and 671 breast cancer deaths were reported for women in 2009 [2]. The incidence of breast cancer is higher in the western countries than in developing countries, but the mortality rate is higher in less developed regions of the world [3]. These differences can in part be explained by different access to medical facilities and treatment strategies.

Factors associated with breast cancer risk can be genetic or non-genetic. Hereditary breast cancer accounts for 5-10% of all breast cancer cases and is mostly caused by germline mutations in the two first identified breast cancer susceptibility genes, BRCA1 and BRCA2 [4]. Exposure to reproductive hormones, such as estrogen and progesterone, are thought to increase breast cancer risk through their influence on cell proliferation [5]. Many non-genetic factors associated with increased breast cancer risk have been identified including age, early menarche and late menopause, late age at first childbirth ( $> 35$  year), no breastfeeding, use of oral contraceptives and post-menopausal hormones, post-menopausal obesity, alcohol consumption, and physical inactivity [6, 7].

The female breast consists of lobules (made of lobular epithelial cells that line the milk-producing glands), ducts (made of duct epithelial cells that line the tubes conveying milk secretion), fatty tissue, and connective tissue. Carcinoma originating from epithelial cells is the most common type of breast cancer [8]. During cancer transformation normal epithelial cells lining the ducts or lobules are replaced by malignant atypical epithelial cells (Figure 1.1). Invasive ductal carcinoma (IDC) and invasive lobular carcinoma (ILC) account for approximately 80% and 10-20% of breast cancer cases, respectively [8].

The overall 5-year breast cancer survival rate is approximately 80% for all patients, but is lower for advanced breast cancer [9]. Locally advanced breast cancer (LABC) constitutes a heterogeneous group of patients with variable prognosis and with a 5-year survival rate of 50-80% [10]. LABC can be defined as the most advanced stage before metastatic disease and constitutes approximately 10% of the newly diagnosed breast cancers [11]. The incidence of LABC is higher in developing countries than in western countries probably due to the occurrence of late-stage disease at the time of diagnosis [11].



**Figure 1.1:** Anatomical illustration of locally advanced breast cancer (LABC). LABC can originate from ductal or lobular epithelial cells. The tumors are either > 5 cm or of any size with extension to chest wall, skin or with lymph node metastasis. The different types of metastatic lymph nodes are illustrated, see Table 1.1.



### 1.1.1 Staging of breast cancer

Breast cancer staging can be defined using the TNM classification system which takes into consideration the extent of the tumor (T), the degree of spread to lymph nodes (N), and distant metastasis (M) (Table 1.1) [12]. The TNM system is used to describe the extent of the disease and is indeed an important prognostic factor for determining treatment options and survival probabilities. The TNM clinical categories are determined by physical examinations and imaging modalities such as mammography and ultrasound of the breast, and often bone scintigram, and computerized tomography (CT) examination of lung and liver. Based on the TNM system, the patients are divided into different breast cancer stages ranging from 0 to IV. Stage 0 is used to describe non-invasive breast cancer, while stages I to III include invasive breast cancer with or without lymph node metastasis. Stage IV describes invasive breast cancer that has spread to other organs [12].

There is no international standard for the staging of LABC. In general, LABC can be defined as T3-T4 (any N) or N2-N3 (any T) without distant metastasis (M0), which includes all patients of stage IIIA-C disease and a subset of stage IIB. According to the TNM system, inflammatory breast cancer (IBC) is considered a subgroup of LABC [12]. However, IBC is often discussed separately due to its distinct clinical presentation and poor prognosis compared to non-IBC [13].

**Table 1.1** TNM clinical classification according to the AJCC/UICC [12]

Characteristic		
T0	No evidence of primary tumor	
T1	Tumor ≤ 2 cm in greatest dimension	
T2	Tumor > 2 cm, but ≤ 5 cm in greatest dimension	
T3	Tumor > 5 cm in greatest dimension	LABC
T4	Tumor of any size with extension to chest wall or skin or inflammatory carcinoma	LABC
N0	No regional lymph node metastasis	
N1	Metastasis in movable ipsilateral axillary lymph node(s)	
N2	Metastasis in fixed ipsilateral axillary lymph node(s)	LABC
N3	Metastasis in ipsilateral infraclavicular or supraclavicular lymph node(s)	LABC
M0	No distant metastasis	
M1	Distant metastasis	

TNM categories associated with locally advanced breast cancer (LABC) are highlighted. AJCC, American Joint Committee on Cancer; UICC, Union for International Cancer Control.

### **1.1.2 Prognostic and predictive factors**

Prognostic factors can predict the outcome of a disease, while predictive factors can predict the response to a specific treatment. The prognostic factors for LABC are similar to the prognostic factors for earlier stage breast cancer with tumor size, grade, and lymph node status being the strongest prognostic factors for breast cancer survival [14].

Estrogen receptor (ER) and progesterone receptor (PgR) are ligand-dependent nuclear transcription factors involved in proliferative activity and reproductive development. Overexpression of ER and PgR is typically observed in breast cancer and is thought to play a major role in breast cancer progression [5]. The mechanisms behind the abnormal expression of these reproductive hormone receptors are still under investigation. Interestingly, both germline and somatic mutations in the ER gene of breast carcinomas are in fact rare [15]. Patients with ER and PgR positive tumors have better prognosis compared to patients that are negative for these hormone receptors [16].

Human epidermal growth factor receptor-2 (HER2, HER-2/neu, c-erbB2) is a relatively newly discovered biological target for the treatment of breast cancer. HER2 is a member of the epidermal growth factor receptor (EGFR) family which regulates several signal transduction pathways of cell growth and differentiation. The expression of HER2 is increased in approximately 20% of breast carcinomas and is associated with increased proliferation, high metastatic potential and poor outcome [17, 18].

Hormone receptor status and HER2 expression are used as target for breast cancer treatment. Thus, they can be defined as both prognostic and predictive factors. The change in tumor size in response to treatment is an important predictive factor for treatment evaluation. In the last decade, molecular characterization by metabolic profiling has provided potential new factors that may play an important role in diagnosis, treatment evaluation, and prognosis of breast cancer [19].

## 1.2 Treatment strategies for LABC

The treatment regimens recommended for LABC patients vary between countries. In general, the patients are often treated with chemotherapy before surgery, so-called neoadjuvant chemotherapy (NAC), to shrink the tumor enough to make surgical removal possible and even allow for breast conserving surgery in exchange of a mastectomy. After surgery, post-operative treatment is usually given in the same way as for those with earlier stage breast cancer. In Norway, guidelines for treatment regimen of LABC are given by the Norwegian Breast Cancer Group ([www.NBCG.no](http://www.NBCG.no)).

### 1.2.1 Neoadjuvant chemotherapy (NAC)

Primary systemic treatment (or NAC) was first described in the 1970's [20] and is now well established in the treatment of LABC [10]. For LABC patients, treatment with NAC is given to make a tumor operable, either by mastectomy or breast-conserving surgery. Overall, NAC offers direct evaluation of treatment effects and the response to NAC has been shown to be an important predictor of survival [21, 22]. Better clinical and pathological response to NAC is associated with prolonged recurrence-free survival [21, 22]. In Norway, the current standard treatment for LABC is a combination of the cytostatic agents 5-fluorouracil, epirubicin, and cyclophosphamide (FEC) and often sequential treatment of FEC and a taxane substance ([www.NBCG.no](http://www.NBCG.no)).

Anthracyclines were discovered in the 1960's and include doxorubicin and epirubicin which are among the most effective chemotherapeutic agents for the treatment of breast cancer. These agents predominately accumulate in neoplastic and proliferating cells where they are capable of inducing DNA strand breakage and apoptosis through their interaction with DNA binding proteins, tumor suppressor gene p53, and DNA intercalation [23-25]. Another relatively new recommended drug group developed in the 1990's for use in the treatment of breast cancer is taxane. Paclitaxel is a taxane drug that causes mitotic arrest by disturbing the breaking and rearranging of microtubules in the cells [26].

### 1.2.2 Post-operative treatment

Post-operative treatment such as radiation, hormone, and biologic therapies are usually given to LABC patients. For women at high risk of recurrence, like LABC patients, the breast cancer survival rate has been shown to significantly improve when treated with radiation therapy [27]. Patients with ER positive tumors could benefit from anti-estrogen drugs, such as tamoxifen, which can result in a reduction of recurrences and breast cancer death [28, 29]. Treatment with trastuzumab, a monoclonal antibody against HER2, can reduce the recurrence rate and mortality of breast cancer [18].

### 1.2.3 Clinical response evaluation

The change in tumor size can be used as a predictive factor of a specific treatment. The tumor response criteria were first published by the World Health Organization (WHO) in 1981 (Table 1.2) [30]. In 2000, an improved and standardized response evaluation system was introduced, known as Response Evaluation Criteria on Solid Tumors (RECIST) (Table 1.2) [31]. Imaging modalities such as mammography, ultrasound, and magnetic resonance imaging (MRI) can be used for the evaluation of treatment response. MRI has been shown to correlate the best with pathological findings compared to clinical examination, mammography, and ultrasound [32]. However, in a neoadjuvant setting when the breast lesions are large (> 5 cm in greatest dimension), the response to treatment can be evaluated clinically using a caliper [31].

**Table 1.2** Clinical response criteria for target lesions according to WHO and RECIST criteria [30, 31]

	<b>WHO*</b>	<b>RECIST</b>
	<b>Bidimensional Product of the two largest diameters</b>	<b>Unidimensional The longest diameter</b>
Complete response (CR)	Disappearance of all target lesions	Disappearance of all target lesions
Partial response (PR)	≥ 50% decrease	≥ 30% decrease
Stable disease (SD)	< 50% decrease to < 25% increase	< 30% decrease to < 20% increase
Progressive disease (PD)	≥ 25% increase	≥ 20% increase

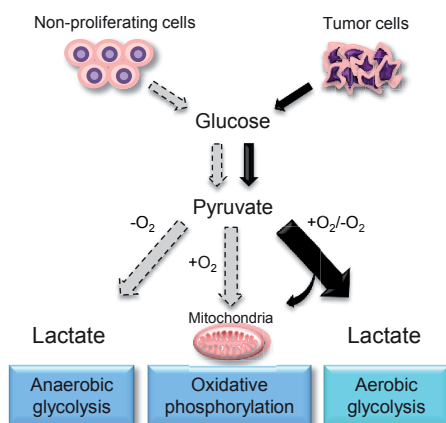
\* Clinical response criteria used in paper I and II.

### 1.3 The biology of cancer

Carcinogenesis is a multistep process that involves essential genomic alternations that collectively dictate malignant growth. Six hallmarks of cancer have been suggested as novel characteristics of cancer cells, including being self-sufficient in growth signals, insensitive to anti-growth signals, limitless replicative potential, evading apoptosis, sustained angiogenesis, and tissue invasion [33]. Two emerging physiological features, reprogramming of energy metabolism and evading immune destruction, have recently been added to the list [34].

#### 1.3.1 Tumor glycolysis

Cancer cells have the ability to adjust their energy metabolism in order to promote rapid and uncontrolled cell proliferation. Glycolysis is a metabolic process in which glucose is converted into pyruvate to produce energy in the form of adenosine triphosphate (ATP). The total number of ATP per glucose molecule depends on the metabolic fate of pyruvate, which in normal cells depend on oxygen availability. In non-proliferating cells under condition of sufficient oxygen supply, pyruvate is completely oxidized in the mitochondria through oxidative phosphorylation which results in high ATP production (Figure 1.2). During anaerobic glycolysis, only a minimum number of ATP is produced by converting pyruvate to lactate. In cancer cells, most pyruvate is converted to lactate regardless of the oxygen levels, so-called aerobic glycolysis. This glycolytic switch in cancer cells was first described by Warburg in the 1950's [35].



**Figure 1.2:** Energy metabolism in non-proliferating and tumor cells. In case of low oxygen supply, normal cells can undergo anaerobic glycolysis and generate lactate instead of mitochondrial oxidative phosphorylation to allow for glycolysis to continue. Tumor cells tend to convert most glucose to lactate regardless of the oxygen supply. This reprogramming of energy supply. This reprogramming of energy metabolism appears to promote tumor growth.

It is not fully understood why cancer cells prefer the lower efficiency of ATP production than mitochondrial oxidative phosphorylation. It has been suggested that aerobic glycolysis protects cancer cells from acid-induced cell toxicity and is an adaptation to intermittent hypoxia in pre-malignant lesions [36]. In addition, increased glycolysis has been shown to facilitate the uptake and incorporation of nutrients needed for cell proliferation [37]. Also, glycolytic intermediates are involved in various biosynthetic pathways that facilitate cell proliferation [37, 38]. The metabolite glycine is an amino acid involved in the nucleotide and protein synthesis, and is derived from the glycolytic intermediate 3-phosphoglycerate, but can also be synthesized from choline through the glycine-betaine pathway. The levels of glycine and lactate have been associated with malignancy and prognosis in different types of cancers [39-45]. However, the molecular mechanisms behind the influence of glycine and lactate on malignant behavior of cancer cells are not fully understood.

### **1.3.2 Tumor hypoxia and angiogenesis**

Normal cells have the capacity to adapt to conditions of low oxygen supply by increasing their oxygenation through the activation of hypoxia inducible factor-1 (HIF-1) transcription factor. HIF-1 regulates multiple downstream genes involved in glucose transportation, the glycolytic pathway, oxygen capacity, and angiogenesis (e.g. vascular endothelial growth factor, VEGF) [46-49]. Hypoxia is typically observed in solid tumors as a result of poor blood supply due to either large tumor size or chaotic and dysfunctional vasculature. Tumor cells appear to have taken advantage of the hypoxic response system to facilitate cell proliferation and angiogenesis which are required for tumor growth and metastasis [50]. Furthermore, HIF-1 plays a regulative role in the production and transportation of lactate by influencing the expression of lactate dehydrogenase (LDH) and monocarboxylate transporters (MCT) [51, 52]. Thus, lactate may act as a downstream marker for aerobic glycolysis and hypoxic response in tumors.

### **1.3.3 Tumor phospholipid metabolism**

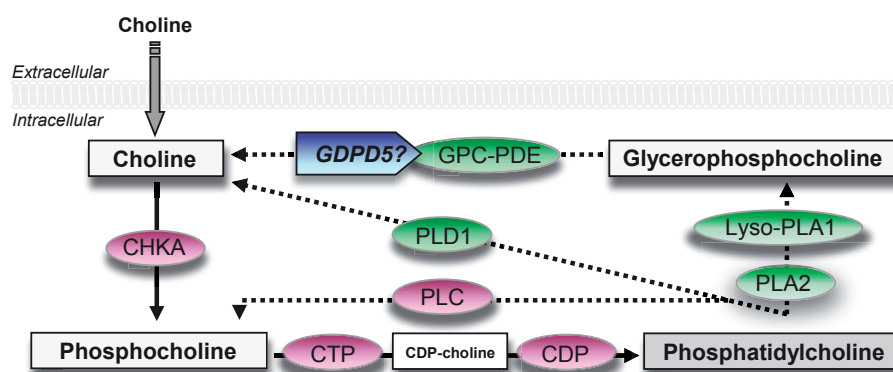
Choline phospholipid metabolism, also known as the Kennedy pathway, is the major biosynthetic pathway of *de novo* phosphatidylcholine (PtdCho) synthesis in mammalian

cells. PtdCho is the most abundant phospholipid in the cells and forms together with other lipids the characteristic bilayer structure of the cell membrane. Choline-containing metabolites (tCho) include glycerophosphocholine (GPC), phosphocholine (PC), and free choline (Cho), and are involved in cell signaling, lipid metabolism, and the structural integrity of the cell membrane. PC is both a precursor and a breakdown product of PtdCho that can act as a secondary messenger with the ability to stimulate cell proliferation through several growth factors [53], while GPC is a breakdown product of PtdCho that may reflect phospholipid membrane turnover [54]. GPC is also an abundant osmoprotective osmolyte that can protect intracellular macromolecules from being denatured during hypertonic stress in kidney cells [55]. Cho is derived from the diet, but it is also a breakdown product of GPC that is used to synthesize PC. However, the daily requirement of Cho from dietary sources are not well defined [56].

Choline phospholipid metabolism is changed in most cancers, including breast cancer [57, 58]. The tCho levels detected with *in vivo* MR spectroscopy have been suggested as a biomarker for the diagnosis and treatment evaluation of breast cancer [58-62]. However, the molecular mechanisms behind the changes in choline phospholipid metabolism observed within breast cancer are not fully understood. The regulation of choline phospholipid metabolism can be affected by growth factor stimulation, cytokines, hypoxic and inflammatory responses, and oncogenic signaling [63-67]. Choline phospholipid metabolism is a complex pathway controlled by several regulatory enzymes (Figure 1.3). Changes in the expression of genes and enzymes involved in the biosynthetic and catabolic pathways of choline phospholipid metabolism, including choline kinase alpha (CHKA), PtdCho-specific phospholipase D (PLD), and PtdCho-specific phospholipase C (PLC), have been found in different types of cancers [57]. Increased activity of the choline transporters such as organic cation transporter-2 (OCT2) and choline transporter-1 (CHT-1) have also been identified [57]. CHK (E.C. 2.7.1.32) is the enzyme at the first step of the Kennedy pathway which regulates the phosphorylation of Cho to PC. Increased CHK activity has been detected in breast cancer tissue compared to normal healthy tissue [68]. CHK inhibition and down-regulation by RNA interference efficiently decreased cellular PC and tCho levels along with proliferation and tumor growth in human breast cancer cells and animal

models [69-72]. Phosphocholine cytidyltransferase (CTP, E.C. 2.7.7.15), which uses PC as a substrate to synthesize cytidine diphosphate choline (CDP-choline), has been found to be underexpressed in cancer cells, leading to elevated PC levels [73].

The GPC levels in choline phospholipid metabolism is dependent on the degradation rate of PtdCho by the two enzymes phospholipase A2 (PLA2, E.C. 3.1.1.4) and lysophospholipase A1 (LYSO-PLA1, E.C. 3.1.1.5), and the degradation of GPC itself into Cho and glycerol-3-phosphate by glycerophosphocholine phosphodiesterase (GPC-PDE, E.C. 3.1.4.2). The gene expressions of PLA2 and LYSO-PLA1 correlate with GPC levels and can be underexpressed in malignant compared to non-malignant mammary epithelial cells [74]. The gene (s) responsible for GPC-PDE has not yet been identified. Glycerophosphodiester phosphodiesterase domain containing 5 (GDPD5) is proposed as a candidate gene for GPC-PDE, as its expression has been shown to affect the enzymatic activity of GPC-PDE and consequently the GPC levels in mouse kidney cells [75]. To date, the role of GDPD5 in choline phospholipid metabolism of human breast cancer have not yet been investigated.



**Figure 1.3:** The biosynthetic (solid lines) and catabolic (dash lines) pathways of choline phospholipid metabolism. GDPD5 have been suggested as a candidate gene for GPC-PDE. However, its role in choline phospholipid metabolism of human breast cancer is still unknown. CHKA, choline kinase alpha; CTP, phosphocholine cytidyltransferase; CDP-Cho, cytidine diphosphate choline; CDP, diacylglycerol cholinephosphotransferase; PLA2, phospholipase A2; Lyso-PLA1, lysophospholipase A1; PLD1/PLC, phosphatidylcholine-specific phospholipase D1/C; GPC-PDE, glycerophosphocholine phosphodiesterase; GDPD5, glycerophosphodiester phosphodiesterase domain containing 5.

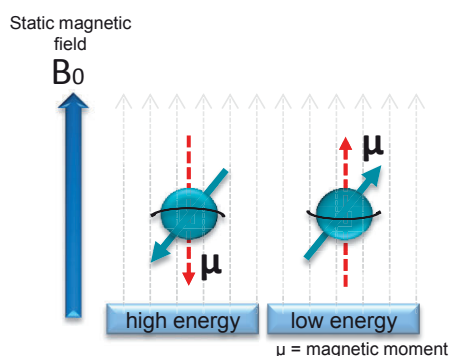


## 1.4 Magnetic resonance spectroscopy (MRS)

MRS is an analytical technique that provides identification and quantification of the metabolites. Metabolomics is the systematic study of metabolites present in a living system such as cells, tissues, biofluids, and organs. MRS metabolomics is emerging, and has provided essential information about the biochemical changes in cancers and other diseases [76-79]. Various metabolic biomarkers related to glycolysis and choline phospholipid metabolism have been reported using MRS analyses [19].

The MR spectrum is a plot of the intensity of MR signals versus the magnetic field frequency, usually given in parts per million (ppm). The MR signals stem from the interaction of radiowaves with atomic nuclei. In the presence of an external magnetic field ( $B_0$ ), atomic nuclei can absorb energy of characteristic frequencies, depending on the physical and chemical environment of the nucleus. In order for a nucleus to give rise to a MR signal, it must have a physical property called spin. The spinning nucleus generates a magnetic moment ( $\mu$ ), which is proportional to its spin quantum number ( $I$ ).

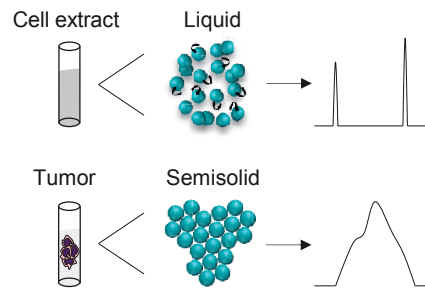
The most interesting nuclei for biological/medical MRS are hydrogen-1 ( $^1\text{H}$ ), carbon-13 ( $^{13}\text{C}$ ), and phosphorous-31 ( $^{31}\text{P}$ ). These nuclei have a spin quantum number  $I = \frac{1}{2}$ , i.e. they have two possible spin states. The spin states are of low or high energy, as the magnetic moment can be directed with or against the  $B_0$ , respectively (Figure 1.4). A small majority of nuclear spins will have their magnetic moment aligned with the  $B_0$  (designated Z-axis). This small excess of nuclei in the low energy state is the basis for the MR signal. By applying a radio frequency (RF) pulse, nuclei in the low energy state will be transferred to the high energy state. The energy difference between the low and



**Figure 1.4:** In the presence of an external magnetic field ( $B_0$ ) two spin states exist, the magnetic moment ( $\mu$ ) of low energy state and high energy state.

high energy state is dependent on the strength of the static magnetic field, thus the higher field strength, the higher sensitivity. Following an RF pulse, the excited nuclei interact with their environment, causing them to lose their excess energy and relax back to equilibrium. The emitted energy can be measured, as an MR signal. The nuclei return to equilibrium through processes characterized by two time constants called longitudinal ( $T_1$ ) and transversal ( $T_2$ ) relaxation.  $T_1$  describes the time it takes for spinning nuclei to re-align with  $B_0$  and is dependent on the nuclei interactions with the environment. Small molecules have low probability for interaction due to their fast movements which result in long  $T_1$ , while lipids and proteins have a higher probability for interaction due to their slow movements and thus exhibit relatively short  $T_1$ . The longitudinal magnetization is fully recovered to its equilibrium value after about five times  $T_1$ .  $T_2$  describes the time it takes for spinning nuclei to lose phase coherence due to magnetic field inhomogeneities and spin-spin relaxation arising mainly from neighboring nuclei. Large molecules, such as lipids and proteins, have higher interaction probability than smaller molecules and therefore shorter  $T_2$  values.  $T_2$  relaxation times is commonly utilized to reduce the signals from lipids and proteins by applying pulse sequences allowing  $T_2$ - weighted MR spectra.

MR spectra signals from solids or semisolids (e.g. tissues) are much broader than those from liquids (e.g. cell extracts). In liquid samples, the molecules are more mobile and the rapid isotropic motions of the nuclei can average the anisotropic nuclear interactions between the nuclei and effectively remove them from the spectrum, which results in spectra with narrow line width (Figure 1.5). In solid samples, the lack of molecular mobility leads to anisotropic nuclear interactions, such as magnetic dipolar interactions, electric quadrupolar, and electron shielding interactions between the nuclei. These interactions result in large anisotropic broadenings and spectra with broad and overlapping signals [80].

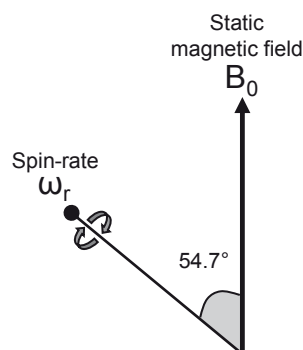


**Figure 1.5:** Liquid and semisolid MRS

### 1.4.1 High resolution magic angle spinning (HR MAS)

For nuclei with spin quantum number  $I = \frac{1}{2}$  (e.g.  $^1\text{H}$ ,  $^{13}\text{C}$ ,  $^{31}\text{P}$ ), line-narrowing in the MR spectra of solid samples can be achieved by imposing a motion on the nuclei which removes anisotropic sources of broadening. The principle of magic angle spinning (MAS) was first described by Andrew and Lowe in 1958 [81, 82]. Rapidly spinning of the solid samples at the magic angle, referring to the angle of 54.7 degrees, will mimic the motion of nuclei in a liquid state; resulting in sharp and highly resolved spectra, comparable with those from liquids.

When a sample is spun about an angle to  $B_0$ , the dipole interaction between the nuclei is dependent on the angle and the spin-rate ( $\omega_r$ ) (Figure 1.6). When the angle is 54.7 degrees, line broadening in solids can be reduced as some of the dipolar interactions are eliminated. Spinning the samples splits the broad signals into narrow lines, but it will also introduce low-intensity lines in the MR spectra that are spin-dependent, the so-called spinning sidebands. The intensity of the sidebands decreases with increasing spin rate. However, high-speed spinning can lead to destruction of tissue structures. The spin rates are chosen to eliminate the sidebands from the spectral region of interest. A wide range of spin rates, spanning from 1 Hz to 12 kHz, has been used for high-resolution magic angle spinning (HR MAS) studies. For samples analyzed with a 600 MHz spectrometer, a spin rate of 5 kHz provides good spectral quality while preserving the tissue structures [83].



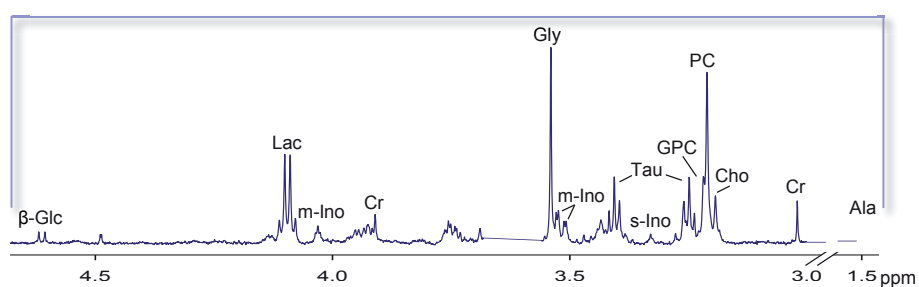
**Figure 1.6:** Schematic illustration of magic angle spinning MRS

*Ex vivo*  $^1\text{H}$  HR MAS MRS has been commercially available since the late 1990's. The technique is non-destructive and requires no difficult sample preparation before analysis. The sample remains intact for further analyses such as histopathology, proteomics, and transcriptomics, thus allowing for a comprehensive and detailed study of the biochemical composition of the tissue. This has contributed to an improved

understanding of biochemical changes that occur in cancer and during cancer treatment. It has been applied to several types of human cancers including brain [84, 85], breast [83, 86], and prostate [87, 88]. In addition, several studies have proven  $^1\text{H}$  HR MAS MRS as a promising tool for diagnosis and treatment monitoring of breast cancer [89, 90].

#### 1.4.2 Analyses of breast cancer spectra

$^1\text{H}$  HR MAS MRS metabolite profiles of breast cancer tissue have been shown to correlate to parameters of clinical importance, such as tumor grade, axillary lymph node status, and hormone receptor status [39, 91, 92]. More than 30 metabolites have been detected and assigned in breast cancer tissue [83]. Part of a  $^1\text{H}$  HR MAS MR spectrum including some of the most studied metabolites in breast cancer tissue is shown in Figure 1.7. Different approaches can be used to extract information from the MR spectra, of which multivariate data analyses and metabolite quantification are most common.



**Figure 1.7:** An example of the metabolite profile of breast cancer tissue obtained by  $^1\text{H}$  HR MAS MRS with the spectral region that was used in paper II. The signals from water, large lipid residuals, and ethanol contamination were removed prior to multivariate data analyses.  $\beta$ -Glc, beta glucose; Lac, lactate; m-Ino, myo-Inositol; Cr, creatine; Gly, glycine; Tau, taurine; s-Ino, scyllo-Inositol; GPC, glycerophosphocholine; PC, phosphocholine; Cho, free choline; Ala, alanine.

### ***Multivariate data analysis***

One of the many challenges for the analysis of  $^1\text{H}$  HR MAS MR spectra is the large number of variables (points in the MR spectra) compared to the low number of samples (individuals). Multivariate statistical methods are specialized to handle such data sets, and can be used in a reliable manner to identify biomarkers and/or discover metabolic features related to the discrimination between distinct classes.

### **Preprocessing**

Spectral preprocessing is a crucial step for building a precise and accurate multivariate model. There are many available methods for preprocessing the MR data. The chosen algorithms and parameter settings should be optimized to increase the quality of the spectra for multivariate modeling. Preprocessing methods including baseline correction, normalization, and peak alignment is usually recommended [93-95]. Mean normalization (also called area normalization) is a common method used to achieve an equal total area for each spectrum, without altering the relative intensities of the metabolite signals within the spectrum. This is used to compensate for individual differences in the samples, such as sample weight and total concentration of the metabolites. The peaks of MR spectra are usually not well aligned due to small variations in pH, temperature, and intermolecular interactions in the samples. Different peak alignment algorithms are available for correcting peak misalignment between the MR spectra, e.g. SpecAlign, *icoshift*, and COW [96-98]. In general, the algorithms are based on the insertion and deletion of spectral data points or intervals to shift regions in the spectrum to align with the corresponding region in a reference spectrum.

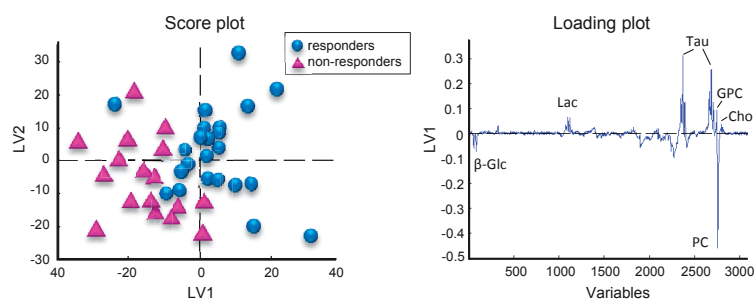
Variable selection for multivariate modeling can be performed by a genetic algorithms (GA), which is a supervised variable selection method based on the principles of genetics and natural selection [99, 100]. GAs generate a population comprising randomly subsets of selected variables (so-called ‘chromosome’) and uses them to produce the next generation via reproduction and mutation. The process is repeated a number of generation until an optimal population consistent of the most useful subsets of variables has been developed.

### **Multivariate methods**

Multivariate statistical methods such as principal component analysis (PCA) and partial least squares discriminant analysis (PLS-DA) can be used for finding linear relationships between the spectral data and clinical features, such as treatment response [101]. PCA explains the underlying variance structure of a data set through linear combinations of the variables. These linear combinations are called principal components (PCs). The first PC (PC1) covers the maximum variation of the data structure, PC2 covers the second largest variation in the data, but is completely uncorrelated to PC1 (orthogonal direction). Each following component accounts for as much of the remaining variability as possible. The goal of PCA is to filter out the noise and redundant data to compute the most important variance structure of the data, usually described by the few first PCs. By plotting the PCs against each other in a score plot, the hidden interrelationships between different variables can be revealed. The loadings show how much each variable contributes to each PC. The corresponding score and loading plots are complementary and can be used to interpret the model. PCA is an unsupervised method, thus it explains the experimental data (e.g. spectral data) without taking into consideration any other relevant information such as clinical data. However, PCA is useful for the initial description of sample patterns and to detect outliers before carrying out more sophisticated multivariate data analyses.

PLS-DA is a supervised data compression method used to detect the relationships between two matrices; experimental data ( $\mathbf{X}$ ) and the response variables ( $\mathbf{Y}$ ). PLS-DA aims to find underlying structures, called latent variables (LVs) that maximize the covariance between  $\mathbf{X}$  (e.g. spectral data) and  $\mathbf{Y}$  (e.g. treatment response). The  $\mathbf{Y}$ -matrix consists of so-called “dummy variables”, classifying each sample in this example as either responders (-1) or non-responders (+1). In a similar manner as for PCA, the corresponding score and loading plots are used to identify the differences in the metabolite profile between classes, and subsequently to discover potential biomarkers for the clinical feature being investigated, see Figure 1.8. The variable importance in the projection (VIP) scores can be used to assist the identification of metabolites of importance for the classification [102].

Multilevel PLS-DA is an extension of the ordinary PLS-DA and can be used to investigate the paired structure within the different subjects [103, 104]. This analysis can only be applied for data with multilevel structure, i.e. when interventions are evaluated on the same subject. In multilevel PLS-DA, the *between* subject variation resulting from differences in age, disease state, genetics, and other factors, is separated from the *within* subject variation, thus enabling the detection of metabolic changes caused by the intervention. The between subject variation is described by the average of the two observations from one subject, whereas the within subject variation is described by the net difference between them [103]. After the split-up of variation, ordinary PLS-DA classifications of the within or between subject variations can be performed.



**Figure 1.8:** A constructed example of the PLS-DA score and loading plots of responders and non-responders to a given treatment. The score plot shows the sample inter-relationships, thus similar samples are located close to each other. The loading plot shows the variable inter-relationship and is used to interpret the reasons behind the object distribution. The scores and variables close to zero have no influence on the classification. In this example, the different classes are well discriminated by latent variable 1 (LV1). Responders have positive scores for LV1 and appear to have more of the metabolites lactate, taurine, GPC and Cho, while non-responders have negative scores for LV1 higher levels of PC and  $\beta$ -glucose.  $\beta$ -Glc, beta glucose; Lac, lactate; Tau, taurine; GPC, glycerophosphocholine; PC, phosphocholine; Cho, free choline.

### **Validation**

Validation of multivariate models is necessary to measure the robustness of the models and to find the optimal dimensionality in order to avoid either overfitting or underfitting. Validation methods such as cross-validation, test set data, and permutation testing are used to assess the significance of the models. During validation the dataset is split in two parts; (1) a training set for model calibration and (2) a test set for model validation. In “leave one out” or full cross-validation only one sample is used for testing at a time, while the remaining samples ( $n-1$  when there are  $n$  observations) are used for training. The procedure must be repeated until all samples have been validated once. The classification result for each sample is summed and the average represents the validated classification result of the model. Full cross-validation may give too optimistic results due to data overfitting, but is a convenient choice for data sets with low sample numbers ( $n \sim 20$ ). For larger data sets, validation by test set data using a defined percentage of the samples for testing and the remaining for training is more appropriate. Limiting the number of LVs is necessary in order to achieve a reliable model. The minimum number of LVs with the minimum classification error determined by cross-validation can be used to optimize the number of LVs.

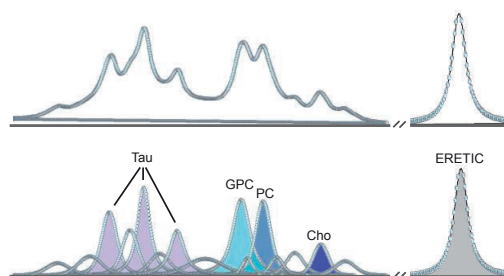
A permutation test can be used to evaluate the statistical significance of the classification results [101]. Permutation testing is performed by randomly assigning the class labels to the samples. The permutation procedure is then repeated a number of times and for each time the permuted classification result is calculated. The classification result of the original model can then be compared to the distribution of classification results from the permutation procedure.



**Metabolite quantification**

MRS is a powerful tool for quantification of metabolites present in a sample since the area of a given signal in the MR spectrum is proportional to the number of nuclei responsible for that signal. The area of a reference signal with known concentration can thus be used to perform absolute quantification. Accurate determination of metabolite concentrations can provide important biochemical information for a better understanding of cancer behavior and progression.

Quantification of metabolites in intact breast cancer tissue is highly challenging due to the inherent complexity of the spectra and overlapping spectral signals from many metabolites. Moreover, the signals are also overlapping with the macromolecules like proteins and lipids. Peak integration is a simple and widely used method for peak area measurement in MR spectra. However, due to overlapping signals, more advanced model fitting methods should be applied, such as curve fitting. PeakFit (PeakFit v 4.12, SeaSolve Software Inc.) is a software that uses nonlinear curve fitting method to calculate the area of overlapping metabolite signals in a spectrum (Figure 1.9) [105]. Prior knowledge of the overlapping metabolite signals is essential to increase the quality of the fitting.



**Figure 1.9:** Metabolite quantification of a  $^1\text{H}$  HR MAS spectrum using a peak fitting algorithm (e.g. PeakFit) and an ERETIC reference signal. PeakFit enables the calculation of area from overlapping signals and by using the ERETIC as a reference absolute concentration of individual metabolites can be quantified. Tau, taurine; GPC, glycerophosphocholine; PC, phosphocholine; Cho, free choline; ERETIC; electronic reference to access in vivo concentration.

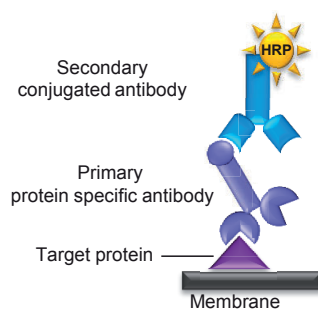
The use of a reference compound for absolute quantification of metabolites in tissue specimens is also challenging. An ideal reference for tissue metabolite quantification should be highly reproducible, not react chemically with the sample, and resonate away from the metabolite signals of interest. Trimethylsilyl propionic acid (TSP) is commonly used as an internal reference in  $^1\text{H}$  HR MAS spectroscopy of tissue [106]. However, the hydrophobic chain of TSP tends to interact with proteins and other membrane components present causing an overestimation of metabolite concentrations [107]. TSP is therefore more suitable as a reference for cell and tissue extracts than tissue samples.

Several studies have used the internal tissue water signal as a reference measured in an additional experiment without water suppression [84, 87]. However, the unsuppressed water signal is typically 1,000-10,000 times larger than most metabolites in the tissue. In addition, the relaxation time and the density of water are not constant in all tissues and tend to change in pathologies [108]. Therefore, extra consideration should be taken when evaluating the quantitative results using internal water as reference.

The electronic reference to access in vivo concentration (ERETIC) published in 1999 by Akoka *et al.* is a promising alternative to the use of an internal reference [109]. The ERETIC signal generates a “synthetic” peak of which the MR characteristics, e.g. frequency, linewidth, and magnitude, are modifiable. In addition, there are no concerns about metabolic activity. Furthermore, the ERETIC signal can easily be moved away from the metabolite region of interest [109, 110]. Calibration of the ERETIC signal to a standard of known concentration (e.g. sucrose or creatine) then permits the use of this signal to quantify metabolites of interest in the sample [110-112].

### 1.5 Gene and protein analyses

The combination of gene, protein and metabolite data is an advantage for the investigation of molecular pathway regulation. Quantitative real-time polymerase chain reaction (qRT-PCR) is a powerful and sensitive gene analysis technique for detection and quantification of a specific target sequence. Real-time detection of PCR products is made possible by using two oligonucleotide primers, forward and reverse, which are designed to specifically bind to the target sequence and a fluorescent molecule that reflects the amount of amplified PCR product. qRT-PCR data can be evaluated without gel electrophoresis resulting in reduced experimental time and increased throughput. Relative quantification of the gene expression can be determined by relating the PCR signal to a reference group, such as untreated controls or normal samples. Immunoblotting (Western blotting) allows for the identification of proteins according to their molecular weight by gel electrophoresis. The proteins are detected by using protein specific antibodies (Figure 1.10).



**Figure 1.10:** The principle of Western blotting analysis. Proteins are separated and transferred from the gel to a membrane. The membrane is exposed to the primary protein specific antibody in the present of a protein-rich solution to reduce non-specific binding. After several washing steps, the membrane is then exposed to the secondary antibody conjugated to a detectable molecule, e.g. horseradish peroxidase (HRP), which produces a colored band when incubated with the appropriate substrate.

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## **2 Aims**

The main objective of this thesis was to explore the metabolite profiles of locally advanced breast cancers and the effects of NAC. More specific, the goals were to:










- Evaluate whether MR metabolic profiling can assist the prediction of clinical treatment response in LABC patients receiving NAC
- Investigate the prognostic value of the MR metabolite profile in LABC patients
- Investigate the role of GDPDs in choline phospholipid metabolism of breast cancer cell lines and patient samples

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### 3 Materials and methods

The present thesis includes three papers presenting data from MR metabolomics, and gene and protein analyses of human breast cancer tissue and cell lines. A summary of the materials and methods used in the thesis is given in Table 3.1.

**Table 3.1** Materials and methods used in the papers I-III.

			Paper I	Paper II	Paper III
Materials		Human samples	Tissue samples n=33p/66s	Tissue samples n=89p/178s	Tissue samples n=19s
		Cell lines	-	-	MCF-12A (n=7) MCF-7 (n=10) MDA-MB-231 (n=8)
Methods		Tumor cell content	Histology sections	Imprint cytology	Imprint cytology
		Metabolomics	<sup>1</sup> H HR MAS MRS	<sup>1</sup> H HR MAS MRS	<sup>1</sup> H HR MAS MRS/ <sup>1</sup> H HR MRS
		Gene expression	-	-	qRT-PCR
		Protein expression	-	-	Western blotting
Data analyses		Metabolite quantification	PeakFit reference: ERETIC	Relative intensity	PeakFit/Integration reference: ERETIC/TSP or TMS
		Multivariate modeling	PLS-DA	Multilevel PLS-DA	-
		Gene and protein expression	-	-	Relative fold change

p, pair (pre- and post-treatment); s, samples; <sup>1</sup>H HR MAS MRS, proton high-resolution magic angle spinning magnetic resonance spectroscopy; qRT-PCR, quantitative real-time polymerase chain reaction; ERETIC, electronic reference to access in vivo concentration; TSP, trimethylsilyl propionic acid; TMS, tetramethylsilane; PLS-DA, partial least squares discriminant analysis.

### 3.1 Human breast cancer patients and cell lines

#### *The patients*

LABC patients (n=122) included in the three presented papers were enrolled in two large clinical studies evaluating predictive factors for response to NAC. The studies were approved by the Regional Ethical Committee (Norwegian Health Region III) and each patient gave written informed consent. The detailed description of the inclusion and treatment protocols is fully described elsewhere [113, 114]. In brief, female patients diagnosed with invasive breast cancer stage IIIA-C and a subset of stage IIB defined as T3-T4 (any N) or N2-N3 (any T) without distant metastasis (M0) were enrolled in 1991-2003. Patients with minor metastatic deposit (e.g. in the bone and liver) in addition to their locally advanced disease at the time of diagnosis were categorized as stage IV disease. These patients were also included in the studies providing they were candidates for surgical treatment of their primary local tumor after NAC. Patients with IBC were excluded in both studies due to their distinct clinical presentation and poor prognosis. Breast cancer tissue samples were obtained from an open biopsy procedure before NAC and during final surgery. The breast cancer tissue samples were snap-frozen immediately (~ 1 min) after removal and stored in -80°C.

#### *Patient treatment protocols*

All patients included in the studies received NAC. In paper I, the patients were treated with weekly doxorubicin (14mg/m<sup>2</sup>) for 16 weeks before surgery. In paper II, first line treatment with four doses of epirubicin (90 mg/m<sup>2</sup>) or paclitaxel (200 mg/m<sup>2</sup>) was administered to the patients every third week. In case of insufficient response or the tumor was still inoperable after four doses, cross-over to second line treatment or extension of four doses of the same first line treatment was given. In paper III, only pre-treatment breast cancer tissue samples were used. All patients underwent a mastectomy and post-operative radiation therapy. Patients with hormone receptor positive tumors (ER and/or PgR  $\geq 10$  fmol/mg protein [115] or  $\geq 10\%$  positive cells detected with immune histochemistry) were treated with tamoxifen for five years after surgery.



### ***Clinical treatment response and breast cancer survival***

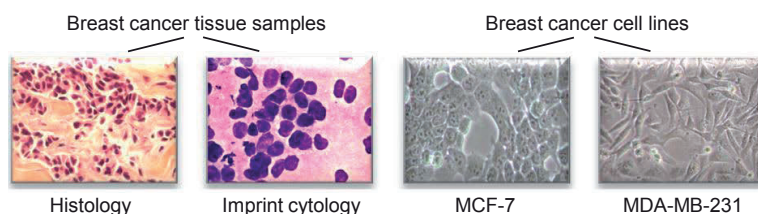
Clinical tumor response was evaluated by comparing caliper measurements pre- and post-treatment and assigned according to the WHO criteria (Table 1.2). Patients included in paper I and II had either a partial response or stable disease in response to NAC. Survival time was defined as the time interval from diagnosis until the end of the observation period (five years). Patients deceased within five years after diagnosis were classified as non-survivors whereas patients surviving five years or more were classified as survivors. Patients that died of other causes than breast cancer were censored.

### ***The cell lines***

All cell lines included in paper III were obtained from American Type Culture Collection (ATCC, [www.atcc.org](http://www.atcc.org)). Non-malignant MCF-12A and two malignant human mammary epithelial cell lines, MCF-7 and MDA-MB-231, were used in the cell experiments. MCF-7 is an estrogen-sensitive and weakly malignant, while MDA-MB-231 is an estrogen-independent and highly malignant breast cancer cell line. The cells were grown in their respective media supplemented with fetal bovine serum (FBS), penicillin, and streptomycin as previously described [116]. All cells were cultured at 37°C in 5% CO<sub>2</sub> and were used while sub confluent (approximately ~70%).

### ***Tumor cell content***

In paper I, breast cancer tissue samples were first analyzed by <sup>1</sup>H HR MAS MRS before formalin-fixed, embedded in paraffin, and stained with hematoxylin-eosin-saffron (HES). In paper II and III, imprint cytology smears were prepared from each tissue sample and stained with May-Grünwald-Giemsa prior to <sup>1</sup>H HR MAS MRS. The tumor cell content was determined microscopically by a pathologist. For cells in culture (paper III), trypan blue staining was used as vital stain for cell counting.



**Figure 3.1:** Microscopic images of breast cancer tissue samples and cultured cells.

### 3.3 $^1\text{H}$ HR MAS and $^1\text{H}$ HR MRS experiments

#### ***Sample preparation***

Patient tissue samples were blinded and randomized prior to  $^1\text{H}$  HR MAS MRS analysis (<http://www.random.org/lists/>). The samples were randomized based on chemotherapy agents (paper II), clinical treatment response, and pre- and post-treatment samples. Pair of samples (pre- and post-treatment) from each patient were analyzed in series to minimize experimental artifacts. Tumor tissue ( $15.5\pm 3.0$  mg) and phosphate buffered saline (PBS, 3  $\mu\text{l}$ ) in  $\text{D}_2\text{O}$  containing 98.2 mM TSP for chemical shift referencing were added to a 30  $\mu\text{l}$  leak-proof disposable insert (Bruker Biospin Corp, USA) and transferred to a MAS rotor.  $^1\text{H}$  HR MAS spectra were obtained using a Bruker AVANCE DRX600 spectrometer (Bruker Biospin GmbH, Germany). Samples were spun at 5 kHz at  $4^\circ\text{C}$  to minimize tissue degradation. Spin-echo spectra (cpmgrp; Bruker) were recorded for all the samples as previously described [39]. In addition, a single pulse experiment including the ERETIC signal (ereticpr.drx; Bruker) as a quantification reference [111] was performed for samples included in paper I and III.

For cell cultures, the lipid and water-soluble metabolites were extracted using a dual-phase extraction method based on methanol/chloroform/water as previously described [74]. The water-soluble and lipid fractions were dissolved in deuterated solvents containing  $0.24\times 10^{-6}$  mol TSP and  $2.17\times 10^{-7}$  mol tetramethylsilane (TMS) respectively, as quantification references and chemical shift standards. Fully relaxed  $^1\text{H}$  HR MRS spectra were obtained using a Bruker AVANCE 500 spectrometer (Bruker Biospin Corp).

**MRS protocols**

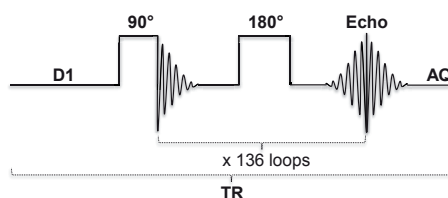
The different MRS protocols for the recorded spectra are summarized in Table 3.2.

**Table 3.2** MRS protocols

Method	Tissue samples		Cultured cells
	<sup>1</sup> H HR MAS MRS Bruker advanced 600 (14.1 T)		<sup>1</sup> H HR MRS Bruker advanced 500 (11.7 T)
Spectrometer			
Pulse program	Spin-echo cpmgpr; Bruker	Single pulse with ERETIC reference ereticpr.drx; Bruker	Single pulse zg; Bruker
Parameters	Paper I + II + III	Paper I + III	Paper III
Flip angle	90°	60°	45°
NS	128	128	128
Time domain size	32K points	64K points	32K points
AQ	1.64 s	3.28 s	0.819 s
Sweep width	10 kHz/16.7 ppm	10 kHz/ 16.7 ppm	6 kHz/ 12.0 ppm
TE	285 ms	-	-
TR	3.93 s	18.28 s	12.70 s

NS, number of scans; AQ, acquisition time; TE, total echo time; TR, repetition time.

The different acquisition times (AQ) used in the spin-echo and ERETIC pulse programs are appropriate for breast tissues. The single pulse spectra with the ERETIC reference of tissue samples and single pulse spectra of cultured cells were acquired with short flip angles (60° and 45°, respectively) and long repetition times to avoid saturation of the signals. The pulse sequence was repeated (NS=128) to achieve a good signal-to-noise ratio (S/N). The spin-echo sequence was used to suppress signals with short T<sub>2</sub> values (e.g. lipids and macro molecules). A total echo time (TE) of 285 ms was obtained by using a Carr-Purcell-Meiboom-Gill (CPMG) pulse sequence with 1 ms echo delay and 136 loops (Figure 3.2). Zero-filling was applied to increase the digital resolution (paper I-III, tissue samples). Spectra were Fourier transformed into 128 K after 0.3 Hz line broadening and chemical shifts were calibrated to the TSP signal at 0 ppm (paper I-III, tissue samples).

**Figure 3.2:** Schematic illustration spin-echo sequence used in paper I-III.

### 3.4 Gene and protein experiments

In paper III, total RNA isolation from human breast cancer tissue samples and cultured cells was performed using the RNeasy Mini Kit (Qiagen) according to the manufacturer's protocol. The concentration and purity of RNA yield were determined with a NanoDrop ND-1000 Spectrophotometer (Thermo Scientific). In addition, the integrity of RNA (RIN) of the tissue samples was measured using Bionalyzer 2100 (Agilent). Total RNA (1  $\mu$ g) was used for preparation of cDNA by SuperScript III First-Strand Synthesis SuperMix (Invitrogen). The mRNA levels of GDPD1-5, CHKA, and PLD1 were measured by qRT-PCR using the iCycler real-time PCR detection system (Bio-Rad) and iQ SYBR Green Supermix (Quanta BioSciences). Gene specific primers (Invitrogen) were designed using the Primer-BLAST tool (<http://www.ncbi.nlm.nih.gov>). The relative fold change (R) in gene expression was calculated based on the threshold cycle (ct) using the  $\Delta\Delta$ ct method as  $R = 2^{-\Delta(\Delta ct)}$  [117], where  $\Delta ct = ct(\text{target gene}) - ct(\text{housekeeping gene})$ , and  $\Delta(\Delta ct) = \Delta ct(\text{experiment sample}) - \Delta ct(\text{control sample})$ .

Protein isolation was carried out using lysis buffer containing a protease inhibitor cocktail (P8340, Sigma-Aldrich). GDPD5 Western blotting for the three tested cell lines was performed as previously described [116]. The proteins were denatured and separated by SDS-PAGE (sodium dodecyl sulfate–polyacrylamide gel electrophoresis). Thirty micrograms of total protein, as determined by a modified Lowry assay (Bio-Rad), was loaded in each lane, and two lanes were loaded with molecular weight standard (BenchMark, Life Technologies). The proteins were transferred to a membrane and incubated for 1 hour with a dilution (1:500) of primary polyclonal anti-GDPD5 antibody (Cat. No. AP10992c, Abgent Inc.) followed by incubation with horseradish peroxidase (HRP) conjugated secondary antibody (Amersham Life Science). Visualization was performed using the Supersignal West Pico chemiluminescent substrate kit (Pierce Biotechnology). The membrane was recorded on Blue Bio film (Denville Scientific). Quantitative densitometry of the GDPD5 proteins was performed using the Gel-analysis-tool in ImageJ (Wayne Rasband, NIH, Bethesda, MD). We did not have sufficient tumor material to run immunoblots on the patient samples.

### 3.5 Data analyses

Tissue samples with low tumor cell count and poor spectral quality were excluded from further analyses.

#### 3.5.1 Multivariate data analyses

The different preprocessing and validation methods of spin-echo spectra used for multivariate data analyses are presented in Table 3.3. Prior to spectral preprocessing, signals from water, large lipid residuals, and ethanol contamination were removed from the spectra. Data analyses were performed in Matlab R2009a (The Mathworks, Inc.) using PLS\_Toolbox 6.2.1 (Eigenvector Research).

**Table 3.3** Multivariate data analyses of spin-echo spectra

	<b>Paper I</b>	<b>Paper II</b>
	PLS-DA/ GA PLS-DA	Multi level PLS-DA/ PLS-DA
<b>Preprocessing methods</b>		
Average	Reduced by a factor of 2	Reduced by a factor of 2
Baseline correction	Baseline offset	Asymmetric least squares and baseline offset
Normalization	Equal total area	Equal total area
Peak alignment	SpecAlign	<i>icoshift</i>
Mean centering	yes	yes
Variable selection	Genetic algorithm	-
<b>Validation methods</b>		
Validation	Full cross-validation	10% random test set
Permutation	-	yes

PLS-DA, partial least squares discriminant analysis; GA, genetic algorithm.

Spectral data from each sample were reduced by a factor of 2 using the mean value of two consecutive data points. Baseline offset was corrected by shifting the minimum intensity value of each spectrum to zero. In paper II, asymmetric least squares baseline correction was used in addition to baseline offset [118]. The spectra were peak aligned using SpecAlign algorithm with the mean spectrum serving as reference (paper I) [96] and *icoshift* (paper II) [97]. Mean centering was performed by subtracting the average spectrum of all the spectra from each spectrum. GA variable selection prior to PLS-DA was performed in paper I.

In paper I, full cross-validation was used due to the low number of samples ( $n \leq 26$ ). In paper II, validation was performed with randomly chosen test set using 90% of the patients for training and the remaining 10% for testing. This procedure was repeated 20 times and the average validated classification results were calculated. To avoid biased results, the same number of LVs was used for all repetitions and was chosen by cross-validation of the whole data set. The VIP scores were used to assist the interpretation of the PLS-DA loadings. Permutation testing was performed by randomly assigning the class labels to the samples and the average results were calculated as described for the original data (90% training set, 10% test set, 20 repetitions). The permutation procedure was repeated 1000 times in which the class labels were reshuffled each time. The classification result of the original data was compared to the distribution of classification results from the permutation. P-values  $\leq 0.05$  were considered significant.

### 3.5.2 Metabolite quantification

The single pulse spectra with the ERETIC reference of tissue samples and single pulse spectra of cultured cells were used for metabolite quantification. Tissue metabolite quantification using curve fitting (PeakFit v 4.12, SeaSolve Software Inc.) and the ERETIC signal as reference was performed in paper I and III. The metabolite concentration was calculated using Equation I [111]. In paper III, metabolite quantification of cell extracts was determined by peak integration (MestReC 4.9.9.6 software, Mestrelab Research) using Equation II [74]. The signal integrals of TSP and TMS were used as references for the water-soluble and lipid extracts, respectively. In paper II, relative metabolite intensities were calculated by integrating the peak areas of spectra normalized to equal total areas after removal of signals from water, lipid residuals, and ethanol contamination (Matlab R2009a, The Mathworks, Inc.).

#### Equation I, tissue samples

$$[MET] \text{ mol/g} = \frac{A_{MET}}{A_{ERETIC}} \times \frac{1}{k_{MET}} \times \frac{n_{ERETIC}}{m_{sample}}$$

$A_{MET}$ : metabolite area  
 $A_{ERETIC}$ : ERETIC area  
 $k_{MET}$ : number of protons of the metabolite signal  
 $n_{ERETIC}$ : number of moles in the ERETIC signal  
 $m_{sample}$ : sample mass (gram)

#### Equation II, cell extracts

$$[MET] \text{ mM} = \frac{I_{MET}}{I_{TSP/TMS}} \times \frac{1}{k_{MET}} \times \frac{n_{TSP/TMS}}{m_{cell}} \times \frac{1}{m_{volume}}$$

$I_{MET}$ : metabolite integral  
 $I_{TSP/TMS}$ : TSP/TMS integral  
 $k_{MET}$ : number of protons of the metabolite signal  
 $n_{TSP/TMS}$ : number of moles in the TSP/TMS signal  
 $m_{cell}$ : cell count  
 $m_{volume}$ : cell volume

Statistical analyses were performed using SPSS (SPSS 16.0 Inc.). The Kolmogorov-Smirnov test was used to evaluate normality of the data. For normal distributed data, the statistical differences between multiple groups and paired samples were determined using two-tailed unpaired and paired T-test, respectively. For non-normal distributed data, the grouped Mann-Whitney and paired Wilcoxon Signed Ranks tests were used. P-values of  $\leq 0.05$  were considered to present significant differences between groups.

In paper I, receiver operating characteristic (ROC) curve analysis was performed using metabolite concentrations obtained from pre-treatment tumor tissue samples to define cut-off levels for prediction of treatment response and breast cancer survival.

### **3.5.3 Gene and protein expressions**

The Grubbs (GraphPad Software) test was performed to detect significant statistical outliers for each gene set (GDPD1-5, CHKA, and PLD1) of the patient tumor samples (significant level  $\alpha \leq 0.05$ ). Maximally one outlier was discarded per set. The normality of the data was evaluated by the Kolmogorov-Smirnov test (SPSS 16.0 Inc.). The unpaired two-tailed T-test (SPSS 16.0 Inc.) was performed to detect significant differences between the tested groups. Pearson correlation (SPSS 16.0 Inc.) was calculated to investigate the linear correlations between GDPD1-5 gene expressions and choline phospholipid metabolites in human breast tumors and cell lines, but also to examine the correlations between GDPD5 *versus* CHKA and GDPD5 *versus* PLD1 gene expressions. In human breast cancer cells, GDPD5 protein levels were also related to choline phospholipid metabolite and CHKA protein levels. P-values of  $\leq 0.05$  were considered to be significant.





## 4 Summary of papers

Paper I

### **Predicting long-term survival and treatment response in breast cancer patients receiving neoadjuvant chemotherapy by MR metabolic profiling**

This paper aimed to evaluate whether MR metabolic profiling can be used for prediction of long-term survival ( $\geq 5$  years) and monitoring of treatment response in LABC patients receiving doxorubicin monotherapy.

$^1\text{H}$  HR MAS MR spectra of pre- and post-treatment tissue samples from LABC patients ( $n=33$ ) were acquired. Tissue metabolite concentrations of PC, GPC, Cho, glycine, and taurine were quantified using PeakFit and the ERETIC signal as reference. ROC curves analysis was performed to define their potential to predict patient survival and treatment response. The MR metabolite profiles were related to long-term survival and treatment response by PLS-DA and PLS-DA with GA variable selection.

A significant decrease in GPC post-treatment was associated with long-term survival ( $p=0.046$ ) and partial response ( $p=0.014$ ) to NAC. Long-term survival was best predicted by GPC using ROC analysis (sensitivity 66.7%/specificity 62.5%), while taurine had the best predictive value of clinical treatment response (sensitivity 72.7%/specificity 63.2%). GA PLS-DA multivariate classification models successfully discriminated between patients with long-term survival ( $\geq 5$  years, survivors) and patients who died of breast cancer recurrence ( $< 5$  years, non-survivors), resulting in 82.7% and 90.2% CV classification accuracy, pre- and post-treatment, respectively. The pre-treatment MR metabolite profiles of survivors were characterized by higher levels

of tCho and lower levels of lactate compared to non-survivors. Classification of clinical treatment response using GA PLS-DA was not successful for this patient cohort.

Our results demonstrate that  $^1\text{H}$  HR MAS MR metabolic characteristics of breast tumors could potentially assist the classification and prediction of long-term survival in LABC patients, in addition to being used for evaluation of treatment response to NAC.

#### Paper II

#### **Prognostic value of metabolic response in breast cancer patients receiving neoadjuvant chemotherapy**

The aim of this paper was to examine the tumor metabolic changes in patients with LABC caused by NAC, and relate these changes to long-term survival ( $\geq 5$  years) and clinical treatment response.

LABC patients (n=89) participating in a randomized multicenter study were allocated to receive either NAC as epirubicin or paclitaxel monotherapy. Tumor tissue samples obtained pre- and post-treatment were analyzed by  $^1\text{H}$  HR MAS MRS. MR metabolite profiles were examined by PLS-DA and paired PLS-DA (or multilevel PLS-DA). The metabolites most important for the classification were identified by VIP scores and quantified by spectral integration of the metabolite peaks.

All patients had a significant metabolic response to NAC, and the pre- and post-treatment spectra could be discriminated with 68.9% and 87.9% CV classification accuracy by PLS-DA and multilevel PLS-DA, respectively ( $p < 0.001$ ). The metabolic responses appear to be similar for the two chemotherapeutic agents. Different metabolic responses to NAC were observed in patients with long-term survival ( $\geq 5$  years, survivors) and patients who died of breast cancer recurrence ( $< 5$  years, non-survivors). Survivors experienced a decrease in the levels of GPC ( $p < 0.001$ ), PC ( $p < 0.001$ ), Cho ( $p = 0.013$ ), glycine ( $p = 0.047$ ), and increase in glucose ( $p = 0.002$ ) levels in response to

NAC, while non-survivors had an increase lactate ( $p=0.004$ ) levels in response to NAC. The metabolic responses to NAC were similar in the different clinical treatment responses.

To conclude, the tumor metabolic response to NAC was related to breast cancer survival, but not to clinical treatment response. Monitoring metabolic responses to NAC by  $^1\text{H}$  HR MAS MRS may provide information related to individual prognosis.

Paper III

**Glycerophosphodiester phosphodiesterase domain containing 5 (GDPD5) expression correlates with malignant choline phospholipid metabolite profiles in human breast cancer**

Choline phospholipid metabolism is altered in cancer. The gene(s) encoding for the GPC-PDE(s) responsible for GPC degradation in breast cancers have not yet been identified. In this paper, we aimed to investigate the role of GDPDs in choline phospholipid metabolism in breast cancer.

Two human breast cancer cell lines ( $n=8$  and  $10$ ) and primary human breast tumor samples ( $n=19$ ) were studied with combined MRS and qRT-PCR to investigate the potential role of GDPD1-5 as GPC-PDE encoding genes and to determine their relationship with CHKA and PLD1 in choline phospholipid metabolism.

Out of five GDPDs tested, GDPD5 was found to be significantly overexpressed in highly malignant ER<sup>-</sup> compared to weakly malignant ER<sup>+</sup> human breast cancer cells ( $p=0.027$ ) and breast tumors from patients ( $p=0.015$ ). GDPD5 showed significantly positive correlations with PC ( $p<0.001$ ), total choline (tCho) ( $p=0.007$ ) and PC/GPC ( $p<0.001$ ) levels in human breast tumors. GDPD5 showed a trend towards negative correlation with GPC levels ( $p=0.130$ ). Human breast cancers with malignant choline metabolite profiles consisting of low GPC and high PC levels highly co-expressed

### Summary of papers

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GDPD5, CHKA, and PLD1, while cancers containing high GPC and relatively low PC levels displayed low co-expression of GDPD5, CHKA, and PLD1. GDPD5, CHKA and PLD1 were significantly overexpressed in highly malignant ER<sup>-</sup> tumors in our patient cohort.

Our study identified GDPD5 as a GPC-PDE that likely participates in regulating choline phospholipid metabolism in breast cancer, which possibly occurs in association with CHKA and PLD1.

## 5 Discussion

The metabolic characterization of breast tumors by  $^1\text{H}$  HR MAS MRS may assist the prediction of long-term survival in LABC patients (paper I and II). The tumor metabolic responses to NAC were related to breast cancer survival, but not to clinically measured treatment response (paper II). High levels of lactate and glycine post-treatment were associated with poor outcome, while decreased choline phospholipid metabolite levels were observed in response to NAC in patients with long-term survival (paper I and II). Furthermore, *GDPD5* was identified as a possible regulatory gene in choline phospholipid metabolism in breast cancer, and high co-expression of *GDPD5*, *CHKA*, and *PLD1* were associated with increased malignancy (paper III).

### 5.1 Patients and tumor samples

The tumor samples obtained from open biopsies before NAC and during final surgery were collected from LABC patients from 1991 to 2003. All samples were immediately (~ 1 min) snap frozen after removal and stored in  $-80^\circ\text{C}$  until used for  $^1\text{H}$  HR MAS MRS analysis in 2008 (paper I) and 2009 (paper II and III). No significant correlations have so far been found between storage time and tissue metabolite degradation determined by  $^1\text{H}$  HR MAS MRS [39, 119]. Furthermore, the tissue metabolite concentrations determined in our study are comparable to those previously reported for breast cancer tissue samples stored for five years or less [39, 111]. The integrity of RNA quantified by RIN-values was good (paper III). Altogether, this suggests that the storage procedure maintains the quality of the samples well, and potential gene and metabolite degradations should be minimal.

As  $^1\text{H}$  HR MAS MRS is a non-destructive method, tissue samples were further used for histological examinations to confirm the tumor cells content (paper I). In paper II and III, imprint cytology was used instead of histological sections to confirm the tumor cell content. Imprint cytology has been found to be a reliable, rapid, and easy complementary examination to histological sectioning [120]. Furthermore, the use of imprint cytology advantageously enabled the tissue samples to be further analyzed for gene and/or protein expressions after  $^1\text{H}$  HR MAS MRS (paper III).

## 5.2 Metabolomics analyses

Metabolomics analyses assess the downstream products of gene and protein expressions, and have shown to provide both predictive and prognostic information for several types of cancers [76, 77]. Multivariate and quantitative analyses of the  $^1\text{H}$  HR MAS MR spectra are of key importance for interpreting findings and validating the results. Therapeutic response is often not associated with the change in one biomarker, but rather with the combined influence of many molecular compounds. Multivariate statistical methods were used to identify patterns of several metabolites simultaneously and to discover metabolic features related to the discrimination between distinct classes. Absolute metabolite quantification has an added value, since the concentrations obtained can be compared to other studies and may be easier to interpret in a clinical setting.

MR metabolite profiles of LABC tumors were related to treatment response and long-term survival by PLS-DA and multilevel PLS-DA multivariate statistical methods. Proper validation of the PLS-DA models is necessary to avoid biased results. In paper I, validation of the multivariate models was performed by full cross-validation. This method is simple and widely used, but is also known to give large variance that may lead to overfitting of data and too optimistic results. However, full cross validation was a convenient choice for this smaller size data set when there were not enough samples for a separate test set. In paper II, validation was performed using randomly selected test sets and permutation testing. To avoid overfitted results, the number of LVs was optimized by cross-validation of the whole data set and the same number of LVs was

used for calculation in all repetitions. It is important to keep in mind that the result of classification models is largely dependent on the validation procedure and also the size of the data set, and that too optimistic results are usually due to inappropriate choice of validation [101].

The study of the metabolic changes in tumors during NAC is important as it can assist in improving treatment of breast cancer patients focusing on personalized treatment strategies. Multilevel PLS-DA is a relatively new method for multivariate investigation of the paired structure within the different subjects [103] and was therefore used in paper II. This method enabled the detection of metabolic changes caused by NAC within each patient by subtracting the between patient variations from the data. Metabolic changes detected by multilevel PLS-DA were significantly better than unpaired PLS-DA, resulting in 87.9% versus 68.9% CV classification accuracy, respectively (paper II). Thus, taking advantage of the multilevel structure in the data set was clearly beneficial.

Metabolites that were found to be important for the multivariate classification models were quantified (paper I and II). To quantify the metabolites in the  $^1\text{H}$  HR MAS MR spectra, the area of the peaks was determined by curve fitting (paper I and III). Spectral prior knowledge (multiplicity etc) is essential for the quality of the fit. Curve fitting is a proper method for area determination of multiple overlapping signals and is a more accurate and reliable method than peak integration. However, curve fitting by Peakfit can be time-consuming. Automatic model-based curve fitting, such as LCModel [121], has been used for quantification of  $^1\text{H}$  HR MAS spectra of brain tissue [122, 123]. LCModel facilitates the separation of overlapping signals by fitting the data to a linear combination of the complete spectra from pure metabolite solutions; so called basic sets [123]. Such basic sets have not been generated for  $^1\text{H}$  HR MAS MRS spectra of breast cancer. Curve fitting using PeakFit can be biased by subjective interpretations. Routines for curve fitting were standardized, and curve fitting was performed by one user (paper I and III). We thus consider the inter-spectral effects on peak area calculations to be small. In paper II, the relative metabolite intensities were found by integrating the peak areas in mean normalized spectra. This approach is useful in terms of confirming the

significant differences in the metabolite levels as observed in the loading plots from multivariate analyses. However, the intensity values are not transferable for comparison with results from other studies.

The electronic external reference method ERETIC used in paper I and III is a promising alternative to the use of internal quantitative references [109-111]. There are no concerns about metabolic activity and visibility when using ERETIC. However, quantification using the ERETIC signal is more sensitive to RF field inhomogeneities of HR MAS probes [124] than chemical internal references such as TSP [111]. The effect of RF field inhomogeneities can be reduced by using an insert which ensure that the sample is within the most homogeneous range of the RF coil, thus minimizing signal loss (paper I-III). A higher relative error for ERETIC (8.4%) compared to TSP (2.7%) has been observed using  $^1\text{H}$  HR MAS MRS for quantification of creatine in a standard solution [111]. However, ERETIC is still considered as the best approach for quantifying tissue metabolites in  $^1\text{H}$  HR MAS MRS, as TSP can bind to proteins and other membrane components present in the sample causing an overestimation of metabolite concentrations. Periodical calibration of the ERETIC signal is necessary for ensuring accurate quantification over time [109, 110]. In this thesis, the samples were randomized and analyzed within a short period of time to reduce the effect of calibration and technical artifacts. Pulse length based concentration determination (PULCON) is another external reference technique that uses the principal of reciprocity to correct absolute intensities relative to an external standard spectrum [125, 126]. To our knowledge, no studies using PULCON for quantitative  $^1\text{H}$  HR MAS MRS have so far been published (Pubmed, Scopus).

Metabolite quantification was related to tissue sample weight, as done in previous studies of  $^1\text{H}$  HR MAS MRS [39, 111, 127].  $^1\text{H}$  HR MAS signals of tumor tissue samples arise from both cancer cells and tumor stroma. The spectra therefore represent the average signal from all the constituents in the sample. In general, this is also the case for other types of molecular profiling analyses, including transcriptomics and genomics.



### 5.3 MR metabolic profiling and clinical treatment response

The most beneficial use of NAC for LABC patients is still under discussion, and both combinations of different chemotherapies, but also monotherapy, have been suggested [10, 128, 129]. Studies investigating chemoresistance to monotherapy as well as the combination of chemotherapies can help optimize and improve the treatment of breast cancer. The clinical response is also of interest as a surrogate marker for survival. Several studies have shown that pathological complete response (pCR) to NAC, which is obtained in 3-26% of breast cancer patients is associated with improved recurrence-free and overall survival [10, 21]. Thus, an improved understanding of breast tumor molecular characteristics would be essential in the design of personalized cancer therapy, thereby achieving better prognosis.

In this thesis, no valid multivariate classification models for the prediction of clinical response could be generated using pre- or post-treatment spectra (paper I and II). In paper I, metabolic changes in response to NAC were evaluated by comparing quantified individual metabolites obtained pre- and post-treatment, because multilevel PLS-DA was yet not implemented as one of our multivariate analytical tools. In patients with partial response, only GPC was found to be significantly decreased, and a decrease in tCho approached significance. In paper II, all patients experienced significant metabolic changes in response to NAC analyzed by multilevel PLS-DA. However, similar metabolic responses were observed in both patients with partial response and with stable disease. In both groups, treatment led to increased levels of lactate and glycine and decreased levels of GPC, while the levels of PC were markedly decreased for some patients. These metabolic changes were similar to those observed for the entire patient cohort.

The tCho level detected with *in vivo* MRS has been suggested as a biomarker for diagnosis and treatment evaluation of breast cancer [57, 58]. Several studies have found decreased tCho levels in response to NAC to be associated with better clinical response [60, 62, 130-132]. Docetaxel treatment of MCF-7 breast cancer xenografts also resulted in decreased *in vivo* tCho levels and cell density [133]. In another study, *ex vivo* PC

levels were found to decrease after treatment with docetaxel in MCF-7 breast cancer xenograft models [134]. Significantly decreased GPC levels in patients with partial response may suggest a better response to NAC (paper I). Unfortunately, GPC cannot be distinguished from the other choline metabolites by *in vivo* MRS due to low spectral resolution.

The lack of patients with progressive disease and complete response in our analyzed cohort could help explain why no clear metabolic differences in response to NAC between the two response groups were observed (paper I and II). According to the protocol, treatment should be interrupted if/when the patients experienced progressive disease. For patients with complete response, no tumor tissue is left for a post-treatment sample. For these patients, examination of metabolic changes in response to NAC of tissue samples taken at an earlier time point than at final surgery would be of interest. Inclusion of pre-treatment samples of patients with progressive disease and complete response could contribute to reveal clearer differences in metabolite profiles between the clinical response groups that can be used to assist the prediction of clinical response.

The finding that all patients had a similar metabolic response to NAC could be due to the fact that only two patients had an equal or increased tumor size after NAC (paper II). Thus, nearly all patients thus had a reduction in tumor size, although the tumor reduction was small for patients with stable disease. In this thesis, treatment response was defined according to the WHO criteria (Table 1.2), which define stable disease as < 50% reduction to < 25% increase in tumor volume. We can postulate that different response criteria for stable disease (lower threshold for reduction in tumor volume) can affect the findings in paper I and II. The differences in response criteria have shown to influence the prediction of response to NAC by *in vivo* MRI [135].

The fact that all patients had a significant metabolic response to NAC could suggest a difference in metabolite profiles due to differences in sampling procedures for the two time points. However, the tumor samples obtained before NAC were excised during open biopsy surgery, which should be quite comparable to the sampling procedure at final surgery. Moreover, all samples were snap-frozen and stored in the same way.

Thus, we consider the differences in sampling procedures at pre and post-treatment to have small effects on the metabolite profiles.

The metabolic response to NAC is also dependent on the molecular effects of the given chemotherapeutic agents. Anthracyclines, such as doxorubicin and epirubicin, are capable of inducing DNA strand breakage and apoptosis [23-25], while paclitaxel causes mitotic arrest by disturbing the breaking and rearranging of microtubules in the cells [26]. However, the main function of all these drugs is to cause disturbance of the cell cycle and cell death. The metabolic responses to epirubicin and paclitaxel could not be distinguished, which suggests that they have the similar effects on tumor cell metabolism (paper II).

#### 5.4 MR metabolic profiling and long-term survival

The definition of long-term survival is not unified in the literature. A long-term survivor is defined by the American Cancer Society as a person who is still alive 5 years after diagnosis [136]. LABC consist of a heterogeneous group of patients with variable prognosis and with a lower 5-year survival rate than early stage breast cancer [10]. We thus consider the use of the term long-term survival to be appropriate for our studies.

Altered cell metabolism is suggested as a new emerging hallmark of cancer [34]. MR detected metabolite profiles have been found to assist the diagnosis and treatment monitoring of breast cancer [89, 90], and have also been found to correlate to parameters of clinical importance such as tumor grade, axillary lymphatic spread, and hormone receptor status [39, 91, 92]. LABC patients constitute a heterogeneous group with variable prognosis, and it is therefore a challenge to identify valid prognostic factors for this patient group. In addition, prediction of survival in LABC patients receiving NAC is difficult as the treatment will affect the prognostic value of tumor size, grade and lymph node status.

Several studies have shown that a pathological complete response to NAC is associated with improved breast cancer survival [21, 22]. However, approximately 80% of patients will have residual tumor in the breast after NAC [22]. Thus, molecular characterization with identification of new prognostic factors and therapeutic targets for breast cancer would greatly benefit the assessment of prognosis.

In this thesis, the potential of MR metabolomics to predict long-term breast cancer survival was investigated. A summary of the main findings is presented in table 5.1. In paper I, metabolic changes in response to NAC were detected by quantification of individual metabolites. Lactate could not be quantified using the present  $^1\text{H}$  HR MAS MRS protocol due to heavily overlapping signals from lipids. In paper II, different metabolic responses to NAC were observed in survivors and non-survivors by multilevel PLS-DA.

Prediction of long-term survival was investigated using  $^1\text{H}$  HR MAS spectra of pre- and post-treatment tumor samples by PLS-DA and metabolite quantification. In paper I, long-term survival could be predicted using pre- and post-treatment spectra. Better classification was obtained post-treatment. In paper II, long-term survival could only be predicted from the post-treatment spectra. These results suggest that the difference between survivors and non-survivors post-treatment is mainly caused by metabolic response to NAC. Thus, the metabolite profiles of post-treatment samples may be a better and more accurate indicator of patient prognosis than pre-treatment samples.

## Discussion

**Table 5.1** Summary of metabolite profiles pre- and post-treatment and metabolic changes observed by multivariate analysis and quantification related to long-term survival in paper I and II.

		Paper I		Paper II	
		Multivariate	Quantification	Multivariate	Quantification
Metabolite profiles	Pre-treatment non-survivors vs survivors*	↑ Lac ↓ tCho	No significant values	No significant model	NA
Metabolic changes in response to treatment	Survivors	NA	↓ GPC and Cho	↓ GPC	↓ Gly, GPC, PC, and Cho
	Non-survivors	NA	No significant values	↑ Lac	↑ Lac
Metabolite profiles	Post-treatment non-survivors vs survivors*	↑ Lac, Gly, and tCho	No significant values	↑ Lac, Gly	↑ Gly

NA, not applicable. \*the results describe the metabolite profiles of non-survivors compared to survivors. Metabolite quantification was performed for Lac (not in paper I), Gly, GPC, PC, Cho, and Tau.

In paper I, higher levels of lactate were observed pre- and post-treatment in non-survivors compared to survivors. In paper II, non-survivors had a significant increase in lactate levels resulted in higher lactate levels in non-survivors compared to survivors at post-treatment (paper II). High lactate levels have been found to correlate with increased risk of radiation resistance, high incident of distant metastases and recurrence, and low survival rates in several types of cancers [42-44]. However, molecular mechanisms behind the role of lactate on malignant behavior of cancer cells are not fully understood. Recently, modification of cell energy metabolism has been suggested as an emerging hallmark of cancer [34]. Cancer cells can reprogram their energy metabolism to convert most glucose to lactate regardless of the oxygen supply, a phenomenon known as aerobic glycolysis (the Warburg effect). Aerobic glycolysis is possibly an adaption to intermittent hypoxia; protecting cancer cells from acid-induced toxicity, and facilitating the uptake and incorporation of nutrients needed for cell proliferation [36, 37]. In return, HiF-1 hypoxia induced gene can accentuate glycolysis by activation of multiple enzymes involved in the glycolytic pathway, including LDH,

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the enzyme responsible for conversion of pyruvate to lactate [46-49, 51, 52]. Lactate may therefore serve as a marker for both aerobic glycolysis and hypoxic responses in tumors. Increased aerobic glycolysis and tumor hypoxic responses have been shown to facilitate cell proliferation, resistance to apoptosis, angiogenesis, and increased risk of metastasis in cancers [37, 38, 50]. Inhibition of LDH has shown to reduce the glycolytic activity associated with a decrease in tumor proliferation of breast cancer animal models [137]. In breast cancer, HiF-1 expression is highly associated with tumor progression, metastasis, therapy resistance and mortality [138, 139]. Anthracyclines have been shown to inhibit the transcriptional activity of HiF-1 by blocking its binding to DNA [140]. Thus, increased lactate levels observed in non-survivors in response to NAC may also be a marker for chemotherapy resistance in these patients. It has also been suggested that the resulting low pH mediated by high lactate levels may enhance the invasiveness of tumor cells and help them evade tumor-attacking immune cells [141]. This thesis suggests that the increased levels of lactate in response to NAC and higher lactate levels post-treatment observed in non-survivors may reflect enhancement of aerobic glycolytic activity and/or tumor hypoxic responses related to higher tumor malignancy and poor prognosis. Coherently, the glucose levels were increased in survivors but not in non-survivors in response to NAC (paper II). Increased glucose may be indicative of decreased aerobic glycolysis and tumor hypoxic response favorable of long-term breast cancer survival.

In response to NAC, survivors had a significant decrease in glycine levels (paper II). This was reflected in the post-treatment spectra, showing significantly higher levels of glycine in non-survivors compared to survivors. The role of glycine in tumor malignancy is still unclear. Glycine is a downstream product of 3-phosphoglycerate, an intermediate of the glycolysis, but it can also be synthesized from Cho through the glycine-betaine pathway. The biomarker potential of glycine has been studied in human brain tumors, where it was found to positively correlate with tumor grade [40, 41]. Higher levels of glycine have been detected in the more aggressive basal-like breast cancer animal model compared to the luminal-like model [142]. This thesis suggests that the decreased glycine levels detected in survivors in response to NAC can possibly

be caused by altered glycolysis and/or reduced Cho levels associated with reduced tumor malignancy.

In paper I, higher levels of tCho were observed in survivors compared to non-survivors before NAC. In response to NAC, survivors experienced a significant decrease in GPC and Cho measured by quantification. After NAC, lower levels of tCho were observed in survivors compared to non-survivors in the loading plot. However, the differences in tCho levels determined by quantification were not significant, probably due to high interpatient variation. In paper II, survivors experienced a significant decrease in GPC, PC, and Cho levels in response to NAC. The loading plot shows decreased GPC levels in survivors, while the levels of PC were markedly decreased for some patients. Overall, choline metabolite levels decreased in response to treatment in survivors, and appear to be higher in non-survivors compare to survivors post-treatment.

The choline phospholipid metabolism is associated with proliferation, oncogenic signaling, and also tumor hypoxic responses [57]. PC and tCho levels have been shown to increase with increased malignancy in breast cancer cells [66]. CHKA, the enzyme that regulates the phosphorylation of Cho to PC, is known to play an important role in malignant transformation in several types of cancers [143]. Moreover, tCho levels have been shown to correlate with tumor grade and pharmacokinetic parameters of breast tumors, indicating a relation between choline phospholipid metabolism and tumor malignancy, but also angiogenesis [144, 145]. Hypoxic tumor regions co-localize with regions of high tCho, possibly occurring through the up-regulation of CHKA by HiF-1 $\alpha$  [65]. This thesis demonstrates that LABC patients with decreased choline phospholipid metabolite levels, in particular GPC levels, in response to NAC have a better survival rate. Furthermore, MR metabolite profiles showing low levels of tCho, lactate, and glycine post-treatment could potentially be predictive of long-term survival. In a recent study, no differences in tumor tCho levels were found between early breast cancer patients with good and poor prognosis [111]. However, the assessment of prognosis in that study was based on the TNM classification system and not survival time.

Five subtypes of breast tumors characterized by gene expression pattern have been identified [146, 147]. A recent study shows the potential of combining transcriptomics and MR metabolic data for a more refined sub-classification of human breast cancers [148]. It is possible that the combined gene expression and MR metabolomics profiles will improve the molecular characteristics of breast cancer and help identify biomarkers, or combination of biomarkers, which in turn can assist treatment stratification and the prediction of patient outcome.

### 5.5 GDPD5 in the regulation of choline phospholipid metabolism

Both PC and GPC are known to be altered in cancer. In ovarian cancer, relatively low GPC compared to PC is typically observed [149]. In brain tumor, GPC levels is the dominant choline component in low compared to high grade gliomas [122]. Elevated GPC levels have been detected in lung [150] and prostate [151] cancer tissues compared to non-involved tissues. In normal mammary cell cultures, the GPC levels are relatively higher than the PC levels. During malignant transformation PC increases while GPC decreases, resulting in a switch from low to high PC/GPC ratio in cell cultures [66]. In a recent study, higher concentrations of GPC have been observed in basal like (poor prognosis) compared to luminal like (good prognosis) breast cancer xenograft models [142]. While recent research studies have focused on the molecular causes leading to elevated PC levels in cancer, relatively little effort has been made to elucidate the molecular causes behind the changes in GPC levels in cancers. The gene or genes responsible for the changes in GPC levels detected in breast cancer is still unknown.

It is important to understand the molecular causes of the GPC levels detected in breast cancer because it is a part of the *in vivo* tCho signal that is increasingly being used in diagnosis and treatment monitoring of breast cancer patients [58-62]. As shown in paper I and II, targeting the enzymes involved in the regulation of GPC levels in breast cancers may be a good therapeutic target for anti-cancer treatment as significant decreased GPC in response to NAC was observed in patients with long-term survival and better clinical response.



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In paper III, the role of GDPD1-5 in the regulation of choline phospholipid metabolism of human breast cancer was studied with combined MRS, gene and protein expressions. Out of five GDPDs tested, GDPD5 was found to be significantly overexpressed in highly malignant ER<sup>-</sup> compared to weakly malignant ER<sup>+</sup> human breast cancer cells and breast tumor samples. GDPD5 showed significantly positive correlations with PC, tCho, and PC/GPC levels in human breast tumors, and a trend towards negative correlation with GPC levels. Human breast cancers with choline metabolite profiles consisting of high PC and low GPC levels highly co-expressed GDPD5, CHKA and PLD1, while cancers containing high GPC and relatively low PC levels displayed low co-expression of GDPD5, CHKA, and PLD1. High correlations were found between gene and protein levels of GDPD5 and CHKA.

GDPD5 is a ubiquitously expressed transmembrane protein in human tissues, but has a relatively low expression in kidney and prostate tissues [152]. It has been suggested as a candidate gene for GPC-PDE as down-regulation of GDPD5 efficiently increased GPC levels, while overexpression of GDPD5 contributes to GPC reduction in mouse renal cells [75]. As a candidate gene for GPC-PDE, the GDPD5 expression is expected to inversely correlate with the GPC level. However, the expression of GDPD5 showed only a modest inverse correlation with GPC levels in breast tumors and cells (paper III). This observation suggests the possibility of additional genes responsible for the altered GPC level observed in breast cancer. Nucleotide pyrophosphatases/phosphodiesterases 6 (NPP6) preferably hydrolyze choline-containing phospholipids or phosphodiester, including GPC [153]. To date, the role of NPP6 is still unknown. The GPC level is also regulated by the gene expression of PLA2 and LYSO-PLA1 [74]. The correlations between these genes and GDPD5 have not been studied.

The strong positive correlations between the expression of GDPD5 and PC, tCho, and PC/GPC levels are probable due to the co-expression of GDPD5, CHKA, and PLD1 observed in breast tumors (paper III). CHKA plays an important role in oncogenic transformation and carcinogenesis in cancers [68, 143, 154, 155]. PLD activity, which degrades PtdCho to Cho, also plays a significant role in oncogenic transformation [156]. Overexpression of CHKA and elevated PC and tCho levels of breast cancer cells have

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been associated with increases in invasiveness and drug resistance [157]. Treatment with the CHK inhibitor Mn58b has shown to reduce PC levels and inhibit proliferation of cancer cells, and Mn58b therefore appears to have a potential as an anticancer drug [158]. The strong positive correlations between GDPD5, CHKA and PLD1 observed suggest the expression of GDPD5 to be associated with malignancy. Targeting GDPD5 will most likely increase GPC levels. However, accumulation of GPC mediated by GDPD5 may disturb the cycle of Cho essential for renewed synthesis of PtdCho in the cell membrane. More studies are needed to investigate the mechanism and effects of GDPD5 for use as a target in cancer treatment.

Overexpression of GDPD5, CHKA, and PLD1 were found in ER<sup>-</sup> tumors compared to ER<sup>+</sup> tumors (paper III). ER status is an important factor for the prediction of prognosis and is routinely used for treatment planning in the clinic. Consistent with our results, overexpression of CHKA has been associated with ER<sup>-</sup> breast tumors in a previous study [68]. However, ER<sup>-</sup> human breast cancer tumors have been related with higher levels of GPC and lower levels of PC compared to ER<sup>+</sup> tumors [92]. The patients included in paper III have been stratified to match the ER status and choline metabolite profiles of the two breast cancer cell lines, MCF-7 and MDA-MB-231, thus a larger cohort is needed to elucidate the relationship between GDPD5 and ER status. This thesis identified GDPD5 as a GPC-PDE gene that likely participates in regulating choline phospholipid metabolism in breast cancer, which possibly occurs in cooperation with CHKA and PLD1.

## 6 Conclusions and future perspectives

In this thesis, MR metabolic profiling of tumor tissue obtained from LABC patients was used to predict long-term survival and clinical treatment response to NAC by multivariate data analyses and metabolite quantification. Furthermore, the role of GDPDs in choline phospholipid metabolism was investigated.

<sup>1</sup>H HR MAS MRS analysis of both pre- and post-treatment tumor tissue samples can be valuable as it provides information on metabolic changes in tumors during NAC. This thesis shows that epirubicin and paclitaxel had similar effects on tumor cell metabolism. It would be of interest to examine the metabolic responses in patients receiving other types of single drugs or multidrug treatment to improve the understanding of treatment effects on tumor metabolism.

No clear differences in metabolic responses were detected between patients with partial response and stable disease, thus the prediction of clinical treatment response by MR metabolomics was not successful. However, it is possible that a cohort including also patients with progressive disease would reveal clearer differences in metabolite profiles between the clinical response groups. Also, the chosen response criteria might have contributed to the unsuccessful prediction of clinical treatment response from metabolite profiles. Different response criteria should be tested, in particular pathological measured response. Molecular characterization of tumors may help stratifying patients for individualized treatment, thereby achieving better prognosis.

MR metabolite profiles of LABC patients contain prognostic information that is associated with survival status. In response to NAC, lactate is increased in non-survivors, while survivors experience a decrease in glycine and choline phospholipid

### Conclusions and future perspectives

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metabolites. These metabolic changes are associated with tumor proliferation, glycolytic activity and hypoxia related to tumor malignancy and prognosis. Metabolite profiles consisting of higher levels of lactate, glycine, and tCho observed in non-survivors post-treatment were shown to be predictive of low breast cancer survival rates. Monitoring metabolic responses to NAC by  $^1\text{H}$  HR MAS MRS may have the potential to assist the prediction of breast cancer survival and help identify new targets for therapeutic treatment.

The relative fold change in gene expression of GDPD5 was correlated with choline phospholipid metabolite levels and with CHKA and PLD1 expressions. Future studies examining the effect of silencing GDPD5 alone or in combination with CHKA and/or PLD1 in breast cancer cells and xenograft models may provide new information about the potential of GDPD5 as anticancer targets of breast cancer. Studies investigating the correlation between GDPD5 and NPP6, PLA2, and LYSO-PLA1 in choline phospholipid metabolism would be of interest. Overexpression of GDPD5, CHKA, and PLD1 were found in ER<sup>-</sup> tumors compared to ER<sup>+</sup> tumors. ER status is associated with treatment response and survival. However, a larger cohort is needed to investigate the correlation between GDPD5 and ER status.

Findings from this thesis show that MR metabolomics can assist the identification of patients at high risk of breast cancer death, and help identify pathways for novel targeted treatment.

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# Paper I

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## Paper II





Prognostic value of metabolic response in breast cancer patients receiving  
neoadjuvant chemotherapy

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## **Abstract**

**BACKGROUND:** Today's clinical diagnostic tools are insufficient for giving accurate prognosis to breast cancer patients. The aim of our study was to examine the tumor metabolic changes in patients with locally advanced breast cancer caused by neoadjuvant chemotherapy (NAC), relating these changes to clinical treatment response and long-term survival.

**METHODS:** Patients (n=89) participating in a randomized open-label multicenter study were allocated to receive either NAC as epirubicin or paclitaxel monotherapy. Biopsies were excised pre- and post-treatment, and analyzed by high resolution magic angle spinning magnetic resonance spectroscopy (HR MAS MRS). The metabolite profiles were examined by paired and unpaired multivariate methods and findings of important metabolites were confirmed by spectral integration of the metabolite peaks.

**RESULTS:** All patients had a significant metabolic response to NAC, and pre- and post-treatment spectra could be discriminated with 87.9%/68.9% classification accuracy by paired/unpaired partial least squares discriminant analysis (PLS-DA) ( $p < 0.001$ ). Similar metabolic responses were observed for the two chemotherapeutic agents. The metabolic responses were related to patient outcome. Non-survivors (<5 years) had increased tumor levels of lactate ( $p = 0.004$ ) after treatment, while survivors ( $\geq 5$  years) experienced a decrease in the levels of glycine ( $p = 0.047$ ) and choline-containing compounds ( $p \leq 0.013$ ) and an increase in glucose ( $p = 0.002$ ) levels. The metabolic responses could not be related to clinical treatment response.

**CONCLUSIONS:** The differences in tumor metabolic response to NAC were associated with breast cancer survival, but not to clinical response. Monitoring metabolic responses to NAC by HR MAS MRS may provide information about tumor biology related to individual prognosis.

## Background

The prognosis of patients with locally advanced breast cancer varies largely due to the heterogeneity of the disease, and 5-year survival rates from 50-80% have been reported [1]. Neoadjuvant chemotherapy (NAC) has been established as a standard treatment for locally advanced breast cancer, with anthracyclines and taxanes being among the most frequently used agents. NAC is provided to make primarily inoperable tumors resectable, and will also increase the rate of breast-conserving surgery without any significant increase in local or distal recurrence [2, 3]. Studies investigating the metabolic responses and chemoresistance to single or a combination of drugs are important for effective treatment and better patient outcome.

Patients with a pathological complete response (pCR) after NAC have improved outcome compared to patients with residual disease, thus treatment response is a prognostic indicator. However, only ~20% of patients will achieve a pCR to NAC [4]. Other prognostic factors of breast cancer include axillary lymph node status, tumor size, Her-2 overexpression, histopathological grade, and hormone receptor status. The status of Her-2 and hormone receptors is also predictive of treatment response. Identification of other markers for prognosis and treatment response may help stratify patients for better individualized treatment.

Several studies have shown altered metabolism in cancer compared to normal tissue. Elevated levels of total choline-containing compounds (tCho) are frequently observed in cancer, and may serve as magnetic resonance spectroscopy (MRS) markers for malignancy, both *in vivo* and *ex vivo* [5, 6]. The tCho signal constitutes signals from glycerophosphocholine (GPC), phosphocholine (PC) and free choline (Cho) which are involved in phospholipid metabolism through the Kennedy pathway. A decreased level of tCho detected by *in vivo* MRS has been suggested as a possible marker for treatment response [7, 8]. Altered concentrations of other tissue metabolites, such as increased levels of lactate, have also been associated with malignancy [9, 10]. Elevated lactate levels may be related to hypoxia, a common feature of solid tumors where glucose is catabolised to lactate due to the lack of oxygen. Also under conditions with sufficient oxygen levels, cancer cells may convert glucose to lactate, described as the Warburg effect.

High resolution magic angle spinning (HR MAS) MRS is a non-destructive technique providing highly resolved MR spectra of intact tissues with minimal sample preparation. HR MAS MR spectra provide an overview of the different metabolites that are present in a tissue sample, and can give insight into the complex processes leading to cancer and other diseases. More than 30 metabolites have been identified in breast tissue using HR MAS MRS [11]. Systematic studies of the metabolic state of biological systems using multivariate analysis methods are referred to as metabolomics. MR metabolomics studies of breast cancer have revealed correlations between tissue metabolic profiles and clinical prognostic factors such as hormone receptor status, grade and lymphatic spread [12-14]. Long-term survival of breast cancer patients has been successfully predicted from breast cancer tissue using multivariate classification models [15, submitted manuscript Giskeødegård et al]. The purpose of this study was to examine the metabolic changes in breast cancer tissues resulting from treatment with NAC, and to relate these changes to treatment response and long-term survival. This is the first study to investigate the metabolic response of NAC in a large breast cancer cohort using *ex vivo* MRS.

## **Methods**

### **Patient and tumor characteristics**

We examined a subcohort of breast cancer patients ( $n = 89$ ) from a larger open-label multicenter study where patients were randomly allocated to receive NAC treatment with either anthracycline (epirubicin,  $90 \text{ mg/m}^2$ ) or taxane (paclitaxel,  $200 \text{ mg/m}^2$ ) monotherapy [16]. The patients were given subsequent adjuvant endocrine treatment according to guidelines from the Norwegian Breast Cancer Group. The inclusion criteria and treatment protocol are fully described elsewhere [16]. Briefly, female breast cancer patients at pre/post menopausal age ( $\leq 70$  years) with locally advanced (stage III,  $T_{3/4}$  and/or  $N_2$ ) non-inflammatory breast cancer with or without limited distant metastasis were recruited in the period 1997-2003. The patients were treated every third week for four cycles. Patients showing a non-satisfactory response were assigned to the opposite treatment. From each patient, an incisional biopsy was taken before treatment with NAC and a post-treatment biopsy was excised during surgical removal of the tumor. The biopsies were immediately snap-frozen and stored in liquid nitrogen in a biobank until use. A part of the pre-treatment tumor biopsy was obtained for routine pathological diagnosis and hormone status assignment. Estrogen (ER) and progesterone receptor (PgR) status were determined by immunohistochemical staining (positive  $\geq 10\%$  staining cells). The study was approved by The Regional Committee for Medical and Health Research Ethics (Norwegian Health Region III) and informed written consent was obtained from all patients

### **Response and survival evaluation**

Response to treatment was evaluated using the WHO criteria by the UICC system [17]. Treatment response was assessed clinically by comparing caliper measurements prior to NAC treatment and after the last cycle. In the subcohort included in this study, the patients were classified to have either partial response ( $\geq 50\%$  reduction in tumor size (the product of the two largest tumor diameters), but not complete response) or stable disease ( $< 50\%$  reduction to  $\leq 25\%$  increase in tumor size). Patients deceased within 5 years after diagnosis were classified as non-survivors whereas patients surviving 5 years or more were classified as survivors.

### **Histopathological examinations**

Prior to HR MAS MRS analysis, imprint cytology smears were prepared from the tissue samples and stained with the May-Grünwald-Giemsa stain (Color-Rapid, Med-Kjemi, Norway). Confirmation of tumor cell content was determined microscopically by a cytopathologist.

### **HR MAS MRS experiments**

HR MAS MRS analyses were performed on a Bruker Avance DRX600 spectrometer (Bruker Biospin GmbH, Germany) equipped with a  $^1\text{H}/^{13}\text{C}$  MAS probe with gradient. The run order of the samples was randomized ([www.random.org](http://www.random.org)) and blindly analyzed during 18 days. Each sample ( $15.1 \pm 2.8$  mg) was cut to fit a 30  $\mu\text{l}$  leak-proof disposable insert (Bruker Biospin Corp, USA) and added phosphate buffered saline (PBS, 3  $\mu\text{l}$ ) in  $\text{D}_2\text{O}$  containing trimethylsilyl tetradeuteropropionic acid (TSP, 98.2 mM) for chemical shift referencing. Samples were spun at 5 kHz and spectra were recorded within 31 minutes per sample at  $4^\circ\text{C}$  to minimize tissue degradation. Spin-echo spectra (cpmgpr; Bruker) were recorded as previously described [14].

### **Data preprocessing**

Twenty eight spectra were excluded from further studies due to low tumor cell content. The resulting data set consisted of 150 spectra from 85 patients (80 pre-treatment and 70 post-treatment spectra). Characteristics of the included patients and tumors are listed in Table 1. The MR spectra were Fourier transformed into 128 K after 0.3 Hz exponential line broadening. Chemical shifts were referenced to the TSP peak at 0 ppm. The spectral region between 4.69-1.45 ppm, excluding the water peak and large lipid residuals, was chosen for analysis. Signals from ethanol pollutions between 3.69-3.57 ppm were removed together with lipid residual signals between 3.01-1.52 ppm. The spectra were baseline corrected using asymmetric least squares [18] with parameters  $\lambda = 1e7$  and  $p = 0.0001$ , and the minimum value of each spectrum was set to zero by subtracting the lowest value. The spectra were normalized to equal total area, and peak aligned using icoshift [19].

### **Multivariate data analysis**

Partial least squares (PLS) analysis is a regression method for analysis of collinear data with numerous variables. The method is based on extraction of underlying structures, or latent variables (LVs), that maximize the covariance between X (the spectra) and a response variable Y [20]. PLS discriminant analysis (PLS-DA) attempts to discriminate between distinct classes. PLS-DA was performed in Matlab R2009a (The Mathworks, Inc., USA) using PLS\_Toolbox 6.2.1 (Eigenvector Research, USA). A PLS-DA model was built on mean-centred spectra from randomly chosen training samples (90 % of the patients) and used to predict the status of test samples (the remaining 10 %). This procedure was repeated 20 times and the average classification results were calculated. The number of LVs to use was chosen by cross-validation of the whole data set and used for all repetitions to avoid biased results. The importance of each variable in the loadings of the PLS-DA was evaluated by variable importance in the projection (VIP) scores [21]. The VIP score positively reflects the variable's influence on the classification, and variables with a score greater than one are generally considered important [21, 22]. To evaluate the statistical significance of the classification results, permutation testing was performed [23]. In permutation testing, the class labels are permuted to resemble random classification. It is then possible to examine if the achieved prediction results of the original data set are significantly different than random predictions. The data set with the permuted class label was divided into training and test sets repeated 20 times as described for the original data set, and the average results were calculated. The permutation procedure was repeated 1000 times, and the prediction error of the original data set was compared to the distribution of prediction errors from the permutation. P-values  $\leq 0.05$  were considered significant.

Multilevel PLS-DA [24, 25] is an extension of ordinary PLS-DA which can be used as a paired analysis for multivariate data. This analysis can only be used when the data has a multilevel structure, i.e. when interventions are evaluated on the same subject. In multilevel PLS-DA, the *between* subject variation is separated from the *within* subject variation. This is useful in metabolic profiling as the variation between subjects, resulting from differences in age, disease state, genetics and other factors, can obscure the metabolic changes caused by the intervention. The between subject variation is described by the average of the two observations from one subject, whereas the within subject variation is described by the net difference between them. Multilevel PLS-DA was used to examine metabolic changes in the



spectra resulting from NAC treatment. The split-up of variation was done using algorithms made available by van Velzen et al [24]. Further PLS-DA classifications of the within subject variation were performed using PLS\_Toolbox as described for the unpaired analyses. The net difference of the spectra pre minus post treatment (positively representing the metabolites higher expressed before treatment) is annotated as control, while the net difference post minus pre treatment (positively representing the metabolites higher expressed after treatment) is annotated as treatment. More specifically,

$$\begin{aligned} \text{control} &= \mathbf{A} - \mathbf{B} \\ \text{treatment} &= \mathbf{B} - \mathbf{A} \end{aligned} \quad (\text{eq. 1})$$

where the matrix **A** represents pre-treatment spectra, and matrix **B** represents the post-treatment spectra.

#### **Univariate data analysis**

To further validate the important metabolites from the PLS-DA models, relative intensities were found by integrating the peak areas of spectra normalized to equal total areas after removal of lipid residuals (Matlab R2009a, The Mathworks, Inc., USA). Normalization of spectra with the lipid residual signals removed will correct for differences in sample size and tumor cell content, as it can be assumed that most of the lipid signals from breast samples do not originate from cancer cells. Group differences were statistically tested by Wilcoxon rank sum tests or Wilcoxon sign rank for paired analyses, and considered significant if the p-values were  $\leq 0.05$ .

## Results

### **Metabolic response to neoadjuvant chemotherapy**

All classification results are summarized in Table 2. An unpaired PLS-DA of the pre- and post-treatment spectra of the whole data set showed a significant difference in the metabolite profiles in response to NAC treatment, indicating a metabolic response to NAC in all patients. However, the specificity of the classification was low (57.1%). When comparing the classification errors of PLS-DA and paired multilevel PLS-DA from 20 different test sets, the multilevel PLS-DA with split-up of the variation decreased the classification error significantly (Wilcoxon rank sum test,  $p < 0.001$ ), showing the beneficial effect of the paired analysis. Treatment and control spectra could be separated with a sensitivity and specificity of 87.9%. Figure 1A shows the scores and loadings of the multilevel PLS-DA. Lactate and PC were of high importance for the discrimination according to the VIP scores in the loadings. The levels of lactate and glycine appear to be increased in response to treatment, while the levels of PC are markedly decreased for some patients. In addition, GPC levels were decreased in response to treatment. No clustering according to the given chemotherapeutic agents could be seen in the multilevel PLS-DA score plot (results not shown), thus the metabolic treatment effects of epirubicin and paclitaxel appear to be indistinguishable.

### **No differences in metabolic response between clinical response groups**

The patients were divided into two groups according to their clinical response (partial response or stable disease), and multilevel PLS-DA was performed on each group separately in order to discover potential differences in metabolic treatment response between the groups. Both for patients with partial response and stable disease there was a significant change in the tumor metabolism in response to NAC treatment, and treatment spectra could be discriminated from controls with high sensitivity and specificity ( $\geq 80.0\%$ ). The metabolic response to NAC as observed in the loading plots was similar for both subgroups, resembling the changes observed for the whole data set (results not shown). Thus, no difference in the metabolic response could be detected between patients with stable disease and partial response.

### **Different metabolic responses correlate with survival**

Accordingly the patients were divided into two groups according to their survival status (5-year survivors or non-survivors). Both for survivors and non-survivors there was a clear change in the tumor metabolism in response to NAC treatment (Figure 1B and C), and treatment spectra could be discriminated from controls with high sensitivity and specificity ( $\geq 82.5\%$ ). However, the metabolic treatment response appears to differ between survivors and non-survivors.

The loadings showed unchanged lactate levels in response to treatment in survivors, while lactate increased in non-survivors with high importance for the discrimination according to the VIP scores. This was confirmed by comparison of the relative intensities from metabolite integrals, showing a significant increase in lactate levels in response to treatment in non-survivors ( $p = 0.004$ ) but not in survivors (Table 3).

Glycine appears to be decreased in survivors according to the loadings, and the difference in relative intensities before and after treatment was significant ( $p = 0.047$ ). For non-survivors, the glycine level appears to be high in some samples from both the control and the treatment group; hence the role of glycine in the loading plot is more difficult to interpret. The glycine change from integrated relative intensities was not significant in non-survivors, with a mean value close to zero.

GPC levels were decreased in the loading plot of survivors with VIP scores showing high importance, while changes in GPC levels in non-survivors were less important for the discrimination. Accordingly, the relative intensities of GPC were significantly lower in response to treatment in survivors ( $p < 0.001$ ) but not in non-survivors.

The loadings show decreased levels of PC in response to treatment in both survivors and non-survivors. However, the change in PC relative intensities was only significant for survivors ( $p < 0.001$ ), but not for non-survivors, possibly due to a high standard error.

Relative intensities of Cho levels were significantly decreased in survivors ( $p = 0.013$ ) in response to treatment, but only a trend of decreased Cho levels was seen in non-survivors ( $p =$

0.084). In addition, glucose was significantly increased in survivors ( $p = 0.002$ ). Cho and glucose were not protruding in the loadings, possibly due to low intensity values.

As an overall measure of the partly overlapping choline-containing metabolite peaks (GPC, PC, and Cho), the changes in relative intensities of tCho were calculated. Survivors had a significant decrease in tCho levels in response to treatment ( $p < 0.001$ ), while a trend of decreased tCho levels were detected in non-survivors ( $p = 0.091$ ).

### **Metabolic traits at pre- and post-treatment**

A PLS-DA of the post-treatment spectra showed a significant difference in the metabolite profiles of 5-year survivors and non-survivors after treatment with 70.1% correct classification (Table 2). According to the scores and loadings shown in Figure 2, the tumors of non-survivors appear to have more of the metabolites lactate and glycine, and less GPC and taurine than survivors post-treatment. PC appears to be present in high levels in some samples of both survivors and non-survivors. The glycine level was denoted to be of major importance according to the VIP scores, and the relative intensities of glycine were significantly higher in non-survivors compared to survivors post-treatment ( $p = 0.033$ , Table 4). Similarly, a trend of higher relative intensities of lactate was observed in non-survivors ( $p = 0.089$ ). No significant differences in the relative intensities of taurine and GPC were observed, however differences in the levels of tCho approached significance ( $p = 0.075$ ) with non-survivors having higher relative intensities than survivors post-treatment.

The metabolic differences between survivor and non-survivors were not seen pre-treatment as the multivariate model could not discriminate the two outcome groups (model not valid). None of the metabolites showed significant differences in relative intensities between survivors and non-survivors pre-treatment (Table 4).

No significant differences in the metabolite profiles at pre- or post-treatment were detected between patients with partial responders and stable disease by PLS-DA. Post-treatment spectra from patients treated with Epirubicin and Paclitaxel could not be discriminated by PLS-DA, further confirming the similarity of the metabolic response of the two chemotherapeutic agents that were used in this study.

## Discussion

In this study we examined the metabolic effect of NAC treatment in patients with locally advanced breast cancer. By comparing MR spectra of biopsies taken pre- and post-treatment, significant metabolic changes in response to treatment were found both by paired and unpaired multivariate models. The results using paired multilevel PLS-DA were however superior to those of unpaired PLS-DA, thus taking advantage of the multilevel structure in the data set was clearly beneficial.

Epirubicin and Paclitaxel appear to affect the metabolism of the tumor cells in the same manners, as evidenced both by indistinguishable metabolic responses and similar metabolic traits of the post-treatment spectra. Anthracyclines work by interfering with the synthesis and function of DNA, while taxanes stabilize the microtubules; thereby inhibiting cell division [26, 27]. However, both treatments will eventually result in cell death. This might explain why the two agents appear to have similar metabolic responses.

Interestingly all patient in our study cohort showed clear changes in the metabolite profiles in response to treatment, including also patients categorized to have a clinically stable disease. No differences in the metabolic responses of the clinical response groups were detected. However, when examining the metabolic changes in survivors and non-survivors independently, a difference in the metabolic response to NAC was seen. Non-survivors had a significant increase in lactate levels in response to treatment, while survivors showed no change in lactate levels. As a result, a trend of higher levels of lactate was detected in non-survivors compared to survivors post-treatment. Increased lactate levels may be a marker for tumor aggressiveness as high levels of lactate have been correlated with low survival rates, high incident of distant metastasis and recurrence, and increased risk of radiation resistance in several types of cancer [28-30]. Modification of cell energy metabolism is typically observed in malignant tumors and is suggested as an emerging hallmark of cancer [31]. Under normoxic conditions, cancer cells can reprogram their energy metabolism to largely depend on aerobic glycolysis as their primary energy pathway resulting in increased lactate production; the so-called Warburg effect. It is not fully known why cancer cells prefer aerobic glycolysis over complete oxidation as this would produce far more ATP. It has been hypothesized that lactate may enhance the invasiveness of tumor cells and the resulting low pH may help tumor cells evading tumor-attacking immune cells [32].

In addition to aerobic glycolysis, breast cancer cells are often hypoxic due to poor blood supply [33]. It can be assumed that the large tumors of patients with locally advanced breast cancer will be affected by hypoxia. Hypoxia can induce the transcription factor hypoxia inducible factor-1 $\alpha$  (HIF-1 $\alpha$ ), which in turn upregulates multiple genes involved in the glycolytic pathway, angiogenesis, cell proliferation, and other mechanisms [33-35]. Furthermore HIF-1 $\alpha$  promotes transcription of lactate dehydrogenase (LDH) and lactate monocarboxylate transporters (MCT), and thus plays an important role in the production and efflux of lactate in cancer cells [36, 37]. Inhibition of LDH by small interfering RNA (siRNA) in mouse breast tumors has been shown to reduce the glycolytic activity associated with a decrease in tumor proliferation and tumorigenic potential [38]. Thus we can suggest that the increased levels of lactate after NAC treatment observed in non-survivors may reflect enhancement of aerobic glycolytic activity and/or hypoxic tumor responses that confer higher tumor malignancy and poor prognosis. In coherence, the glucose levels were increased in response to treatment in survivors but not in non-survivors. Increased glucose may be indicative of decreased aerobic glycolysis and tumor hypoxic response favorable of long term breast cancer survival.

Survivors had a significant decrease in glycine as a response to treatment, while it remained unchanged in non-survivors. This was reflected in the post-treatment spectra, showing significantly lower levels of glycine in survivors. In a previous study, we also found decreased glycine levels after NAC to be associated with long term breast cancer survival [15]. The biological role of glycine in tumor malignancy is still unclear. Several studies have elucidated the biomarker potential of glycine in human brain tumors, where it was found to positively correlate with tumor grade [39, 40]. Higher levels of glycine have also been detected in pre-clinical studies of the more aggressive basal-like breast cancer model compared to the luminal-like model [41]. In patients, high glycine levels detected in malignant breast tumors have been correlated with poor prognosis [42]. Glycine is mainly synthesized from 3-phosphoglycerate, an intermediate of the glycolysis. In addition, glycine can be synthesized from Cho through the glycine-betaine pathway. We can postulate that the decreased glycine levels after NAC treatment detected in survivors are caused by altered glycolysis and/or reduced Cho levels associated with reduced tumor aggressiveness.

A significant decrease of GPC, PC, Cho levels and the combined tCho level was detected in survivors in response to treatment, whereas non-survivors experienced only a trend of

decrease in Cho and tCho levels. As a result, lower tCho levels in survivors compared to non-survivors post-treatment approached significance. In a previous publication, we showed that GPC and Cho concentrations significantly decreased in patients with long-term survival ( $\geq 5$  years), while non-survivors ( $< 5$  years) had no significant changes in choline phospholipid metabolites in response to NAC [15]. Choline phospholipid metabolites are important biological compounds in cell membrane synthesis and turnover. In addition, tCho levels have been associated with increased malignancy and activation of oncogenic signaling in breast cancer cells [43, 44]. Higher tCho concentrations have been detected in high-grade breast tumors and tumors with higher pharmacokinetic parameters measured with dynamic contrast enhanced MR imaging, indicating a correlation between choline phospholipid metabolism and tumor malignancy and angiogenesis [45, 46]. As previously mentioned, cancer cells may undergo adaptive responses to hypoxia by inducing HiF-1 $\alpha$ . Increased tCho levels and choline kinase alpha (CHKA) expressions has been detected in prostate cancer cells and xenografts models under hypoxic compared to normoxic conditions [47]. In the same study, the authors found hypoxic tumor regions to be co-localized with regions of high tCho, which possibly occurred through the up-regulation of CHKA by HiF-1 $\alpha$ . CHKA is known to play an important role in malignant transformation in several types of cancer [48]. Overexpression of CHKA and elevated PC and tCho levels of breast cancer cells have been associated with increases invasiveness and drug resistance [49]. Decreased choline phospholipid metabolism after NAC treatment may be associated with lower malignancy that potentially can be used as a predictor of breast cancer survival.

The metabolic responses to NAC treatment appear to be similar in patients with partial response and stable disease. None of the patients in this study had a progressive disease, whereas patients with a complete response would not have any tumor tissue left for a post-treatment biopsy. By definition the group with stable disease can have up to 50% reduction in tumor volume, and indeed only two patients in this study had an equal or increased tumor size after NAC. In that respect, almost all patients had a biological effect of the treatment although the tumor reduction was small for patients with a stable disease. It is conceivable that a cohort including also patients with progressive disease would reveal clearer differences in metabolic response between the clinical response groups. It is however noteworthy that all patients in this study in general had a decrease in tCho after NAC, as tCho is suggested as an *in vivo* biomarker for clinical treatment response.

In this patient cohort, the prediction of overall survival was accomplished with 70.1% classification accuracy using post-treatment spectra, but no prognostic information could be extracted from the pre-treatment spectra. This shows that the difference between survivors and non-survivors post-treatment results from a metabolic response to the treatment. The observed higher levels of lactate and glycine in non-survivors compared to survivors support our previous studies postulating high lactate and glycine levels to be predictive of low breast cancer survival rates (< 5 years).

Prediction of survival in patients receiving NAC is challenging. As NAC will downstage and potentially completely remove the disease, standard prognostic indicators such as tumor size and lymph node status are no longer fully applicable after NAC. Several studies have shown that a pathological complete response after NAC is associated with better survival rates [4]. However, approximately 80% of patients will have residual tumor in the breast after treatment [4]. Our study shows that the metabolic response to treatment may be an indicator of patient prognosis.



## **Conclusions**

By comparing HR MAS MR spectra from biopsies excised before and after NAC treatment, we have revealed significant metabolic changes in breast cancer tumors as a response to treatment. Different metabolic responses could be related to patient outcome, but did not separate patients with partial response from those with stable disease. Non-survivors had increased tumor levels of lactate after treatment, while survivors experienced a decrease in the levels of glycine and choline-containing compounds. These differences in tumor response may reflect tumor aggressiveness associated with breast cancer survival. Monitoring metabolic responses to NAC by HR MAS MRS may provide information about tumor biology related to prognosis, and help identify pathways for targeted therapies.

## **Authors' contributions**

MCD carried out the HR MAS MRS and imprint cytology experiments. GFG carried out Matlab programming and preprocessing of the spectral data. MDC and GFG performed the statistical analyses, interpretations of the results and writing of article. IG, TFB, and BS participated in the design of the study, interpretations of the results and writing of article. AB analyzed the imprint cytology samples and helped to draft the manuscript. PEL and SL recruited the patients, collected the tumor biopsies and helped to draft the manuscript. All authors read and approved the final manuscript.

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## **Competing interests**

The authors declare that they have no competing interests.

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**Table 1** Patient and tumor characteristics

		<u>Survivors</u> (n=60)	<u>Non-survivors</u> (n=23)	<u>NA*</u> (n=2)
Mean age (±SD)	years	51.1±10.6	49.3±8.3	46.4±2.6
Mean tumor dimensions (mean ±SD)	mm	67.9x67.9 ±18.0x19.8	78.6x77.3 ±22.0x24.0	65.0x51.5 ±7.1x26.2
NAC treatment	Epirubicin	25	8	-
	Paclitaxel	23	5	2
	Both <sup>†</sup>	12	10	-
Treatment response	Partial response	40	11	1
	Stable disease	20	12	1
AJCC	IIB	21	7	1
	IIIA	25	11	1
	IIIB	12	2	-
	IV	2	3	-
ER status	+	41	7	2
	-	19	15	-
	unknown	-	1	-
PgR status	+	32	14	2
	-	28	18	-
	unknown	-	1	-
Nodes	+	32	14	1
	-	28	9	1
Metastasis	+	2	2	0
	-	58	21	2

\*NA, not applicable - One patient without following up and one patient dead by other causes;  
AJCC, American Joint Committee on Cancer; Both<sup>†</sup>, sequential treatment with Epirubicin and Paclitaxel

**Table 2** Classification results from PLS-DA and multilevel PLS-DA

				<b>Class. model</b>	<b>No. of LVs</b>	<b>Variance X/Y (%)</b>	<b>Sensitivity/ Specificity (%)</b>	<b>Class. accuracy (%)</b>	<b>Permutation p-value</b>
Paired data	All samples	Control vs Treatment	(n=65p)	Multilevel PLS-DA	2	58.9/50.9	87.9/87.9	87.9	<0.001
	Partial response	Control vs Treatment	(n=37p)	Multilevel PLS-DA	2	55.7/61.7	80.0/80.0	80.0	<0.001
	Stable disease	Control vs Treatment	(n=28p)	Multilevel PLS-DA	2	63.2/61.3	88.7/88.7	88.7	<0.001
	Survivors	Control vs Treatment	(n=44p)	Multilevel PLS-DA	2	60.0/50.5	83.0/83.0	83.0	<0.001
	Non-survivors	Control vs Treatment	(n=19p)	Multilevel PLS-DA	2	70.6/63.9	82.5/82.5	82.5	0.006
Unpaired data	All samples	Pre- vs Post-treatment	(n=65p)	PLD-DA	2	50.3/29.2	80.7/57.1	68.9	<0.001
	Pre-treatment	Partial response vs Stable disease	(n=48) (n=32)	PLS-DA	2	51.5/19.3	56.7/60.2	58.4	0.231
	Post-treatment	Partial response vs Stable disease	(n=41) (n=29)	PLS-DA	NaN	-	-	-	-
	Pre-treatment	Survivors vs Non-survivors	(n=57) (n=20)	PLS-DA	NaN	-	-	-	-
	Post-treatment	Survivors vs Non-survivors	(n=47) (n=21)	PLS-DA	3	62.8/32.1	58.4/75.3	70.1	0.009
	Post-treatment	Epirubicin vs Paclitaxel	(n=29) (n=23)	PLS-DA	2	45.7/26.8	45.0/48.3	46.5	0.245

The sensitivity is for detecting a treatment/stable disease/non-survivor/Paclitaxel spectrum; Variance X/Y, amount of variance from X/Y explained by the model; NaN, no valid model; p, pairs.

**Table 3** Changes in relative intensities of metabolites in response to NAC

Metabolite	ppm	Survivors		Non-survivors	
		Mean $\pm$ SE	p-value	Mean $\pm$ SE	p-value
Lactate	4.08-4.13	2.8 $\pm$ 15.3	0.815	97.1 $\pm$ 26.4	0.004**
Glycine	3.54-3.56	-19.6 $\pm$ 8.0	0.047*	0.8 $\pm$ 14.3	0.601
GPC	3.22-3.24	-59.6 $\pm$ 14.6	< 0.001**	-11.8 $\pm$ 15.7	0.469
PC	3.21-3.22	-95.4 $\pm$ 24.3	< 0.001**	-67.4 $\pm$ 44.2	0.227
Cho	3.20-3.21	-16.6 $\pm$ 6.3	0.013*	-17.8 $\pm$ 6.3	0.084
tCho	3.20-3.24	-167.2 $\pm$ 36.7	< 0.001**	-95.3 $\pm$ 57.5	0.091
Taurine	3.40-3.43	-0.8 $\pm$ 13.2	0.861	6.9 $\pm$ 12.5	0.398
$\beta$ -Glucose	4.61-4.64	17.8 $\pm$ 5.1	0.002**	-0.2 $\pm$ 8.8	0.841

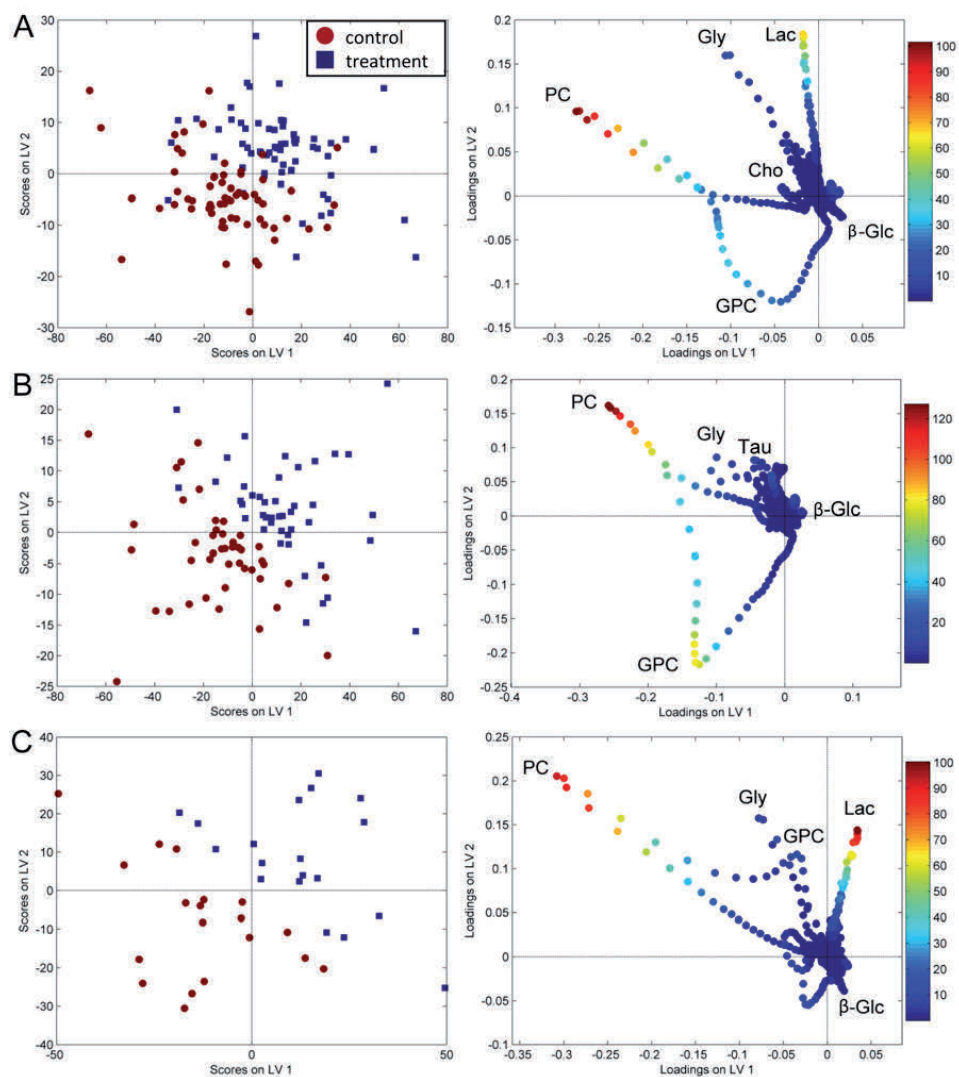
The values (post- minus pre-treatment) of relative intensities are integrated peak areas from spectra normalized to equal total areas. Wilcoxon sign rank tests were used for paired statistical analyses. \* p < 0.05, \*\* p < 0.01.



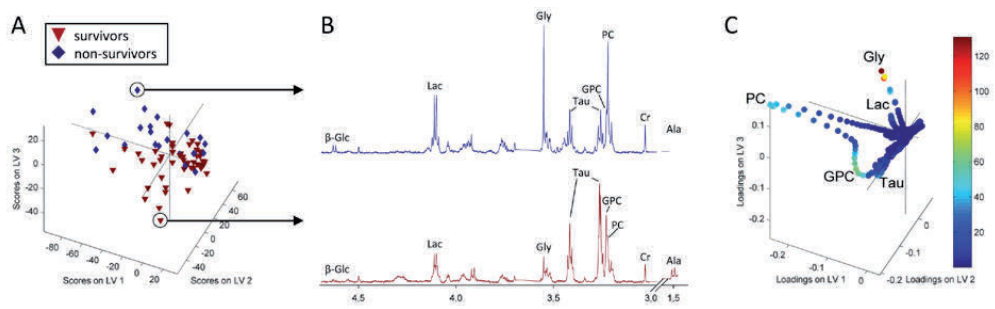
**Table 4** Relative intensities of metabolites at pre- and post-treatment

Metabolites	ppm	Pre-treatment (mean $\pm$ SE)			Post-treatment (mean $\pm$ SE)		
		Survivors	Non-survivors	p-value	Survivors	Non-survivors	p-value
Lactate	4.08-4.13	185.8 $\pm$ 11.4	164.6 $\pm$ 13.8	0.534	196.2 $\pm$ 12.7	250.6 $\pm$ 26.0	0.089
Glycine	3.54-3.56	115.0 $\pm$ 6.4	120.8 $\pm$ 11.0	0.542	91.2 $\pm$ 4.1	111.4 $\pm$ 8.4	0.033*
GPC	3.22-3.24	167.3 $\pm$ 12.4	170.1 $\pm$ 23.9	0.949	115.6 $\pm$ 6.7	153.9 $\pm$ 24.1	0.144
PC	3.21-3.22	247.9 $\pm$ 17.0	285.4 $\pm$ 34.9	0.338	158.0 $\pm$ 16.1	205.5 $\pm$ 28.1	0.105
Cho	3.20-3.21	95.4 $\pm$ 3.9	108.7 $\pm$ 8.3	0.225	79.5 $\pm$ 3.7	85.9 $\pm$ 6.2	0.276
tCho	3.20-3.24	498.3 $\pm$ 26.4	551.3 $\pm$ 46.8	0.253	344.9 $\pm$ 22.3	434.6 $\pm$ 44.6	0.075
Taurine	3.40-3.43	242.6 $\pm$ 9.6	222.8 $\pm$ 12.4	0.393	248.0 $\pm$ 8.1	222.3 $\pm$ 9.3	0.144
$\beta$ -Glucose	4.61-4.64	48.4 $\pm$ 3.3	49.3 $\pm$ 6.0	1.000	63.6 $\pm$ 4.3	53.5 $\pm$ 6.6	0.172

The values of relative intensities are integrated peak areas from spectra normalized to equal total areas. Wilcoxon rank sum tests were used for statistical analyses. \*p < 0.05, \*\*p < 0.01.



**Figure 1** Scores and loadings from multilevel PLS-DA. Separation of treatment and control spectra based on (A) the whole data set, (B) 5-year survivors, and (C) non-survivors. The variables in the loadings are colored according to VIP scores, indicating the importance of each variable in the discrimination. The control spectra equal the difference between pre- and post-treatment spectra, while the treatment spectra equal the post-pre treatment difference. Lac, lactate; Gly, glycine;  $\beta$ -Glc,  $\beta$ -glucose.



**Figure 2 PLS-DA of the MR spectra from biopsies excised post-treatment.** (A) A score plot separating survivors and non-survivors, (B) Representative spectra showing the metabolic differences of the tumors of survivors and non-survivors. (C) The loadings of the PLS-DA model with variables colored according to the VIP scores.  $\beta$ -Glc,  $\beta$ -glucose; Lac, lactate, Gly, glycine; Cr, creatine; Ala, alanine

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