



UNIVERSITI PUTRA MALAYSIA

***EVALUATING A RAPID METHOD TO QUANTIFY MULTIPLE GENE
EXPRESSION IN ACUTE MYELOID LEUKAEMIA***

LEE CIN DEE

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EXPRESSION IN ACUTE MYELOID LEUKAEMIA**

By

LEE CIN DEE

**Thesis Submitted to the School of Graduate Studies, Universiti Putra Malaysia,
in Fulfilment of the Requirements for the Degree of Master of Science**

July 2013

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Abstract of thesis presented to the Senate of Universiti Putra Malaysia in fulfilment
of the requirement for the degree of Master of Science

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By

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July 2013

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Acute myeloid leukaemia (AML) is a clonal disease characterized by the proliferation and accumulation of myeloid progenitor cells in the bone marrow and peripheral blood. Prognostic markers are needed to predict patient's response to therapy and reduce under- or over-treatment. Age, white blood counts and cytogenetics are currently routine prognostic markers but are limited by the test and the number of patients who can benefit from it. Large scale gene profiling methods have further identified genetic aberrations such as microdeletions and mutations associated with pathogenesis of disease and outcome. Thus, further screening and confirmation using reliable and accurate high-throughput methods are required. A pool of genes with potential markers was isolated from good and poor prognosis patients in the previous study, where subtractive hybridisation was applied on randomly selected patient based on their prognosis. The expressions of these markers were then evaluated on leukaemia cell lines. This study, aims to further examine the expression of these markers on AML samples and confirm its prognostic properties. Thirty newly diagnosed acute myeloid leukaemia (AML) cases were included in the study. The diagnosis and treatment outcome of these cases were retrieved from haematological reports and clinical data from the hospital involved. Nineteen potential genes identified from earlier study and four housekeeping genes were selected and the level of expression was determined using the GeXP method and confirmed using the real-time PCR method. Results revealed that several genes including CALM2, CSTB and TMSB4X may be related to good prognosis while SON, PGK1 and SF3B1 may be related to poor prognostic in acute myeloid leukaemias. The GeXP method has several advantages over real-time PCR including the requirement for less samples, simultaneous optimization and examination of all target and reference genes in a reaction and no requirement for repeated standard curves which are all important considerations to the study of clinical samples. This study has provided much insight into reliable techniques for selection of biomarkers and identified potential prognostic markers for acute myeloid leukaemias. This will in turn lead towards more-directed therapy for patients.

Abstrak tesis yang dikemukakan kepada Senat Universiti Putra Malaysia sebagai memenuhi keperluan untuk Ijazah Master Sains

**EVALUASI KAEDAH PANTAS UNTUK MENGUKUR ESPRESI GEN
DALAM LEUKEMIA MYELOID AKUT (AML)**

Oleh

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Leukemia myeloid akut (AML) adalah penyakit klonal yang dicirikan oleh proliferasi dan pengumpulan sel anak myeloid di dalam sum-sum tulang dan darah periferi. Penanda ramalan perlu untuk meramal respons pesakit terhadap terapi serta mengawal terhadap pemberian ubatan kekurangan atau melampau. Umur, bacaan sel darah putih dan sitogenetik adalah penanda ramalan rutin tetapi terhad kepada kemampuan ujian tersebut disamping hanya memanfaatkan sebilangan pesakit sahaja. Kaedah profil gen secara besar-besaran telah mengenal pasti aberasi genetik seperti *microdeletions* dan mutasi yang berkenaan dengan patogenesis penyakit dan kesannya. Oleh itu, saringan lanjut dan pengesahan dengan bilangan sampel yang tinggi dengan kaedah ujian yang dipercayai serta tepat adalah perlu. Sekumpulan gen dengan penanda berpotensi telah diasingkan daripada sampel pesakit prognosis baik dan buruk dalam kajian sebelum ini. Ekspresi penanda-penanda ini kemudiannya telah dinilai pada *cell line*. Kajian ini bertujuan untuk memeriksa ekspresi penanda-penanda tersebut pada sampel AML dan seterusnya mengesahkan ciri-ciri prognostiknya. Tiga puluh kes AML baru disertakan ke dalam kajian ini. Diagnosis dan kesan rawatan diperoleh daripada laporan hematologi dan data klinikal dari hospital yang terlibat. Sembilan belas gen berpotensi yang dikenalpasti daripada kajian sebelum ini, yang mana kaedah “subtractive hybridization” telah digunakan terhadap pesakit yang dipilih secara rambang berdasarkan prognosis mereka. Empat gen rujukan juga telah dipilih dan tahap ekspresi gen-gen tersebut ditentukan menggunakan kaedah GeXP dan disahkan melalui kaedah *real-time PCR*. Keputusan mendedahkan bahawa beberapa gen termasuk CALM2, CSTB and TMSB4X mungkin berkaitan dengan prognosis baik manakala SON, PGK1 and SF3B1 mungkin berkaitan dengan prognosis buruk dalam AML. Kaedah GeXP mempunyai beberapa kelebihan berbanding dengan *real-time PCR* iaitu keperluan sampel yang sedikit, pengoptimuman serentak dan pemeriksaan semua gen sasaran dan rujukan dalam satu reaksi serta tidak perlu pengulangan lengkung standard dalam setiap esei. Semua ini adalah pertimbangan penting dalam kajian berkaitan sampel klinikal. Kajian ini telah memberi pemahaman kepada teknik yang dapat dipercayai bagi pemilihan penandabio dan mengenalpasti penanda prognostik berpotensi bagi

AML. Dengan ini, ia akan dapat membawa kepada terapi yang lebih sesuai dan berkesan kepada pesakit.



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This thesis was submitted to the Senate of Universiti Putra Malaysia and has been accepted as fulfilment of the requirement for the degree of Master of Science. The members of the Supervisory Committee were as follows:

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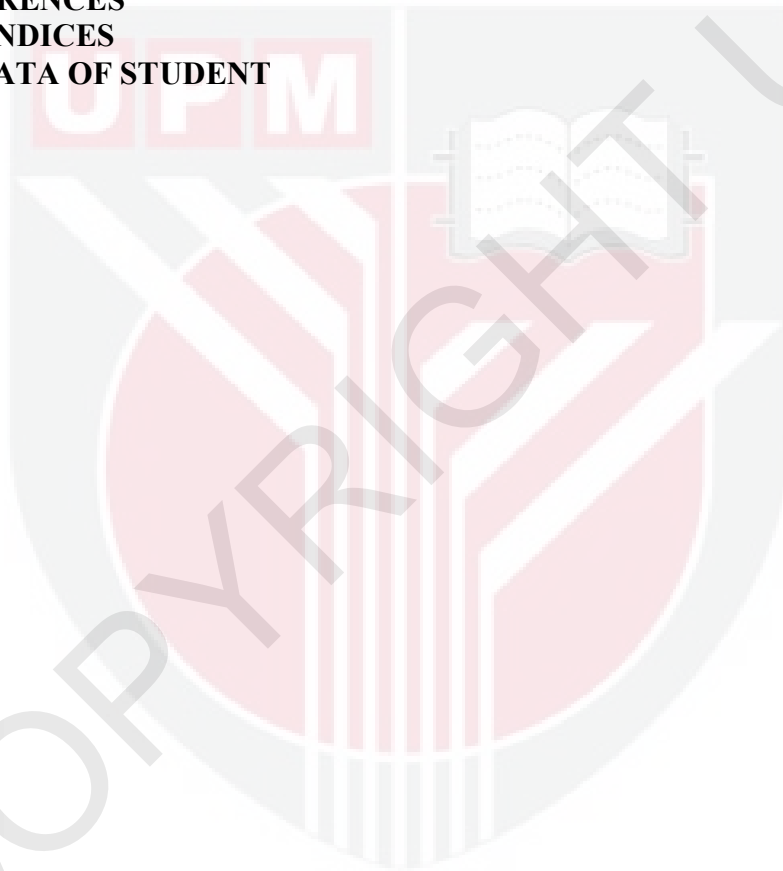
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LIST OF ABBREVIATIONS

AAI	Anti-apoptosis index
ALL	Acute Lymphoblastic Leukaemia
AML	Acute myeloid leukaemia
ANAE	Alpha naphthyl acetate esterase
ANBE	Alpha naphthyl butyrate esterase
AP	Acid phosphatase
APML	Acute promyelocytic leukaemia
ASO	Allele-specific oligonucleotide
BAALC	Brain and Acute Leukemia, Cytoplasmic
BLAST	Basic local alignment search tool
BMA	Bone marrow aspirate
BMT	Bone marrow transplantation
bp	Base pair
CAE	Chloroacetate esterase
CBF	Core-binding factor
cDNA	Complementary DNA
CEBPA	CCAAT enhancer-binding protein- α
CLL	Chronic Lymphoid Leukaemia
CML	Chronic Myeloid Leukaemia
cMPO	Cytoplasmic myeloperoxidase
CN-AML	Cytogenetically normal acute myeloid leukaemia
CR	Complete remission
CR1	First complete remission
C _T	Threshold cycle
DEPC	Diethylpyrocarbonate
DFS	Disease-free survival

DI	Deformability index
DMSO	Dimethyl sulfoxide
DNA	Deoxyribonucleic acid
EDTA	Ethylenediaminetetraacetic acid
ERG	ETS-related gene
EtBr	Ethidium bromide
FAB	French-American-British
FISH	Fluorescence in-situ hybridization
FLT3	Fms-like tyrosine kinase 3
GEP	Gene expression profiling
GeXP	GenomeLab GeXP Genetic Analysis System (Beckman Coulter)
GVL	Graft-versus-leukaemia
HBSS	Hank's Balanced Salt Solution
HCT	Haematopoietic cell transplantation
HIDAC	High-dose Ara-C
HSC	Hematopoietic stem cell
HSCT	Hematopoietic stem cell transplantation
ITD	Internal tandem duplication
LSCs	Leukemic stem cells
MDR	Multidrug resistance
MDS	Myelodysplastic syndromes
MGG	May-Grünwald/Giemsa
MIC-M	Morphologic, Immunologic, Cytogenetic and Molecular Genetics
MK	Monosomal karyotype
M-MLV	Moloney murine leukaemia virus
MoAb	Monoclonal antibodies

MPO	Myeloperoxidase
MRD	Minimal residual disease
mRNA	Messenger RNA
NCBI	National Center for Biotechnology Information
NGS	Next generation sequencing
NPM1	Nucleophosmin 1
NSE	Non-specific esterase
OS	Overall survival
PAS	Periodic acid–Schiff
PBF	Peripheral blood film
PBMC	Peripheral blood mononuclear cells
PBS	Phosphate buffer saline
PCR	Polymerase chain reaction
PTD	Partial tandem duplication
qPCR	Real-time PCR
RFU	Relative fluorescence unit
RNA	Ribonucleic acid
RPMI	Roswell Park Memorial Institute
RT	Reverse transcription
RTK	Receptor tyrosine kinase
SBB	Sudan black B
SD	Standard deviation
SEM	Standard error of mean
SNP	Single nucleotide polymorphism
SSCP	Single-strand conformation polymorphism
WBC	White blood cells
WHO	World Health Organization

CHAPTER 1

INTRODUCTION

Acute myeloid leukaemia (AML) is a clonal disease characterized by the proliferation and accumulation of myeloid progenitor cells in the bone marrow, which ultimately leads to hematopoietic failure (Robak and Wierzbowska, 2009). More than one quarter of a million adults throughout the world are diagnosed annually with acute myeloid leukaemia (AML) (Rowe and Tallman, 2010). Compared to younger adults, older AML patients are more likely to have AML with poor-risk cytogenetics (Sekeres, 2008). The duration of survival also varies in these patients. Age, white blood and cytogenetics are current risk factors and are essential to provide risk-adapted therapy to reduce over-treatment or under-treatment of patients. However, these are useful for only a fraction of patients as only 40 percent of patients have normal karyotype. Older adults with leukaemias typified by core-binding factor (CBF) abnormality (Sangle and Perkins, 2011) experiencing five-year overall survival (OS) rates is only 20 percent and even worse, zero percent for those with poor-risk features (Farag et al., 2006). Younger adults with AML who receive standard remission induction therapy experience complete remission (CR) rates of 65 to 85 percent, a full 25 percent higher than all older adults (Sekeres, 2008). To date, gene expression profiling of AML has largely confirmed the presence of well-established recurring cytogenetic abnormalities, such as translocations, deletions, point mutations, as well as microaberrations in apparently normal karyotypes. This has led to the identification of sets of genes reflective of these abnormalities (Willman, 2008) and identified new prospective prognosis categories. Genome wide search for suitable markers has identified multitudes of genes and uncharacterized transcripts but has not led to the identification of many novel therapeutic targets in AML. Selection of potential markers requires further screening, quantification and confirmation of genes expressed in a sufficiently large number of acute myeloid leukaemia samples. Current gold standard using real-time polymerase chain reaction (PCR) method is laborious and time consuming. The GenomeLab GeXP system provides an alternative method for rapid, simultaneous quantification of gene expressions in multiple samples. We hypothesized that GenomeLab GeXP system would be able to quantify multiple gene expressions more rapidly as compared to conventional PCR and there would be a significant correlation between treatment outcomes of the patients with their level of gene expressions.

1.1 Aim

To screen and confirm a panel of genes as well as to identify prognostic markers for acute myeloid leukaemias (AML).

1.2 Objectives

The objectives of the study are:-

- a) To quantify expression of genes in acute myeloid leukaemia samples using the GenomeLab GeXP Genetic Analysis System.
- b) To compare and confirm expression levels of selected genes in acute myeloid leukaemia samples from GenomeLab GeXP Genetic Analysis System with real-time PCR method.
- c) To correlate treatment outcome of acute leukaemia patients with level of gene expression in samples.



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