



Evaluation of Long Non Coding RNA (CCAT1) as a Prognostic Biomarker in Acute Myeloid Leukemia

A Thesis

"Submitted for degree of science as a partial fulfillment for
requirements of Master of science"

Submitted by

Rehab Raafat Abd-ELmaksoud

B.Sc. in Biochemistry, 2012

(Faculty of Science - Ain Shams University)

Under Supervision of

Prof. Dr. Magdy Mahmoud Mohamed

Professor of Biochemistry

Faculty of Science

Ain Shams University

Dr. Eman M. Saleh

Assistant professor of Biochemistry

Faculty of Science

Ain Shams University

Dr. Nashwa Nagy EL-Khazragy
Consultant of Clinical Pathology
Faculty of Medicine
Ain Shams University

*Biochemistry department
Faculty of Science
Ain Shams University
2020*



Ain-Shams University
Faculty of Science
Biochemistry Department

Approval sheet

Name of candidate/ **Rehab Raafat Abd-ELmaksoud**

Title of the thesis: **Evaluation of Long Non Coding RNA (CCAT1) as a Prognostic Biomarker in Acute Myeloid Leukemia.**

This thesis has been approved for submission by:

Supervisors:

Prof.Dr.Magdy Mahmoud Mohamed

Professor of Biochemistry, Faculty of Science, Ain Shams University

Dr. Eman M. Saleh

Assistant professor of Biochemistry, Faculty of Science, Ain Shams University

Dr. Nashwa Nagy EL-Khazragy

Consultant of Clinical Pathology, Faculty of Medicine, Ain Shams University

Examiners committee:

Prof. Dr. Mona Ahmed Sadek

Professor of Biochemistry, Nutrition department, Faculty of Women for Arts, Science and education, Ain Shams University

Prof. Dr. Samar Samir Youssef

Professor of Biomedical Technology, National Research Center.

Prof. Dr. Magdy Mahmoud Mohamed

Professor of Biochemistry, Faculty of Science, Ain Shams University

Head of Biochemistry Department

Prof. Dr. Kholoud Salah El-Din

ACKNOWLEDGMENT

First and for most thanks to **ALLAH** who gives me the power to go forward in a way illuminated with his merciful guidance

No words can express my profound thanks for deep gratitude to **Prof. Dr. Magdy Mahmoud Mohamed** for constructive guidance and his continuous efforts and facilities he offered throughout his supervision. I am also thankful to him for his continuous support faithful advice and continuous encouragement during the execution of the work. It is an honor to me that he is my supervisor and I will never forget his valuable supervision.

I am sincerely grateful to **Dr. Eman M. Saleh** for providing invaluable guidance throughout this research. I would also like to thank her for her friendship and empathy.

I would like to express my thanks and gratitude to **Dr. Nashwa EL-Khazragy** for her sincere constructive help and valuable contribution throughout the experimental work and for suggesting several important improvements in the manuscript of the thesis and for sustained encouragement continuous support grate assistance and kind supervision.

My thanks are due to my sincere colleagues for their respectable dealing and sincere cooperation.

DEDICATION

TO MY FAMILY

SPECIAL DEDICATION FOR ALL MY

FAMILY ESPECIALLY

MY FATHER AND MY MOTHER

ALSO MY HUSBAND

FOR THEIR CONTINUED SUPPORT AND

ENCOURAGEMENT THROUGHOUT MY

WORK

LIST OF ABBREVIATIONS

Ago2	Argonaute protein 2
ALL	Acute lymphoblastic leukemia
AML	Acute myeloid leukemia
APL	Acute promyelocytic leukemia
Ara-C	Cytosine arabinoside
AS	Antisense
AT1R	Angiotensin II type 1 receptor
ATRA	All-trans-retinoic acid
AUC	Area under the curve
<i>BANCR</i>	BRAF-activated non-protein coding RNA
BLACAT1	Bladder cancer-associated transcript 1
CBC	Complete blood picture
CCA	Cholangiocarcinoma
CCAT1	Colon cancer-associated transcript-1
CCATs	Colon cancer associated transcripts
cDNA	Complementary DNA
CEBPA	CCAAT enhancer-binding protein- α
ChIRP-Seq	Chromatin Isolation by RNA purification
CI	Confidence interval
CLIP	Crosslinking immunoprecipitation
CLL	Chronic lymphocytic leukemia
CML	Chronic myeloid leukemia
CN-AML	Cytogenetically normal acute myeloid leukemia
CNV	Copy number variation
CRC	Colorectal cancers
CRISPRs	Clustered regularly interspaced short palindromic repeats
dsRBD	double-stranded RNA binding
EC	Esophageal cancer
<i>EGOT</i>	Eosinophil granule ontogeny transcript
EMPs	Early myeloid progenitors
FAB:	French-American-British
FRET	Fluorescence resonance energy transfer
G2DHE	GATA2 distal hematopoietic enhancer
GBC	Gallbladder cancer:
GC	Gastric cancer
GCF	First-degree relatives of patients with gastric cancer
HCC	Hepatocellular carcinoma
HGNC	The HUGO Gene Nomenclature Committee
HK	Housekeeper gene
HMGA2	High mobility group AT-hook 2

HS	highly significant
HSCs	Hematopoietic stem cells
IQR	Interquartile range
IT	Intronic
ITDs	Internal tandem duplications
<i>LINC</i>	Long intergenic non-coding
LNA	Locked nucleic acids
LncRNAs	Long non-coding RNAs
LPS	Lipo poly saccharide
LSC	leukemic stem cell
M0	Minimally differentiated Acute Myeloblastic leukemia
M1	Myeloblastic leukemia
M2	Myelocytic leukemia
M3	Promyelocytic leukemia
M4	Myelomonocytic leukemia
M5:	Acute monocytic leukemia
M6	Acute erythroid leukemia
M7	Acute megakaryoblastic leukemia
MBC	metastatic breast cancer
MGB	Minor groove –binding
miRNAs	Micro RNAs
MRD	Minimal/measurable residual disease in AML
MTX	Methotrexate
<i>NEAT1</i>	Nuclear paraspeckle assembly transcript 1
NF- κ B	Nuclear factor- κ B
NPM1	Nucleophosmin 1
NSCLC	Non-small cell lung carcinoma
NUD	Nonulcer dyspepsia
OS	Overall survival
p-ALL	pediatric Acute Lymphocytic Leukemia
PAZ	Piwi/Argonaute/Zwilli domain
PBS	Phosphate-buffered saline
PDCD4	programmed cell death 4
PLTs:	Platelets
poly IC	polyribonucleosinic–polyribocytidylic acid
pre-miRNA	Precursor miRNA
pri-miRNA	primary miRNA
PSPs	paraspeckle proteins
PTEN	phosphatase and tensin homolog
RFS	Shorter relapse-free survival
RISC	RNA-induced silencing complex
RNaseP	Ribonuclease P

ROC Curve	Receiver operator characteristic curve
RTqPCR	Real-time quantitative PCR
SCT	Rtem cell transplant
SnoRNA	Small nucleolar RNA
SnoRNP	Small nucleolar RNA protein
SNP	Single-nucleotide polymorphism
SPEM	Spasmolytic polypeptide- expressing metaplasia
STAT5	Signal transducer and activator of transcription 5
SZ	Schizophrenia
T2D	Type 2 diabetes
TC	Tongue cancer
TKDs	Tyrosine kinase domains
TNF- α	Tumor Necrosis Factor- α
TPM1	Tropomyosin1
WHO	World Health Organization

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ABSTRACT

Colon cancer-associated transcript-1 (CCAT1) is a long noncoding RNA that maps to chromosome 8q24.21, it was first discovered to be upregulated in colorectal cancer. Recent studies have observed the CCAT1 overexpression in primary human solid cancers as in AML. Moreover, it repressed monocytic differentiation and promoted cell growth of HL-60. The present study aims to investigate the correlation of CCAT1 expression with clinic-pathological features and the clinical prognosis of the patients with AML. To find out the association between CCAT1 expression and expression of miRNA-155 as a targeting gene for CCAT1 and to improve our understanding of the roles and the clinic implications of CCAT1 in the development and progression of AML. This study obtained by measuring the expression of CCAT1 and miR-155a of 50 AML patients. The results of the present work showed that CCAT1 and miR-155a were increased by 3.0 and 5.6 folds respectively in AML compared to normal controls and also upregulation of both biomarkers was significantly associated with high risk AML. It could be concluded that CCAT1 and miR-155a can be considered as a diagnostic and prognostic biomarker in AML.

Key words

Leukemia, Acute myeloid leukemia, Long Non Coding
RNA and MicroRNA-155a

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