

significantly more common with total body irradiation involving a myeloablative regimen and peripheral stem cell transplantation from a fully matched related donor. GvHD can be acute or chronic based on the clinical presentation and its occurrence after or before 100 days after allo-HSCT. aGvHD may occur beyond this arbitrary cut-off of 100 days. The widely accepted National Institutes of Health consensus criteria have been used to classify GvHD. GvHD is divided into four subclasses: 1) Classic aGvHD: Diagnostic and distinctive features of chronic GvHD (cGvHD) are absent. Clinical features of aGvHD and present within 100 days of allo-HSCT or donor lymphocyte infusion (DLI). 2) Persistent and/or recurrent late-onset aGvHD: Features of classic aGvHD without diagnostic manifestations of cGvHD occurring beyond 100 days after allo-HSCT or DLI. 3) Classic cGvHD: Present at any time after HSCT. Diagnostic and distinctive features of cGvHD are present without aGvHD. 4) Overlap syndrome: Features of both cGvHD and aGvHD can be seen. The most commonly affected organs are: Skin, eyes, oral mucosa, liver, GIS tract, genital organs, lungs, joints and fascia. The most important step for the prevention of GvHD is minimizing risk factors with donor selection and a preparative regimen. GvHD prophylaxis is essential for patients undergoing allo-HSCT. Guidelines for GvHD prophylaxis have been proposed by the European Group for Blood and Marrow Transplantation and European LeukemiaNet. The most common form of GvHD prophylaxis has been the combination of cyclosporine and a short course of methotrexate, which demonstrated improved survival compared to either drug alone. Both cyclosporine and tacrolimus decreased the proliferation of T-lymphocytes. Tacrolimus plus methotrexate is better in decreasing the risk for aGvHD than the combination of cyclosporine and methotrexate, particularly in unrelated HSCT. Both regimens are considered as cornerstones for most GvHD prevention strategies for patients receiving allo HSCT. The effects of the addition of corticosteroids to the combination of cyclosporine and a short course of methotrexate have shown conflicting results. Calcineurin inhibitors and Ruxolitinib, a JAK 1/2 inhibitor, are also used as prophylactic treatment. Unfortunately, there is no standard indication or timing for the initiation of therapy for GvHD. Many agents have been tested alone or in combination with corticosteroids. Extracorporeal photopheresis (ECP), mycophenolate mofetil, sirolimus, everolimus, rituximab, and ibrutinib are available options.

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Abstract 032

CHRONIC LYMPHOCYTIC LEUKEMIA (CLL): IMMUNOGENETICS AND DIAGNOSIS

Meryem Sener

Düzce Atatürk State Hospital, Türkiye

CLL is a monoclonal proliferation of mature B lymphocytes defined by an absolute clonal count $\geq 5 \times 10^9/L$ in blood. CLL is clinically heterogeneous: some patients remain asymptomatic for years, whereas others need multiple lines of therapy.

BCR biology and immunogenetics. A central driver of CLL biology is B-cell receptor (BCR) signaling. Compared with normal B cells, CLL cells display low IgM expression, variable responses to antigen, and tonic activation of anti-apoptotic pathways. Gene-expression and tissue array studies show up-regulation of BCR-pathway genes in lymph nodes and marrow versus blood, highlighting microenvironmental homing. The IGHV mutation status is a key immunogenetic marker: about 60% of patients have IGHV mutated $\geq 2\%$ from germline (typically indolent course), while $\sim 40\%$ have unmutated IGHV ($<2\%$), associated with faster progression and shorter survival before the era of BCR-targeted therapies. Roughly 30% of cases carry stereotyped BCRs; certain stereotyped subsets (e.g., 1 and 2) predict higher-risk disease. Cytogenetic lesions. Recurrent abnormalities identified by FISH (and, when needed, stimulated metaphase karyotype) include del(13q14.3) (most common; favorable when isolated), trisomy 12 (intermediate risk), del(11q22.3) involving ATM (bulky nodes, aggressive disease in younger patients), and del(17p13.1) affecting TP53 (worst prognosis, poor response to traditional chemotherapy). Complex karyotype (≥ 3 abnormalities) adversely impacts time to treatment and overall survival. Because clonal evolution can occur even without therapy, FISH (\pm cytogenetics) should be reassessed before each line of treatment, particularly to detect new del(17p). Gene mutations and microRNAs. CLL genomes are relatively simple (≈ 20 nonsynonymous changes and ≈ 5 structural lesions on average) and lack a unifying driver. Recurrently mutated genes include SF3B1, NOTCH1, MYD88, ATM, and TP53. NOTCH1 mutations ($\sim 15\%$) often co-occur with trisomy 12 and may confer reduced sensitivity to anti-CD20 antibodies and increased risk of Richter transformation; SF3B1 relates to DNA-damage responses; TP53 mutations rise from $\sim 5\%$ in early untreated disease to $\sim 40\%$ in advanced disease, frequently coexisting with del(17p). ATM mutations (10–15%) often accompany del(11q). MYD88 mutations are enriched in IGHV-mutated CLL and associate with a more indolent course. Non-coding alterations are also relevant: del(13q14.3) deletes the miR-15/16 cluster, derepressing anti-apoptotic programs (e.g., BCL2); loss of miR-181a and over-expression of miR-155 further support leukemic survival. Immune dysregulation. Beyond the malignant clone, CLL features innate and adaptive immune defects: reduced complement, qualitative neutrophil and NK-cell dysfunction, CD4 $^{+}$ T-cell exhaustion with impaired cytotoxicity, Th1 \rightarrow Th2 polarization, and T-regulatory expansion. Hypogammaglobulinemia is common ($\approx 85\%$ over the disease course), with low IgG/IgA correlating with infections. Diagnosis and differential. CLL is most often detected incidentally via lymphocytosis. Flow cytometry confirms a characteristic phenotype—CD19 $^{+}$, CD20 (dim), CD22 $^{+}$, CD23 $^{+}$, CD200 $^{+}$, CD5 $^{+}$, with dim surface Ig (kappa or lambda). When blood clonal B cells are $\geq 5 \times 10^9/L$, no additional testing is needed to confirm CLL. Take-home. Integrating flow cytometry, cytogenetics (FISH/karyotype), and targeted sequencing with IGHV status and non-coding lesions underpins modern risk stratification and sharpens diagnostic certainty in CLL.

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