

Chronic lymphocytic leukemia and prolymphocytic leukemia. Two coins or two sides of the same coin?

Laura Magnano,^{1,2*} Alba Navarro,^{2,3*} Mónica López-Guerra,^{1,2,3} Guillem Clot,^{2,3} Sílvia Beà,^{1,2,3} Gabriela Bastidas,⁴ Dolors Costa,^{1,2,3} Andrea Rivero,⁴ Marta Garrote,⁴ Eva Giné,^{2,3,4} María Rozman,^{1,2,3} Marta Aymerich,^{1,2,3} Dolors Colomer,^{1,2,3} Armando López-Guillermo,^{2,3,4} Elías Campo,^{1,2,3} Neus Villamor^{1,2,3} and Estella Matutes¹

**LM and AN contributed equally as co-first authors*

¹Hemathopatology Unit, Department of Pathology, Hospital Clínic of Barcelona; ²Institut d'Investigacions Biomèdiques August Pi i Sunyer (IDIBAPS); ³Centro de Investigación Biomédica en Red de Cáncer (CIBERONC) and ⁴Hematology Department, Hospital Clínic of Barcelona, Barcelona, Spain

Correspondence: LAURA MAGNANO - lmagnan@clinic.cat

doi:10.3324/haematol.2020.253062

Supplementary table.

	B-PLL	CLL	B-PLL + CLL
Morphology	Medium to large sized lymphoid cells with a round nucleus, prominent single nucleolus, and moderately basophilic cytoplasm	Lymphocytes with clumped chromatin and smudge cells	Mixture of prolymphocytes and CLL cells
Immunophenotype	B-lymphocytes lambda+, CD5 ⁺ , FMC7 ⁺⁺ , CD10 ⁻ , CD23 ⁻ CD200 ⁻ and CD43 ⁻ . The antigen intensity of CD20, CD22 and CD79b was normal	B-lymphocytes CD5 ⁺ , CD23 ⁺ , CD43 ⁺ , CD200 ⁺ , CD10 ⁻ , CD20 and CD22 weakly positive and weak kappa light chain restriction	Three populations: 1. CLL phenotype with kappa light chain restriction 2. Phenotype of the B-PLL cells with lambda light chain restriction 3. Polytypic B-cell phenotype
Fluorescence <i>in situ</i> hybridization (FISH)	<i>MYC</i> (8q24) rearrangement <i>BCL6</i> , <i>BCL2</i> , <i>CCND1</i> and <i>CCND2</i> were not rearranged <i>TP53</i> was not deleted. The t(11;14)(q13;q32) was absent	<i>MYC</i> (8q24) rearrangement was not detected <i>ATM</i> , <i>D12Z3</i> , <i>DLEU</i> , <i>LAMP1</i> and <i>TP53</i> was normal.	--
Molecular analysis	<i>CCND1</i> , <i>SOX11</i> , <i>HDGFRP3</i> , <i>DBN1</i> , <i>CCND2</i> , <i>CCDN3</i> , <i>FMOD</i> , <i>KSR2</i> , <i>MYOF</i> , <i>MME</i> , <i>CXCR</i> , and <i>CAMSAP2</i> were not overexpressed No mutations in <i>TP53</i> or in hotspot regions of <i>BRAF</i> , <i>MYD88</i> , <i>NOTCH2</i> , <i>NOTCH1</i> , and <i>MAP2K1</i>	--	--
Sequencing study	IGHV5-51 family	IGHV1-69 family	IGHV5-51 family IGHV1-69 family