

GENETIC ALTERATIONS IN ACUTE LYMPHOBLASTIC LEUKEMIA

UAB

Elena Esperanza Cebollada

Introduction

Acute Lymphoblastic Leukemia (ALL) is a neoplasm of immature lymphoid progenitors, characterized by **clonal expansion** of leukemic cells in the **bone marrow (BM)**. It can affect **both children and adults**, but is more prevalent between ages of 2 and 5 years. The majority of ALL cases are **aneuploidy** or harbor recurring **structural chromosomal rearrangements** that are important in initiating events in leukemogenesis and which subdivides between the subtypes B and T, but that are insufficient to explain the biology and heterogeneity of ALL. For that reason it is **necessary** a thorough **study** about **genetics** of the disease.

Methods and objectives

Bibliographic search of reviews and original articles in databases such as PubMed (NCBI) has been made in order to accomplish the following goals: present the current situation of the disease and how the genetic study has allowed us to understand the disease as well as the risk stratification, and develop new therapies.

Clinical diagnostic



Figure 1: Bone marrow aspiration and biopsy from National Cancer Institute <<http://www.cancer.gov>> [26/05/2015]

Morphology

Immunophenotype

Genetic analysis

- **ALL-L1**
- **ALL-L2**
- **ALL-L3**
- **ALL-B:** CD19, CD20, CD22, CD24, CD79a, CD10, cIgM and mIgM
- **ALL-T:** CD2, CD3, CD5, CD1a, CD4 and CD7
- **Conventional cytogenetics**
- **Molecular cytogenetics**
- **PCR and CGH**

Techniques

1956 The human chromosome number is 46

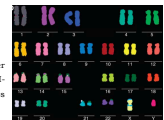
1985 Invention of polymerase chain reaction (PCR)

Development of conventional cytogenetics

1982 Fluorescence *in situ* hybridization was developed

1992 Comparative genomic hybridization (CGH) was developed

Figure 2: Human male Karyotype after hybridization with of a seven-fluorochrome M-FISH mix from Naturel protocols <www.nature.com> [26/05/2015]



GENETIC ALTERATIONS

Cytogenetic alterations	Genetic lesion	Associated clinical features and specific treatments	Prognosis
Changes in chromosomal Number 25%	Hyperdiploidy (>50)	20% with <i>FLT3</i> activation	Good prognosis
	Hypodiploidy (<44)	High frequency of RAS pathway and IKAROS gene family mutations	Poor prognosis
Structural abnormalities chromosome 50%	B-ALL		
	<i>BCR-ABL</i> t(9;22)	Associated with <i>IKZF1</i> or <i>CDKN2A</i> deletions. Treatment with tyrosine kinase inhibitors like imatinib but resistance develops rapidly. <i>BCR-ABL</i> -like with deletions in <i>IKZF1</i> , rearrangements in <i>CRLF2</i> and <i>JAK</i> mutations.	Poor prognosis
	<i>MLL</i> rearrangements	Unregulated <i>FLT3</i> . Use of cytarabine for some rearrangements. Treatment with <i>FLT3</i> inhibitors like sorafenib or crenalanib.	Improved outcome
	<i>ETV6-RUNX1</i> t(12;21)	Intensive chemotherapy that includes asparaginase. Sometimes present <i>iAMP21</i> with multiple copies of <i>RUNX1</i> . Current development of treatment in the UK	Good prognosis
	<i>E2A-PBX1</i> t(1;19)	Increased incidence in African Americans. Intensified chemotherapy	Generally excellent prognosis
	T-ALL		
	<i>NOTCH1</i> t(7;9)	Resistant tumours, gain of function that activates <i>MYC</i>	
	<i>HOX</i> rearrangements	Elevated expression; <i>HOX11</i> inhibition of PP2A and PP1 phosphatases	<i>HOX11</i> T-ALL has better prognosis than other T-ALL molecular
	<i>TAL1/SCL</i> t(1;14)	Dimerize <i>E2A</i> and HEB transcription factors, blocking T cell differentiation	Good and poor outcomes
	<i>LYL1</i> t(7;19)	Dimerize <i>E2A</i> and HEB transcription factors, blocking T cell differentiation	

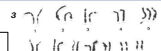


Figure 3 and 4: Hyperdiploidy (3) and Hypodiploidy karyotype from Quintero M, Rojas-Atencio A, Ruiz A, González M, Herrera J, Atencio F, Delgado W, Urdaneta K, Pérez F, 2003. Anomalías cromosómicas en pacientes venezolanos con mieloma múltiple. Scielo. Vol. 44

Figure 5: Chromosomal translocation *BCR-ABL* from Leucemia linfocítica aguda infantil: Toriberto (PDQ). Instituto Nacional del Cáncer. p. 1-73

Figure 6: (AMP21). A) Partial G-banded karyotypes showing pairs of chromosomes 21 from six patients. In each pair the normal chromosome 21 is on the left and the abnormal homologue is on the right. B) G-banding and mBAND partial karyotypes of normal left and abnormal right chromosomes 21 from *iAMP21* from Harrison C.J, 2009. Cytogenetics of paediatric and adolescent acute lymphoblastic leukaemia. *British Journal of haematology*. Vol. 144, p. 147-156

Cytogenetic technologies permit the detection of different types of chromosomal and genetic abnormalities. There are three types of chromosomal aberrations: those involving changes in chromosome number, those with structural abnormalities and those that present a normal karyotype. The genetics of these chromosomal alterations allow us to know the incidence and prevalence of each one, use it for monitoring the disease, learn about the biology of the disease, the risk stratification and the potential markers for therapy. **Hyperdiploidy**, with gain of at least 5 chromosomes, is one of the most frequent alterations in childhood, and is associated with a favourable outcome. Hyperdiploidy includes **quasitri/tetraploidy**. However, **hypodiploidy** with fewer than 44 chromosomes is associated with poor prognosis. The recurring **chromosomal rearrangements** differentiate, B-ALL or T-ALL and the new rearrangements are critical for leukemogenesis and commonly perturb genes encoding regulators of haematopoiesis, tumour suppressors, oncogenes or tyrosine kinases, but in most cases they are primary events that need others to produce disease. Moreover, some patients present a **normal karyotype (diploid)**, which has an improved outcome.

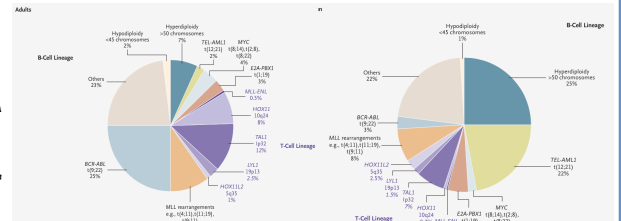
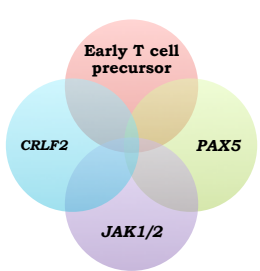


Figure 7: Estimated Frequency of Specific Genotypes of ALL in Children and Adults from Pui C.H, Robinson L, Look A. T, 2008. Acute lymphoblastic leukemia. *Lancet*. Vol. 371, p. 1030-1043. Mechanisms of disease Acute Lymphoblastic Leukemia. *The New England Journal of Medicine*. Vol. 350, p. 1535-1548

Novel alteration



Novel perspectives

Personalized medicine

There is no consensus on what constitutes an optimal treatment

Develop less toxic treatments while preserving earlier gains in efficacy

Studies have begun to identify a number of polymorphisms, such as *ARID5B*, *IKZF1*, *CEBPE* and *CDKN2A*

New epigenetic studies

Conclusion

ALL is the most common and heterogeneous neoplasm in childhood and its also affects adults. Early diagnosis is important to perform a good treatment and get complete remission.

Genetics have allowed us to identify a large number of chromosomal alterations that are associated with biological features. The genetics alterations has been used to define B-ALL and T-ALL, prognostic and risk stratification.

Conventional cytogenetic analysis should be a mandatory routine examination.

Further genetic study must be carried out to understand the disease and create specialized treatments.

References

- [1] Chiaretti S, Zini G and Bassan R, 2014. Diagnosis and Subclassification of Acute Lymphoblastic Leukemia. *Mediterranean Journal of Hematology and Infectious Diseases*. Vol. 6.
- [2] Harrison C.J, 2009. Cytogenetics of paediatric and adolescent acute lymphoblastic leukaemia. *British Journal of haematology*. Vol. 144, p. 147-156
- [3] Mullighan C.G, 2012. Molecular genetics of B-precursor acute lymphoblastic leukaemia. *The Journal of Clinical Investigation*. Vol. 122, num. 10, p. 3407-3415
- [4] Pui C.H, Robinson L, Look A. T, 2008. Acute lymphoblastic leukemia. *Lancet*. Vol. 371, p. 1030-1043
- [5] Pui C.H, Mullighan C.G, Evans W.E and Relling M.V, 2012. Pediatric acute lymphoblastic leukemia: where are we going and how do we get there?. *Blood*. V.120, p.1-3