



UNIVERSITI PUTRA MALAYSIA

***CLINICAL EVALUATION AND PROTEOMIC PROFILES OF ACUTE
MYELOID LEUKEMIA PATIENTS, SAUDI ARABIA***

ALMAIMAN AMER ABDULRAHMAN

IB 2015 25



**CLINICAL EVALUATION AND PROTEOMIC PROFILES OF ACUTE
MYELOID LEUKEMIA PATIENTS, SAUDI ARABIA**

By

ALMAIMAN AMER ABDULRAHMAN

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia, in
Fulfillment of the Requirements of the Degree of Doctor of Philosophy**

December 2015

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DEDICATIONS

Dedicate to my father, my mother and my wife



Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfillment of
the requirements for the degree of Doctor of Philosophy

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ALMAIMAN AMER ABDULRAHMAN

December 2015

Chairman: **Prof. Rasedee Abdullah, PhD**

Faculty: **Institute of Biosciences**

Acute myeloid leukemia (AML) represents a group of clonal hematopoietic stem cell disorders which fail to differentiate and proliferate result in the accumulation of non-functional myeloblasts. In AML, response of patients to therapy is variables and there is no reliable marker to predict treatment response or prognosis of the disease. In this study, the main objective was to determine proteomic profiles of AML in patients referred to the King Faisal Specialist Hospital and Research Center, Riyadh, Saudi Arabia. The AML patients were categorized according to risk degree based on the probability of survival. Clinical data were collected from 22 patients (16 males and 6 females) with consent. A clinical data form was developed to collect information on the diagnosis, prevention, and follow-up monitoring of AML patients.

The clinical data showed that most patients (14) were cytogenetically and genetically normal and classified under the intermediate-risk category. Six patients expressed complex CCAAT/enhancer binding protein (CEBPA), FMS-related tyrosine kinase (FLT), isocitrate dehydrogenase (IDH) and Wilms tumor 1 (WT1) gene abnormalities, 2 patients showed inversion at chromosome 16 (inv.16) and 1 had t(15:17) chromosomal translocation.

The high abundance protein in the samples must be depleted before subjecting to proteomic analyses. In the current study, the Pierce Albumin and IgG Removal, Albumin Depletion, and ProteoPrep® Immunoaffinity Albumin and IgG Depletion Kits were compared in the optimization of the samples. The Pierce Albumin and IgG Removal Kit was found to be the best depletion method for high abundance proteins.

The protein expressions were compared among patients with different risk categories, at diagnosis and after remission. The AML samples from peripheral blood and bone marrow were analyzed by liquid chromatography tandem mass spectrometry (LC-MS/MS). At diagnosis, in both the peripheral blood and bone marrow samples, 21 proteins were significantly ($P<0.05$) different in differential expressions among groups. The total number of proteins detected in peripheral blood was similar to those detected in bone marrow. However, there were differences in proteomic profiles between samples collected at diagnosis and remission. Most differentially expressed proteins were down-regulated in peripheral blood at remission. Among the AML cases in this study, 144 differentially expressed proteins were identified, and differences in their expression levels correlated with AML risk categories. The study showed that amphiregulin precursor (AR) (colorectum cell-derived) was expressed in low-risk AML patients only, while haptoglobin α and β and cytoplasmic tyrosyl-tRNA synthetase (EC 6.1.1.1) were highly expressed in intermediate-risk AML patients only. Lysine-arginine-ornithine-binding periplasmic protein (LAO) was expressed in intermediate and high-risk and not in the low-risk AML patients.

In conclusion, the study showed that complete clinical data are essential for the determination of correlation between proteomic profile, risk categories and prediction of response to chemotherapy in AML patients. AR , haptoglobin α and β and LAO may serve as potential biomarkers for the determination of risk categories and responsiveness of AML patients to chemotherapy.

Keywords: Acute myeloid leukemia, risk categories, proteomics.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai
memenuhi keperluan untuk ijazah Doktor Falsafah

**PENILAIAN KLINIKAL DAN PROFIL PROTEOMIK LEUKEMIA MIELOID
AKUT PESAKIT, ARAB SAUDI**

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Leukemia mieloid akut (AML) mewakili sekumpulan gangguan sel dasar hematopoiesis berklon di mana kegagalan untuk membeza dan memproliferat mengakibatkan terkumpulnya mieloblas yang tidak berfungsi. Dalam AML, gerak balas pesakit terhadap terapi adalah berbeza dan tiada satu penanda yang betul boleh dipercayai untuk meramal gerak balas terhadap rawatan atau prognosis penyakit ini. Dalam kajian ini, objektif utama adalah menentukan profil proteomik AML untuk pesakit yang dirujuk kepada King Faisal Specialist Hospital and Research Center, Riyadh, Arab Saudi. Pesakit AML dikategorikan mengikut tahap risiko berasaskan kemungkinan mandiri. Data klinikal telah dikumpulkan daripada 22 pesakit (16 lelaki dan 6 perempuan) dengan izin. Borang data klinikal telah diwujudkan mengumpul keterangan mengenai diagnosis, pencegahan, dan pemantauan susulan serta pesakit AML.

Data klinikal menunjukkan bahawa kebanyakan pesakit (14) adalah normal sitogenetik dan genetiknya dan diklasifikasi di bawah kategori risiko sederhana. Enam pesakit menyatakan kompleks protein pengikat CCAAT/peningkat (CEBPA), tirosine kinase terkait-FMS (FLT), isositrat dehidrogenase (IDH) dan keabnormalan gen tumor Wilms 1 (WT1), 2 menunjukkan pembalikan pada kromosom 16 (inv.16) dan 1 dengan translokasi kromosom t(15:17).

Protein berlebihan tinggi dalam sampel mesti disingkirkan sebelum perlakuan analisis proteomik. Dalam kajian ini, tiga kaedah untuk pengoptimuman sampel, iaitu kit Pierce Albumin and IgG Removal, Albumin Depletion, and ProteoPrep® Immunoaffinity Albumin and IgG Depletion telah dibanding. Kit Pierce Albumin and IgG Removal didapati kaedah yang terbaik untuk penyaringan protein berlebihan tinggi.

Penyataan protein telah dibandingkan di kalangan pesakit berlainan kategori risikonya, semasa diagnosis dan selepas kebah. Sampel AML daripada darah periferi dan sumsum tulang telah dianalisiskan melalui spektrometri jisim seiring kromatografi cecair (LC-MS/MS). Pada masa diagnosis, dalam kedua-dua sampel darah periferi dan sumsum tulang, 21 protein didapati berbeza secara tererti ($P<0.05$) dengan nyata pembezaannya di kalangan kumpulan. Bilangan protein yang dikesan dalam darah periferi sama dengan sumsum tulang. Bagaimanapun, terdapat kelainan dalam profil proteomik antara sampel yang diambil semasa diagnosis dan kebah. Kebanyakan protein nyata pembezaan telah terkawal-turun dalam darah periferi pada masa kebah. Di kalangan kes dalam kajian ini, 144 protein nyata pembezaan dikenal pasti, dan kelainan dalam tahap penyataan berkorelasi dengan kategori risiko AML. Kajian itu menunjukkan bahawa pelopor amfiregulin (AR) (terbitan sel kolorektum) ternyata dalam pesakit AML berisiko rendah sahaja, sementara haptoglobin α dan β dan sintetase tirosil-tRNA sitoplasma (EC 6.1.1.1) ternyata tinggi dalam pesakit AML berisiko sederhana sahaja. Protein periplasma pengikat-lisina-arginina-ornitina (LAO) ternyata dalam pesakit AML yang berisiko sederhana dan tinggi dan bukan dalam yang berisiko rendah.

Kesimpulannya, kajian ini menunjukkan bahawa data klinikal lengkap adalah perlu untuk penentuan korelasi antara profil proteomik, kategori risiko dan ramalan gerak balas terhadap kemoterapi dalam pesakit AML. Pelopor amfiregulin, haptoglobin α dan β dan LAO mungkin boleh bertindak sebagai biopenanda berpotensi dalam penentuan kategori risiko dan tahap gerak balas pesakit AML terhadap kemoterapi.

Katakunci: leukemia mieloid akut, kategori risiko, proteomik.

ACKNOWLEDGEMENTS

A number of people have been instrumental in bringing this thesis to its proper end. I would like to express my sincere appreciation to everyone who has supported me throughout this study. First and foremost, I would especially like to acknowledge and greatly thank my supervisor, Professor Rasedee Abdullah, for his unending support, mentorship, and for giving me the opportunity to pursue my PhD degree in the interesting fields of genomics and proteomics. His never failing enthusiasm and encouragement are thankfully appreciated.

To my supervisory committee: Prof. Ahmad Bustamam, Prof. Zeenathul Nazariah Alauddin, Dr. Ayodele Alaiya and Dr. Eltayeb Eid, for their kind acceptance, support and provision of excellent working condition. You have all encouraged me to work independently and your support and enthusiastic advice have been beneficial to me during these challenging years.

I would specially like to thank Dr. Alaiya and Ms. Zakia Shinwari for their invaluable guidance on proteomics works and for keeping their proteomics lab door widely opened for me. I am most grateful to the members of the ‘Oncology Center and the Department of Pathology and Laboratory Medicine at King Faisal Specialist Hospital and Research Center (KFSH&RC) in Riyadh’ for productive collaboration and friendship. In particular, Dr. Nasir Bakhshi, Dr. Walid Rasheed, Dr. Mahmoud Aljurf, Dr. Tareq Owaideh, Dr. Asim Belgumi, and Ms. Ghada Al juhani. The support from Research Center, Office of Education and Training, at KFSH&RC is also acknowledged.

Finally, I would like to thank the most important persons in my life; my always supportive family, (my father AbdulRahman and my mother Madawie) for their supports, understanding and endurance throughout this long journey.

I certify that a Thesis Examination Committee has met on 8 December 2015 to conduct the final examination of Almaiman Amer Abdulrahman A on his thesis entitled "Clinical Evaluation and Proteomic Profiles of Acute Myeloid Leukemia Patients, Saudi Arabia" in accordance with the Universities and University Colleges Act 1971 and the Constitution of the Universiti Putra Malaysia [P.U.(A) 106] 15 March 1998. The Committee recommends that the student be awarded the Doctor of Philosophy.

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LIST OF ABBREVIATIONS

ADH	Alcohol dehydrogenase
ALL	Acute lymphoid leukemia
AmBic	Ammonium bicarbonate
AML	Acute myeloid leukemia
BM	Bone marrow
BMC	Bone marrow cell
BMP	Bone marrow plasma
BSA	Bovine serum albumin
CBC	Complete blood count
CDK	Cyclin-dependent kinase
CEBPA	CCAAT/enhancer-binding protein
CHAPS	3[(3-Cholamidopropyl) dimethylammonio] propanesulfonic acid
CLL	Chronic lymphoid leukemia
CLP	Common lymphoid progenitor
CML	Chronic myeloid leukemia
CMP	Common myeloid progenitor
CN-AML	Normal cytogenetic-acute myeloid leukemia
CPF	Core binding factor
CR	Complete remission
CSF-1	Colony-stimulating factor 1
CV	Coefficient of variation
Da	Dalton
DBP	D-binding protein precursor
EDTA	Ethylenediaminetetraacetic acid
DE	Dimensional electrophoresis
Del	Deletion
DNA	Deoxyribonucleic acid
DTT	Dithiothreitol
ETO	Eight twenty-one proteins
FAB	French-american-british
FLT	Fms-like tyrosine
Hb	Hemoglobin
HCl	Hydrogen chloride
Hct	Hematocrit
HDMS	High-definition mass spectrometry
HIC	Hydrophobic interaction chromatography
HIDAC	High dosage cytarabine
HAS	Human albumin serum
HSCs	Hematopoietic stem cells
HTLV-1	Human T-lymphotropic virus
IA	Immunoaffinity

IAA	Iodoacetamide
ICE	Ifosfamide, carboplatin, and etoposide
IDH	Isocitrate dehydrogenase
IEF	Isoelectric focusing
IgG	Immunoglobulin
Inv	Inversion
IPA	Ingenuity pathway analysis
IPG	Immobilized ph gradient
LC/MS/MS	Liquid chromatography/ tandem mass spectrometry
LT-HSC	Long-term hematopoietic stem cell
M1	Acute myeloblastic leukemia with minimal maturation
M2	Acute myeloblastic leukemia with maturation
M3	Acute promyelocytic leukemia
M4	Acute myelomonocytic leukemia
M5	Acute monocytic leukemia
M6	Acute erythroid leukemia
M7	Acute megakaryocyte leukemia
MapK	Mitogen-activated protein kinase
MALDI	Matrix-assisted laser desorption ionization
MDR	Multidrug resistant
MLL	Multi-lineage leukemia
MLP	Multiple lymphomatous polyposis
MPO	Myeloperoxidase
MRD	Minmal residual disease
MRN	Medical record number
MSE	Data-independent acquisition
Mg	Microgram
MI	Microliter
UPLC	Ultra performance liquid chromatography
NaCl	Sodium chloride
NK cells	Natural killer cells
NPM	Nucleophosmin
PAGE	Polyacrylamide gel electrophoresis
PB	Peripheral blood
PBC	Peripheral blood cell
PBS	Phosphate-buffered saline
PBP	Peripheral blood plasmas
PBMC	Peripheral blood mononuclear cell
PCA	Principle component analysis
PH	Partial pressure of (element)
Plt	Platelet
PML	Promyelocytic leukemia
PMSF	Phenylmethylsulfonyl fluoride
PTM	Post-translational modification

RAR	Retinoic acid receptor
RBC	Red blood cell
RBM	Round per minute
Rh	Rhesus
RNA	Ribonucleic acid
RT	Room temperature
RUNX1	Runt-related transcription factor 1
SDS	Sodium dodecyl sulfate
ST-HSC	Short-term hematopoietic stem cell
TCR	T-cell antigen receptor
TET2	Ten eleven translocation 2
TKD	Tyrosine kinase domain
TOF	Time-of-flight
Tris	Tris (hydroxymethyl) aminomethane
WBC	White blood cell
WHO	World health organization
WT1	Wilms tumor 1

CHAPTER 1

INTRODUCTION

1.0 Leukemia and proteomics

Acute and chronic hematological malignancies or “blood cancers” form a distinct subset of cancers that originate in the bone marrow or lymph nodes (Aquino, 2002; Wartenberg *et al.*, 2008). Leukemia is a group of disorders characterized by the accumulation of abnormal leukocytes in the bone marrow and blood circulation. The occupation of these abnormal cells may cause bone marrow failure (Lane and Gilliland, 2010).

Leukemogenesis is a multistep process with several factors that could influence normal hematopoiesis, including over-expression of certain oncogenes, aberrant intracellular pathways, behavior of oncoproteins and expression of chromosomes (Reikvam *et al.*, 2011). Acute myeloid leukemia (AML) is a hematological malignancy characterized by clonal proliferation of immature myeloid precursors and arrest in the maturation of these cells (Rubnitz *et al.*, 2010). These abnormalities cause accumulation of leukemic blast cells in the bone marrow and eventually in peripheral blood. The bone marrow infiltration by the immature cells causes a decrease in blood cell production and thereby reducing the peripheral blood numbers of mature erythrocytes (RBCs), leucocytes (WBCs) and platelets (Plts), causing anemia, thrombocytopenia that eventually lead to hemorrhage, neutropenia and loss of resistance to infections. Thus, in AML, patients are initially presented with symptoms often related to pancytopenia, anemia, weakness, fatigue, infections and/or bleeding (Hamid, 2013).

The incidence of AML is about five cases per 100,000 individuals annually and it accounts for approximately 80 % of acute leukemias in adults and 15 to 20 % in children (Robison *et al.*, 2002; Deschler and Lübbert, 2006; Chen *et al.*, 2014). In infants, leukemia is unique in epidemiological, biological, and clinical characteristics. Most of the acute lymphoblastic leukemia (ALL) and AML cases in infants are characterized by high leukocyte count, extramedullary disease, propensity for expression of lymphoid and myeloid phenotypic markers, and translocation of the mixed-lineage leukemia (MLL) (ALL-1, HRX, Htrx-1) gene at chromosome band 11q23 (Reikvam *et al.*, 2011), rapid tumor cell proliferation and a predominance of blast cells. Acute lymphoblastic leukemia is the most common form of leukemia which accounts for 75 to 80 % of all acute leukemia cases in children and adolescents, while AML accounts for 15 to 20% (Yeates *et al.*, 2009). With modern intensive chemotherapy and supportive care, the prognosis of ALL and to a lesser extent AML in children has improved significantly over the past decades (Shipley and Butera, 2009).

The majority of leukemia studies focused on the correlation between leukemic cell phenotypes with cytogenetic and clinical response with the induction and consolidation therapies. Others have evaluated clinical outcomes of different AML subtypes. Few studies have demonstrated the potential of proteomics in the characterization, diagnosis and treatment of hematological malignancies (Luczak *et al.*, 2012). The weakness of leukemia studies lies in the relatively low sample size and more importantly, in the lack of validation of results and with no follow-up pilot clinical trial on the discoveries from their studies.

Currently, apart from the clinical evaluation coupled with hematological, cytogenetic and molecular tests to monitor patient's responses, there is no available objective protein marker for accurate prediction and monitoring of treatment response in AML. There is therefore a need to develop protein markers that could be complementary to currently diagnostic tools in the management of AML patients.

Recent advancements in proteomic technologies have generated vast interest in the pursuit for biomarkers for various hematological malignancies. Large-scale analysis of proteins from cells, tissues, fluids, or organs, using the classical proteomic platforms has yielded information on the disease heterogeneity at different stages of development and progression. Global differential protein profiling analyses or expression proteomics have resulted in identification of disease-related or tissue-specific proteins that could potentially be useful as disease biomarkers (Alaiya *et al.*, 2011).

This quest to translate basic discoveries into patient care regimes has resulted in many proteomic studies describing potential biomarkers. It is disappointing that despite the technological advances, very few studies have found way into clinical trials. The majority of the published proteomic studies have limitations, including inadequate sample representation, non-standardized sample handling and processing, and extreme dynamic range of serum proteins and above the modest sample size, which does not accurately represent the clinical cohorts (Eun *et al.*, 2004; Visanji *et al.*, 2012). It is therefore important that polypeptides identified as potential biomarkers are validated in appropriately processed, well-characterized clinical samples using established techniques, such as immunochemistry or PCR-based methods (Pitkanen and Lukasiuk, 2011).

The understanding of the molecular mechanisms in treatment responses and disease recurrence is limited in AML. Proteomics is the logical approach because proteins change with cellular responses to internal environment, external stimuli, and disease development.

The majority of available biomarkers are single biomolecules with low sensitivity and specificity. Therefore, the use of a combination of measurable protein panels for a more accurate diagnosis and prediction of disease prognosis in AML.

1.1 Hypothesis

Proteomic profiling in combination with clinical data would support the diagnosis, prediction of progression, and risk categorization of acute myeloid leukemia.

1.2 Problem statement

Cancer is among the main causes of death due to disease in developed countries and developing countries (Siegel *et al.*, 2014). Several studies have demonstrated the potential of proteomics and clinical data in the characterization, diagnosis, and treatment of AML (Luczak *et al.*, 2012). However, to date no protein marker has been identified that can accurately be used in the prediction and determination of treatment response in AML. The discovery of AML diagnostic protein markers will complement the currently available diagnostic tools in the management of AML patients.

1.3 General objective

The general goal of this study was to evaluate the AML risk categories and correlate their global protein expressions with the response to induction and consolidation treatments and overall outcome of the disease.

1.4 Specific objectives of the study

The specific objectives of the study are to:

1. Evaluate the clinical data of acute myeloid leukemia.
2. Correlate the proteins fingerprinting with clinical data of AML patients.
3. Optimize high abundance plasma protein removal for accurate and reproducible proteomic analysis in AML.
4. Determine the proteomic profiles of AML using Synapt G2 platform.

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