Interphase FISH Analysis of 9p21 Deletion in Childhood Acute Lymphoblastic Leukemia

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Submitted for Partial Fulfillment of Master Degree in Clinical and Chemical Pathology

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List of Abbreviations

ALL : Acute lymphoblastic leukemia

AML : Acute myeloid leukemia

AP : Acid phosphataseAT : Ataxiatelangiectasia

BM : Bone marrow

CALLA : Common ALL antigenCBC : Complete blood cell countCD : Cluster of differentiation

CGH : Comparative genomic hybridizationCML : Chronic myelogenous leukemia

CR : Complete remissionCSF : Cerebrospinal fluidDW : Distilled waterEBV : Epstien-Barr virus

EDTA : Ethylene diamine tetra acetic acidFAB : French, American, and BritishFCL : Folliclular center lymphoma

FCS: Fetal calf serum

FISH : Fluorescence in situ hybridization **FLT3** : FMS-related tyrosine kinase-3

Hb : Hemoglobin HM : Hepatomegaly HS : Highly significant Ig : Immunoglobulin **IPT** : Immunophenotyping IR : Incomplete remission LDH : Lactate dehydrogenase LN : Lymphadenopathy LOH : Loss of heterozygosity

MALT : Mucosa-associated lymphoid tissue

MPO : Myeloperoxidase

MRD : Minimal residual disease

MTAP : Methylthioadenosine phosphorylase

MTS-2 : Multiple tumor suppressor 2

List of Abbreviations (Cont...)

NB : Neuroblastoma

NOS : Not otherwise specified

NS : Non- significant
PB : Peripheral blood
S : Significant
SBB : Sudan black

SIg : Surface immunoglobulin

SM : Splenomegaly

SSC : Standard saline citrate

TCR : T cell receptor

TdT : Terminal deoxynucleotidyl transferase

TF : Transcription factor **TK** : Tyrosine kinase

TLC : Total leucocytic count TSG : Tumor suppressor genes

WBC: White blood cell

WCPP: Whole chromosome painting probe

WHO : World Health Organization

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برَحْمَتِكَ فِي عِبَادِكَ الصَّالِحِينَ)

صدق الله العظيم

النمل. اية رقو ١٩



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INTRODUCTION

cute lymphoblastic leukemia (ALL) is a malignant disease resulting from the accumulation of genetic alterations of B or T lymphoid precursor cells (*Meshinchi and Arceci*, 2007). It is considered the most common cancer among persons under 15 years of age and accounting for > 30% of all childhood malignancies (*Ries et al.*, 1999).

Pediatric ALL is one of the success stories of cancer research and treatment. Not only this fatal disease is now curable in the majority of patients, who have access to appropriate therapy and support (*Pui*, 2004), but much of its cellular and molecular biology has been uncovered (*Cogen and Franco*, 2003; *Pui et al.*, 2004).

A number of clinical and laboratory features evident at diagnosis, have prognostic value for predicting the outcome of patients treated for ALL. The identification of these prognostic factors has provided a mean of stratifying patients into different risk groups and "tailoring" treatment accordingly (*Carrol, 2003; Bhatias, 2004*).

Molecular characterization of the genetic changes has yielded a wealth of information on the mechanism of leukemogenesis. These findings have also allowed the development of sensitive techniques such as fluorescence in situ hybridization (FISH) for identification of underlying molecular defects, which can be applied to evaluate disease prognosis,

monitor response to treatment and predict minimal residual disease (*Lee et al.*, 2007).

Genetic alterations of tumor suppressor genes (TSG) such as p53, RB gene, p15 and p16 contribute to leukemic transformation of hemopoietic stem cells or their committed progenitors by changing cellular functions (*Krug et al.*, 2002; *Berlin et al.*, 2003).

Alterations of the 9p21 locus have been implicated in many types of cancer including ALL, indicating a role for the tumor suppressor genes CDKN2A (MTS1) and CDKN2B (MTS2), which encode for p16^{INK4a} and p15^{INK4b}, respectively. Loss of cell proliferation control and regulation of the cell cycle are known to be critical to cancer development (*Sarina et al.*, 2009).

Both p16^{INK4a} and p15^{INK4b} tumor suppressor genes counteract the activity of cyclins, cyclin dependent kinase (cyclin D – CDK 4/6 complexes) and other regulatory proteins of the cell cycle such as p53 and pRb. Dysregulation of cell cycle control is crucial in the development and progression of ALL. Thus, deletions of p16 or p15 located at 9p21 may play a role in leukemogenesis, have a prognostic significance and provide new targets for therapeutic interventions (*Lee et al.*, 2007; *Lin et al.*, 2007; *Sarina et al.*, 2009).

AIM OF THE WORK

The present work aims to detect del 9p21 in pediatric ALL patients, by FISH technique; in order to evaluate the impact of such deletion on patients response to therapy and to correlate it to standard prognostic factors.

ACUTE LYMPHOBLASTIC LEUKEMIA

DEFINITION:

cute lymphoblastic leukemia (ALL) is a malignant (clonal) disease of the bone marrow in which early lymphoid precursors proliferate and replace the normal hematopoietic cells of the marrow. ALL may be distinguished from other malignant lymphoid disorders by the immunophenotype of the cells, which is similar to B- or T-precursor cells. Immunochemistry, cytochemistry, and cytogenetic markers may also aid in categorizing the malignant lymphoid clone (*Seiter*, 2013).

ALL is considered the most common cancer in children and is among the most curable of the pediatric malignancies (*Alison et al.*, 2006).

INCIDENCE AND EPIDEMIOLOGY:

I. Age

ALL is the most common cancer diagnosed in children and represents 23% of cancer diagnoses among children younger than 15 years. There has been a gradual increase in the incidence of ALL in the past 25 years. A sharp peak in ALL incidence is observed among children aged 2 to 3 years (>80 per million per year), with rates decreasing to 20 per million for ages 8 to 10 years. The incidence of ALL among children aged 2 to 3 years is approximately fourfold greater than that for infants and is nearly tenfold greater than that for adolescents aged 16 to 21 years (*Shah and Coleman*, 2007).