consistently associated with better outcomes and healthcare experiences.

Aims: This study uses the Lymphoma Coalition (LC) 2020 Global Patient Survey (GPS) on Lymphomas and CLL to describe the global differences in patients' information experiences at diagnosis, as well as to compare the areas of need for more information.

Methods: Globally, 9,179 patients with lymphoma or CLL from 89 countries took part in the LC 2020 GPS. The countries were grouped into regions, and regions with greater than 200 patient respondents were included in the analysis. The five regions analysed were Asia (AS) (n = 2326), Oceania (OC) (n = 695), Europe (EU)(n = 4343), North America (NA) (n = 1543), and South America (SA) (n = 214).

Descriptive analyses of questions relating to patients' information experiences at diagnoses and areas in which they needed more information were performed in IBM SPSS v27.

Results: All the regions differed significantly ($p < 0.05$) in the demographic categories of age, sex, education level, and household status.

When asked which time point patients had the greatest need for information, over half of patients in all the regions reported the time point as 'within the first month following diagnosis' (AS-62%, OC-58%, EU-57%, NA-53% and SA-59%) (Table 1).

Relating to how patients felt about the amount of information they were given upon diagnosis with lymphoma, patients from AS were the most prevalent in reporting they were not given enough information (55%) followed by patients from NA (36%). Additionally, only 30% of patients from AS reported receiving the right amount of information, while 60% and more, of patients from NA, EU, SA, and OC reported the same (60%, 67%, 71% and 70% respectively) (Table 1).

When asked about the specific areas patients needed more information in, the most commonly reported areas in all the regions were 'treatment options' (AS-76%, OC-44%, EU-50%, NA-61% and SA-40%), 'diagnosis and what it means' (AS-58%, OC-45%, EU-56%, NA-51% and SA-38%), and 'treatment side-effects' (AS-61%, OC-44%, EU-45%, NA-38% and SA-41%). Patients also reported needing information on 'support for self care', 'psychological support', 'support for their families', and 'fertility' (Table 1). Only 2% of patients from AS reported not needing any additional information compared to the other regions (OC-19%, EU-11%, NA-16% and SA-18%) (Table 1).

Conclusion: Access to timely and credible medical information remains an essential aspect of a successful patient experience and this study shows that patients with lymphoma have diverse information experiences and needs. It is therefore important that doctors provide information that address(es) each patient's unique information needs. In the future, LC would like to explore how demographic differences may have confounded results.

Keywords: Cancer Health Disparities

Conflicts of interests pertinent to the abstract

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141 | IMPACT OF DISEASE TREATMENT ON THE OUTCOME OF PATIENTS WITH CHRONIC LYMPHOCYTIC LEUKEMIA (CLL) WITH COVID-19: A MULTICENTER STUDY ON BEHALF OF GELLC

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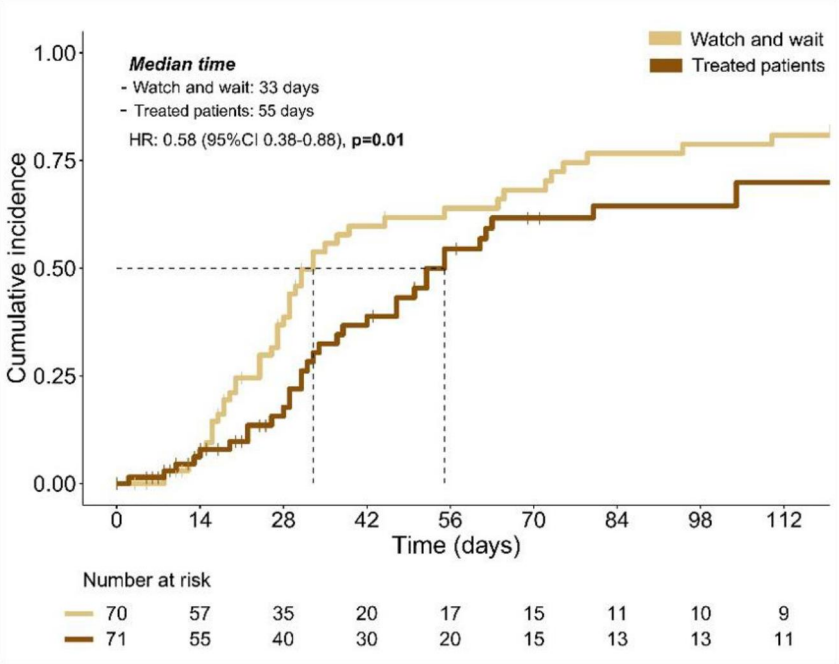
FIGURE 1 Time to PCR negativity according to CLL status



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Introduction: Patients (pts) with CLL are at risk of more severe COVID-19 clinical forms and worse survival compared to general population. Besides age and comorbidities, CLL treatments can aggravate an immune status otherwise impaired by the disease itself, which could also influence COVID-19 outcome. The aim of our study was to focus on COVID-19 outcomes according to CLL treatment at the time of COVID-19.

Patients and Methods: 321 pts with CLL and COVID-19 from 52 Spanish centers were included. Pts were classified in two cohorts according to time of COVID. First cohort were pts from the first wave (1W) of COVID and included 166 pts infected from March 1 to May 31, 2020; the second wave (2W) included 155 patients infected from August 1 to January 31, 2021. Clinical characteristics, CLL treatment status and COVID outcomes were analyzed and reported from the whole series, and from the two cohorts separately. Finally, we collected data referred to SARS-CoV-2 infection status and response, including Polymerase Chain Reaction (PCR) negativity for COVID19 and presence of serum neutralizing antibodies.

Results: Median age was 73 years (37-94) and 65% (n = 210) were male. A total of 160 (50%) were on watch and wait (W&W) approach, 61 (19%) were previously treated [26 of them (43%) ended treatment <12 months before COVID], and 100 (31%) were on active CLL treatment at the time of COVID diagnosis (72 BTKi, 16 BCL-2i, 9 alkylating drugs and 3 others). 1W cohort presented with more pneumonia (87% vs. 72%, p = 0.001), supplemental oxygen requirements (82% vs. 70%, p = 0.018) and admissions (92% vs 71%, p < 0.01) than those from 2W. Conversely, no significant differences in overall survival (OS) were found between the two cohorts. Considering the whole series, age and D-dimer levels were statistically associated with OS (p < 0.01). In addition, W&W patients presented better OS compared to patients on active or previous CLL treatment finished <12 months prior COVID infection (HR 1.7 [95% CI 1.09-2.81], p = 0.02). Finally, median time to PCR negativity was 33 days for W&W patients compared to 55 days for treated patients (p = 0.01) (Figure 1). Serological test was performed in 84 out of 321 cases (26%), with 47 patients (56%) becoming positive (IgG+). No significant differences in terms of seroconversion were found according to CLL treatment status. With a median follow-up of 60 days

(range 0-320), no SARS-CoV-2 reinfections were reported and, among IgG+ cases, none of the patients became seronegative.

Conclusions: CLL remains a high-risk disease for COVID-19 regardless of best understanding of SARS-CoV-2 management and improved health-care conditions during the 2W. Of note, patients in W&W have better OS compared to those previously treated or in active treatment at COVID diagnosis, suggesting that CLL treatment is worsening COVID-19 outcomes. Finally, PCR clears earlier in W&W patients than in treated cases.

Keywords: Chronic Lymphocytic Leukemia (CLL)

No conflicts of interest pertinent to the abstract.

142 | DISSECTING THE GENETICS OF DIFFERENT ANATOMICAL COMPARTMENTS OF SMALL LYMPHOCYTIC LYMPHOMA WITH A MULTIREGIONAL SEQUENCING APPORACH

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Background: Small lymphocytic lymphoma (SLL) is a model that can inform on whether spatial heterogeneity exists in leukemic B-cell tumors, as it is the sole entity that markedly involves both blood and lymph nodes in all cases. Circulating tumor DNA (ctDNA) recapitulates disease genetics in aggressive lymphomas but its role advantage multiregional sequencing of peripheral blood and lymph node biopsy is unexplored.

Methods: Patients with SLL (n = 12) were referred to our institution and provided with: *i)* tumour gDNA extracted from fresh frozen lymph node cells or formalin-fixed paraffin-embedded (FFPE) lymph node biopsies; *ii)* tumour gDNA extracted from sorted peripheral blood (PB) CD19+/CD5+ cells; *iii)* ctDNA from plasma; and *iv)* germline gDNA extracted from CD3+ T-cells and/or granulocytes for comparative purposes. The CAPP-Seq assay was used for the mutational profiling and comprised a panel of 124 genes relevant in B cell malignancies. Copy number variants (CNVs) were identified with the GATK4 CNV workflow.

Results: Overall, the analysis of the three SLL compartments analyzed (i.e. lymph node biopsy, circulating PB CD19+ cell compartment, and plasma ctDNA) identified a total of 46 mutations. The most frequently mutated genes were *TRAF3* and *ASXL1*in 3/12 (25.0%) patients each, followed by *NOTCH1*, *EGR2*, and *SF3B1* in 2/12 (16.7%) patients each (Figure 1A). By comparing the representation of gene mutations in the different anatomical compartments investigated in SLL, 10/46 (21.7%) mutations were identified in all three compartments, whereas the remaining mutations were differently distributed among the three examined compartments. More precisely, 6/46 (13.0%) mutations were exclusive of the lymph node biopsy, 15/46 (32.6%) were exclusive of the circulating PB CD19+ cell compartment, and only a small fraction of mutations (2/46; 4.3%) were detectable uniquely in the plasma ctDNA (Figure 1B). Interestingly, from a translational perspective, a *BIRC3* mutation that may harbor potential predictive value, has been identified only in the circulating PB CD19+ cell compartment. In addition, a bioinformatic algorithm for CNVs analysis has been applied to 8 patients in order to identify potential additional differences between the lymph node biopsy and the circulating PB CD19+ cell compartment. This algorithm showed 100% concordance with FISH karyotype and allowed the detection of at least one CNVs difference in 3/8 patients (37.5%).

Conclusions: These results suggest that the multiregional sequencing of the different anatomical compartments of SLL is essential to gain a comprehensive view of the disease mutational landscape. This observation may have clinical relevance when treatment tailoring is based on specific gene mutations used as molecular predictors that might be present in only one specific anatomical compartment of the disease.

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Keywords: Diagnostic and Prognostic Biomarkers, Chronic Lymphocytic Leukemia (CLL)

No conflicts of interest pertinent to the abstract.

143 | KINASE-DEAD BRUTON'S TYROSINE KINASE (BTK) C481F/Y MUTANTS CONFER IBRUTINIB RESISTANCE THROUGH ACTIVATION OF HEMATOPOIETIC CELL KINASE (HCK)

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Introduction: Ibrutinib is a once-daily BTK inhibitor used in the treatment of various B-cell malignancies and chronic graft-versus-host disease. Ibrutinib forms a covalent (irreversible) bond with C481 of BTK to inhibit kinase activity and reduce downstream B-cell receptor (BCR) signaling. In some patients who develop resistance to ibrutinib during treatment, acquired mutations at C481 disrupt binding of ibrutinib to BTK. The best characterized mutation is C481S, which results in reversible binding and decreased affinity for ibrutinib, while retaining intact mutant BTK kinase activity. Other clinically identified mutations are less well understood; better