# Monoclonal B-Cell Lymphocytosis: Update on Diagnosis, Clinical Outcome, and Counseling

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Keywords

Monoclonal B-cell lymphocytosis, chronic lymphocytic leukemia, classification, diagnosis, clinical management Abstract: Monoclonal B-cell lymphocytosis (MBL) is a clonal B-cell disorder characterized by less than 5  $\times$  10<sup>9</sup>/L B lymphocytes in the peripheral blood, with a characteristic immunophenotype and no lymphadenopathy or organomegaly. The vast majority of MBL cases express the immunophenotype of chronic lymphocytic leukemia (CLL; CLL-like MBL), although non-CLL MBL also exists. CLL-like MBL, which is the focus of this review, is divided into low-count MBL (median B-cell count: 0.001 imes10<sup>9</sup>/L, typically identified in population-based screening studies using highly sensitive flow cytometry assays) and high-count MBL (clinical MBL, median B-cell count:  $2.9 \times 10^{9}$ /L, typically identified during the workup of low-level lymphocytosis). Low-count MBL has an exceedingly small risk of progression to CLL, and these patients do not require any specific follow-up. In contrast, patients with high-count MBL have a 1% to 2% per year risk of progression to CLL requiring therapy, as well as a higher risk of infectious complications and secondary malignancies. Although the overall survival of high-count MBL patients collectively is similar to the age- and sex-matched general population, 5-year survival for high-count MBL with higher-risk biologic parameters appears to be slightly lower than that of the general population. This review summarizes key concepts in the classification, diagnosis, and biology of CLL-like MBL and addresses several important issues in clinical management. [Editor's Note: Corrections were made to this article on February 12, 2014.]

### **Background and Definitions**

The 1996 National Cancer Institute-Working Group (NCI-WG) criteria defined chronic lymphocytic leukemia (CLL) as a clonal lymphoproliferative disorder characterized by more than  $5 \times 10^{9}$ /L lymphocytes in the peripheral blood that coexpress CD19, CD5, and CD23, and have weak expression of CD20, CD79b, and surface immunoglobulin.<sup>1,2</sup> In the past 25 years, widespread use of 3- and 4-color flow cytometry has made it possible to detect monoclonal B cells at very low levels in apparently healthy individuals. In a public health study conducted by the US Centers for Disease Control in the 1990s, 11 out of 1926 (0.6%) individuals in the general population aged 40 to 76 years were found to have a clonal population of B cells with a CLL phenotype.<sup>3,4</sup> Subsequent studies also identified clonal B-cell populations with a non-CLL phenotype, similar to that of low-grade non-Hodgkin lymphomas (eg, marginal zone lymphoma).<sup>5</sup> Using biospecimens from the observational cohort of the PLCO (Prostate, Lung, Colon, and Ovary Cancer Screening Trial) study, investigators were able to demonstrate the presence of a monoclonal B-cell lymphocytosis (MBL) clone in virtually all patients (44 out of 45) who subsequently developed CLL.<sup>6</sup> This study convincingly demonstrated that CLL is almost always preceded by MBL. In 2005, the International Familial CLL Consortium proposed the term monoclonal B-cell lymphocytosis to describe very low levels of circulating monoclonal B cells that were identified by means of immunophenotypic characterization in the peripheral blood of apparently healthy subjects.<sup>7</sup>

In alignment with this proposal, the 2008 International Working Group of CLL (IWCLL) revised the diagnostic criteria for CLL and also formally recognized MBL as a separate entity.8 In contrast to the 1996 NCI-WG criteria, which defined CLL as more than  $5.0 \times 10^9$ /L lymphocytes in the peripheral blood with a characteristic immunophenotype, the 2008 IWCLL guidelines revised it to more than  $5.0 \times 10^{9}$ /L B lymphocytes. Patients with less than 5.0  $\times$  10<sup>9</sup>/L B lymphocytes in the peripheral blood were considered to have the small lymphocytic lymphoma (SLL) variant of CLL if pathologic lymphadenopathy was present, and MBL if there was no lymphadenopathy, splenomegaly, hepatomegaly, or cytopenias. Individuals with a clonal B-cell process consistent with MBL but without a CLL immunophenotype were classified as non-CLL phenotype MBL if they were CD5+, or CD5-ve MBL if they did not express CD5.

The natural history and management of non-CLL phenotype MBL and CD5-ve MBL are distinct from CLL-like MBL, but are beyond the focus of this review. The current diagnostic criteria for MBL are summarized in Table 1.

#### Prevalence

The size of the B-cell clone has a significant impact on its clinical relevance, making it important to distinguish between low-count MBL (typically identified through population screening) and high-count MBL (recognized during the evaluation of low-level lymphocytosis). Early population-based screening studies using 2-color flow cytometry identified a monoclonal B-cell population in 0.1% to 3% of the general population.<sup>4,9,10</sup> Subsequent 
 Table 1. Diagnostic Criteria for Monoclonal B-Cell

 Lymphocytosis

1. Documentation of clonal B-cell population by 1 or more of the following:

a. Light chain restriction,  $\kappa{:}\lambda$  ratio >3:1 or <0.3:1 or >25% B cells lacking or expressing low-level surface immunoglobulin

b. Heavy chain monoclonal IGHV rearrangements

2. Absolute B-cell count <5 x 10<sup>9</sup>/L

3. Presence of a disease-specific immunophenotype\*

4. No other features of a lymphoproliferative disorder or autoimmune/infectious condition:

a. Normal physical examination (no organomegaly or lymphadenopathy)

b. Absence of B symptoms, such as fatigue, night sweats, or weight loss

c. No evidence of an underlying autoimmune/infectious disease

CLL, chronic lymphocytic leukemia; *IGHV*, immunoglobulin heavy chain; MBL, monoclonal B-cell lymphocytosis.

studies using 4- to 8-color flow cytometry identified MBL in up to 6% of the general population.<sup>11-13</sup> A large population-based study utilizing 8-color flow cytometry to examine  $5 \times 10^6$ /L B cells per patient found that 73 out of 608 patients (12%) older than 40 years had CLL-phenotype MBL.<sup>14</sup> Table 2 summarizes all published studies that have reported on the prevalence of MBL to date.

The median clonal B-cell count in the peripheral blood of individuals with low-count MBL is only 0.001  $\times 10^{9}/L$ .<sup>15</sup> This is in contrast to the median clonal B-cell count of 2.9  $\times 10^{9}/L$  observed in high-count MBL.<sup>16,17</sup> More than 95% of patients with high-count MBL have an absolute B-cell count of more than 0.45  $\times 10^{9}/L$ . Given these facts, as well as the important differences in the biology and outcomes of patients with low- and high-count MBL, a threshold of 0.5  $\times 10^{9}/L$  has been proposed in order to distinguish between these conditions.<sup>15</sup> Prospective studies following patients with both low- and high-count MBL for an extended period are needed in order to confirm the biologic and prognostic importance of this threshold.

The change in the lower boundary of what constitutes CLL (from an absolute lymphocyte count [ALC] of  $\ge 5 \times 10^{9}$ /L to a B-cell count of  $\ge 5 \times 10^{9}$ /L) reclassified many patients who were previously considered to have CLL as having high-count MBL. A populationbased study in Olmsted County, Minnesota evaluated

<sup>\*</sup>CLL-like phenotype MBL cells coexpress CD5, CD19, CD23, CD20 (dim), and surface immunoglobulin (dim). Atypical-CLL phenotype MBL cells express CD5 with CD19, but are either CD23– or express CD20 (bright) or surface immunoglobulin (bright). Non-CLL phenotype MBL cells do not express CD5, but are CD20+, and express surface immunoglobulin (bright). It is important to exclude mantle cell lymphoma, which characteristically has t(11;14).

Reference	Study	Ν	Median	Flow Cytometry			CLL-Like	Non-CLL
Year	Population		Age (Range)	No. of Colors Markers Assessed		No. of Cells Exam- ined	MBL Phenotype Prevalence	MBL Phenotype Prevalence
Frequency of	MBL among healthy	residen	tial popula	tion and l	blood donors			
Shim <sup>4</sup> 2007	US general population	1926	53 (40-78)	2	CD19 or CD20, CD45, CD3, CD5	NR	0.6%	NR
Rachel <sup>9</sup> 2007	US blood donors	5141	45 (18-79)	2	CD19, CD5 In select samples: CD2, CD3, CD4, CD7, CD8, CD10, CD14, CD20, CD23, к, λ	NR	0.14%	NR
Dagklis <sup>13</sup> 2009	Italy general population	1725	55 (18-102)	5	CD5, CD19, CD20, κ, λ	5×10 <sup>5</sup>	5.2%	2.3%
Nieto <sup>14</sup> 2009	Spain outpatient clinic	608	62 (40-97)	8	CD3, CD5, CD8, CD10, CD19, CD20, CD23, CD45, CD56, κ, λ, Bcl2	5×10 <sup>6</sup>	12%	2.3%
Frequency of	MBL among outpat	ient clint	ic patients,	excluding	familial CLL patients			
Rawstron <sup>10</sup> 2002	UK outpatient clinic	910	>40	4	CD20, CD76b, CD19, CD5, κ, λ, CD5	2×10 <sup>5</sup>	3.5%	1.0%
Ghia <sup>11</sup> 2004	Italy outpatient clinic	500	74 (65-98)	4	CD5, CD19, к, λ or CD5, CD20, CD79b, CD19	2×10 <sup>5</sup>	4.4%	2%
Rawstron <sup>12</sup> 2008	UK outpatient clinic	1520	74 (60-80)	4	CD19, CD5, κ, λ	5×10 <sup>5</sup>	5.1%	1.8%
Frequency of MBL among clinically unaffected relatives of CLL patients								
Rawstron <sup>21</sup> 2002	Healthy first- degree relatives of 21 CLL families	59	NR (23-86)	4	CD20, CD76b, CD19, CD5, κ, λ, CD5	NR	13.6% in first-degree relatives	NR
Marti <sup>20</sup> 2003	First-degree rela- tives of 9 kindreds of familial CLL	33	NR	2	CD19 or CD20, CD45, CD3, CD5	NR	18%	NR
Matos <sup>22</sup> 2009	First-degree relatives of 42 families with sporadic CLL	167	NR (18-84)	4	CD20, CD79b, CD19, CD5	3×10 <sup>5</sup>	3.6%	0.6%

Table 2. Prevalence of Monoclonal B-Cell Lymphocytosis

CLL, chronic lymphocytic leukemia; MBL, monoclonal B-cell lymphocytosis; NR, not reported.

the incidence of CLL and high-count MBL from 2000 to 2010. The incidence of high-count MBL was 3.5 per 100,000 individuals, according to the IWCLL 2008 criteria. Of the 123 patients who were classified as having Rai stage 0 CLL by the NCI-WG 1996 criteria, 36 patients were reclassified as MBL by the IWCLL 2008 criteria.<sup>18</sup> This reclassification also shifted the stage distribution at diagnosis for those who remained in the CLL category, with an increased proportion of patients with Rai stage I or II disease at diagnosis. Reclassifying some of the lowest risk patients from Rai stage 0 to MBL also changed the natural history of those patients

who remained in the Rai stage 0 category under IWCLL 2008, resulting in a shorter time to first treatment.<sup>18</sup>

#### **Risk Factors for Developing MBL**

Few risk factors for the development of MBL or CLL have been identified. Consistent with the fact that CLL has the strongest family history of any hematologic cancer, the prevalence of MBL in families where at least 2 first-degree relatives are affected by CLL (eg, familial CLL; MBL prevalence, 12% to 18%) is 2- to 3-fold higher than that of the general population.<sup>19-21</sup> Studies suggest that relatives of patients with sporadic CLL also have an increased prevalence of MBL.<sup>22</sup> Increasing age and male sex are associated with an increased risk of developing MBL. Several groups have identified heritable germline gene polymorphisms associated with increased risk of CLL,<sup>23,24</sup> and initial studies suggest that these single nucleotide polymorphisms may confer this risk by increasing the likelihood of developing MBL.<sup>25</sup>

Recent studies have shown that up to one-third of patients with CLL will demonstrate stereotyped B-cell receptors (BCR), characterized by nonrandom combinations of immunoglobulin heavy-chain variable *(IGHV)* genes.<sup>26</sup> Structural similarity of these BCRs suggests that such receptors may bind to a similar yet unidentified antigen(s), with potential relevance to disease pathogenesis. Approximately 25% of CLL patients demonstrate stereotyped complementarity determining region 3 (CDR3) sequences, compared with less than 5% of individuals with low-count MBL.<sup>13</sup> One recent study found CDR3 stereotypy in 5.5% of individuals with low-count MBL, compared with 22% of high-count MBL patients and 20% of patients with Rai stage 0 CLL.<sup>27</sup>

Chronic infections may also contribute to the risk of developing CLL in some patients. In a populationbased study of 4249 CLL patients conducted in Denmark from 1977 to 1997, prior history of pneumonia was associated with significantly increased risk for CLL (odds ratio [OR], 1.4) compared with 15,690 frequency-matched controls.<sup>28</sup> Analysis from the Surveillance, Epidemiology and End Results (SEER) database also suggested that patients with CLL (n=10,171) were at increased risk for sinusitis, pharyngitis, bronchitis, pneumonia, influenza, cellulitis, and herpes zoster (OR range, 1.08-1.24) relative to 122,531 frequencymatched controls.<sup>29</sup> A link between infection and risk of CLL was also observed in a nationwide analysis of 4 million adult males who were admitted to Veterans Affairs hospitals.<sup>30</sup>

In a recent study, MBL was detected in 28.5% of patients (35 out of 123) with chronic hepatitis C virus (HCV),<sup>31</sup> with a trend toward increased frequency among patients with more advanced disease. Interestingly, the distribution of cases among the subtypes of MBL differed in HCV-infected patients relative to the general population. All phenotypes occurred at a higher frequency in the HCV-infected patients than in the uninfected control group. Although CLL-like MBL accounts for approximately 70% of cases in the general population, only 37% of the HCV patients with MBL had this phenotype. Atypical CLL and non-CLL types of MBL constituted 46% and 17% of the cases, respectively. The authors concluded that persistence of the HCV antigen may signal through the BCR chroni-

cally, resulting in clonal expansion of B cells. Additional research to determine which specific antigenic stimuli can lead to MBL is ongoing, and will likely provide clues to the stimuli that lead to CLL.

#### **Biologic Insights**

Although both CLL-like MBL and CLL share the same immunophenotypic markers, studies that describe their underlying biologic differences are limited. It was initially thought that low-count MBL was always a monoclonal process; however, single-cell analytic studies have showed that low-count MBL can be oligoclonal or polyclonal.<sup>32</sup> A recent study identified constitutive activation of lymphoid enhancer binding factor-1 (LEF-1) and the Wnt pathway in patients with CLL and MBL (absolute B-cell count of  $0.7-2.4 \times 10^{9}$ /L), but not in normal B cells, suggesting that the Wnt signaling pathway may be active and play a role in the pathogenesis of MBL and CLL.33 The IGHV gene mutation status and genetic abnormalities detected by fluorescence in situ hybridization (FISH) are generally similar among patients with high-count MBL and Rai stage 0 CLL (Table 3), although they are markedly different in individuals with low-count MBL.<sup>12,16,34,35</sup> In low-count MBL, both IGHV 4-34 and IGHV 3-23 genes are underrepresented and IGHV 1-69 usage is absent, whereas these IGHV gene families are much more common in CLL.13,14

In addition to the known common recurrent genetic alterations identified by FISH,36 recent genetic studies in CLL using massively parallel sequencing have identified novel mutations in NOTCH1, SF3B1, MYD88, ZMYM3, MAPK1, FBXW7, and DDX3X genes.<sup>37</sup> Of these, NOTCH1 (present in approximately 10% to 15% of CLL patients) and SF3B1 (present in approximately 10% to 15% of CLL patients) have been shown to be independent predictors of poor outcomes in CLL patients.<sup>38,39</sup> In a small study of 63 high-count MBL patients, SF3B1 mutation was detected in only 1 patient (1.5%), and 2 patients (3.2%) harbored NOTCH1 mutations.<sup>40,41</sup> A recent study evaluated the IGHV gene mutation status and FISH risk category in low-risk MBL, high-risk MBL, and CLL. Investigators demonstrated that low-count MBL clones appear to display a much lower frequency of chromosomal alterations that are restricted to del(13q) and trisomy 12, with a high prevalence of IGHV-mutated cases. In contrast, del(11q) was seen more often in high-count MBL, and del(17p) and NOTCH1 mutations were only found in CLL.<sup>42</sup> These data support the notion that evolution from low-count MBL to high-count MBL-and subsequently CLLoccurs in a stepwise fashion, with gradual acquisition of high-risk genetic abnormalities.

Reference	N	Median B-Cell	IGHV mutation status		FISH Results			
Year		Count, × 10 <sup>9</sup> /L (Range)	Mutated <i>IGHV</i> , %	<i>IGHV</i> Gene Usage	del(13q), %	Trisomy 12 (%)	del(11q), %	del(17p), %
Rawstron <sup>12</sup> 2008	309	3.3 (0.01-4.9)	90	3-07, 3-23, 4-34	58	21	6	3
Shanafelt <sup>35</sup> 2009	302	2.8 (0.02-4.9)	77	3-07, 1-69, 4-34, 3-23	44	18	2	3
Rossi <sup>16</sup> 2009	123	2.8 (0.2-4.9)	80	4-34, 3-23, 1-69, 3-30	35	18	0	4
Molica <sup>34</sup> 2011	105	3.9 (1.0-4.9)	70	3-23, 4-34, 1-69, 3-30	70	15	2	0
Henriques <sup>42</sup> 2013	51	2 (0.3-4.9)	73	3-23	31	20	4	0

Table 3. IGHV Mutation Analysis, IGHV Gene Usage, and FISH Analysis in High-Count Monoclonal B-Cell Lymphocytosis

FISH, fluorescence in situ hybridization; IGHV, immunoglobulin heavy chain.

# General Approach to the Workup of Lymphocytosis

A general approach to evaluating patients with lymphocytosis is shown in the Figure. It is important for clinicians to recognize that patients found to have non-CLL phenotype MBL require a complete evaluation for an underlying lymphoproliferative disorder appropriate for the histologic profile of the clonal B cells. For most cases of non-CLL phenotype MBL, this involves the typical non-Hodgkin lymphoma staging evaluation, including computed tomography (CT) scans of the chest, abdomen, and pelvis, as well as bilateral bone marrow biopsy.

Prior to classifying patients as having CLL phenotype MBL, it is important to consider whether they may have SLL (Table 1 and Figure). In a study that evaluated 36 patients with lymph node tissue containing CLL-type cells and less than  $5 \times 10^{9}$ /L peripheral blood monoclonal B cells, 24 (67%) patients had stable/improved lymph-adenopathy and 12 (33%) patients required treatment for CLL after a median follow-up of 23 months.<sup>43</sup> Features associated with progressive disease requiring treatment included lymph nodes larger than 1.5 cm and the presence of proliferation centers in the biopsied tissue.

It is well recognized that CT scans at the time of diagnosis will upstage approximately 25% of patients with newly diagnosed, Rai stage 0 CLL.<sup>44</sup> One recent study of 240 patients with Binet stage A CLL (according to the 1996 NCI-WG criteria) evaluated the effects of wholebody CT on disease classification.<sup>45</sup> Of the 240 cases of Binet stage A CLL, 69 patients had high-count MBL when classified using the 2008 IWCLL guidelines. CT scans identified a lymph node larger than 1.5 cm in 29 patients with high-count MBL, resulting in reclassification to SLL. After a median follow-up of 35 months, however, only 5 of the 66 patients with high-count MBL had progressed to CLL requiring therapy, with no difference observed among MBL patients who were reclassified as having SLL based on imaging. Collectively, these studies suggest that there may be a "nodal equivalent" of MBL, but indicate that there is no current clinical justification for routine CT scans in patients with CLL-phenotype MBL.

Ideally, these patients should be seen by a hematologist/oncologist at least once for a review of systems and a physical examination, with particular attention to a thorough family history. A bone marrow aspirate and biopsy is not required at the time of diagnosis. Additionally, there are no formal recommendations to test for various prognostic markers available to predict time to treatment and overall survival (as are available in CLL) for patients with MBL, outside of a research setting. Individuals with low-count MBL have an exceedingly low risk of progression to CLL requiring therapy, and therefore could be followed by their regular primary care physician for routine medical care. Patients with high-count MBL should be made aware of B-type symptoms, including fevers, night sweats, weight loss, and fatigue. They should also be informed of the risks of progression to CLL requiring therapy (which occurs at a rate of approximately 1% to 2% of cases per year). Annual follow-up by a hematologist/oncologist is generally advised in order to monitor the B-cell clone size and assess for clinical progression of disease. General recommendations for follow-up of MBL are summarized in Table 4.

### Key Questions Regarding the Natural History and Clinical Management of Patients With MBL

#### What Is the Natural History of MBL?

Since the prevalence of low-count MBL is at least 100 times more than that of CLL, it is apparent that only a



Figure. A schematic approach to incidentally-discovered lymphocytosis.

\*Treat the underlying infectious and autoimmune condition appropriately; if lymphocytosis does not resolve, consider peripheral blood flow cytometry.

†Phenotype of CLL cells is as follows: positive for CD19, CD5, and CD23; and weak expression of CD20, CD79b, and surface immunoglobulin.

‡Occasionally, some patients who have an increased ALC that is predominantly due to a reactive lymphocytosis are found to have a very small B-cell clone on flow cytometry that is not the etiology of the increased ALC. Such patients with a clonal B-cell count of less than 500 cells/uL should be considered low-count MBL.

ALC, absolute-lymphocyte count; CLL, chronic lymphocytic leukemia; IWCLL, International Working Group of CLL; MBL, monoclonal B-cell lymphocytosis; SLL, small lymphocytic leukemia.

subset of individuals with low-count MBL progress to overt CLL. Few studies have longitudinally examined the progression of low-count MBL. After a median follow-up of 34 months, Fazi and colleagues evaluated 76 individuals with low-count MBL using 5-color flow cytometry and demonstrated that the size of the B-cell clone in 90% of individuals was stable over time.<sup>46</sup> In another study of 78 individuals with low-count MBL, expansion of CLL cells occurred in 7.5% of patients after a median follow-up of 65 months. No individuals with low-count MBL had progressed to CLL that required therapy.<sup>47</sup>

More studies have evaluated clinical outcomes in patients with high-count MBL than in low-count MBL.

Given that the threshold to distinguish high-count MBL from Rai stage 0 CLL was somewhat arbitrarily selected, rather than focusing on what proportion of MBL patients progress to meet criteria for a CLL diagnosis, a more appropriate and clinically relevant question is: What is the rate of progression of high-count MBL to CLL requiring therapy? Several studies<sup>12,16,34,35,48-50</sup> have reported the rate of progression of high-count MBL to CLL requiring treatment and are summarized in Table 5. The median duration of follow-up in these studies ranged from 1.5 years to 6.7 years. The rate of progression to CLL requiring treatment was heterogeneous and ranged from 0% to 5% per year. The vast majority of these studies were retrospective; as

Factors to Consider	Low-Count MBL	High-Count MBL		
Risk of progression requiring therapy	Extremely low	1% to 2% per year		
Patient counseling	Yes	Yes		
History and physical examination	No modification to general medical care	Annually		
CBC with differential	Routine	Annually		
Screen for secondary nonhematologic malignancies	Age-appropriate cancer screening	Age-appropriate cancer screening; consider whole body skin examination for skin cancer screening		
Follow-up of infectious complications	No	Yes		

Table 4. General Recommendations for Follow-Up of Monoclonal B-Cell Lymphocytosis

CBC, complete blood count; MBL, monoclonal B-cell lymphocytosis.

Table	5. Progression	1 of High-Count	Monoclonal B-	Cell Lymphoc	ytosis to CLL R	equiring Treatment
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Reference, Year	N, Location	Median Follow-Up, Years (Range)	Rate of Progression
Rawstron, <sup>12</sup> 2008	185, UK	6.7 (0.2-11.8)	1.1% per year
Shanafelt, <sup>17</sup> 2009	302, USA	1.5 (0.3-7.9)	1.4% per year
Rossi, <sup>16</sup> 2009	123, Italy	3.6 (NR)	4% per year in the first 7 years, and then 0%
Molica, <sup>34</sup> 2011	124, Italy	2.8 (0.2-10)	2.5% per year
Fung, <sup>48</sup> 2007	46, Canada	2.5 (0.1-10)	0%
Kern, <sup>49</sup> 2011	298, Germany	NR	5% per year
Xu, <sup>50</sup> 2009	20, China	3.8 (1.5-11.3)	4% per year

CLL, chronic lymphocytic leukemia; NR, not reported.

such, accurate determination of clinical features in some patients was not always possible. Also, it appeared in some of the studies that the rate of progressive CLL requiring treatment was higher in the first few years following diagnosis. Based on current knowledge, the best estimate of the rate of progression of high-count MBL to CLL requiring therapy is approximately 1% to 2% per year.<sup>51</sup>

# What Are the Risk Factors of Progression From MBL to CLL Requiring Therapy?

Whereas the risk factors for disease progression in CLL (eg, non-del[13q14] FISH abnormality, unmutated IGHV, and expression of CD38, ZAP-70, and CD49d) have been well defined, there are limited studies examining the role of these risk factors on the natural history of high-count MBL. In a retrospective study from the Mayo Clinic involving 302 high-count MBL patients, expression of CD38 was associated with faster progression, but there were insufficient events to assess the impact of IGHV mutation, ZAP-70 expression, or chromosomal abnormalities to evaluate their association with progression.<sup>17</sup> Rossi and associates studied the impact of several prognostic markers among 123 patients with high-count MBL, and found that IGHV mutation analysis, CD38 and CD49d expression, and FISH analysis predicted for a faster time to progression on univariable analysis.<sup>16</sup> However, on multivariate analysis, only high-risk FISH category (trisomy 12 or del[17p]) remained significant. Kern and colleagues showed that

among 298 high-count MBL patients, ZAP-70 expression, unmutated *IGHV*, and trisomy 12 or del(11q) were associated with progression on univariate analysis. However, on multivariable analysis, only unmutated *IGHV* status remained significant.<sup>49</sup>

Several studies have also reported on overall survival in patients with high-count MBL.12,52 In the UK series of high-count MBL, 62 out of 185 patients (34%) died after 6.7 years of follow-up. However, only 4 deaths (2%) were attributed to progressive CLL.<sup>12</sup> In a retrospective study of 312 patients with high-count MBL seen at the Mayo Clinic, overall survival was not significantly different from that of age- and sex-matched controls in the general population.<sup>52</sup> This is in contrast to patients with Rai stage 0 CLL, whose overall survival was significantly inferior to that of the general population. Notably, however, the survival of patients with high-count MBL relative to the population was influenced by biologic characteristics of the B-cell clone. Patients with high-count MBL who were negative for CD38 had a survival identical to that of the general population, but 5-year survival for CD38+ highcount MBL patients was approximately 10% to 20% lower than that of the general population. Together, these findings lend support to considering both the absolute B-cell count<sup>27,28</sup> and biologic characteristics of the clone in future efforts to predict clinical outcome in patients with MBL.

Even fewer data are available on overall survival in individuals with low-count MBL. Bennett and colleagues

reported on the outcomes of individuals with low-count MBL detected during routine screening of normal 60- to 80-year-old patients seen in the clinic.<sup>47</sup> They identified 78 individuals with low-count MBL and 126 age-matched controls that did not have any abnormal circulating B cells. Among those for whom follow-up data were available, there were 9 deaths (23%) in the MBL group compared with 36 deaths (29%) among controls, after a median follow-up of 5.5 years. This report suggests that individuals with low-count MBL have no significant difference in overall survival when compared with those among an age-matched general population.

## Are Patients With MBL at Increased Risk of Other Complications Associated with CLL?

MBL and Infections Infections are a major source of morbidity and mortality in patients with CLL, and are directly or indirectly related to the cause of death in 30% to 50% of CLL patients.<sup>53,54</sup> In addition to hypogammaglobulinemia that is thought to occur from defective functioning of the nonmalignant B cells, abnormalities in T-cell function and neutrophil and monocyte function have been reported.55,56 Recent studies evaluating the risk of infection in high-count MBL suggest that these individuals are at a higher risk for infectious complications. In a case control study from the Mayo Clinic, infection risk was compared among local cohorts of patients with highcount MBL (n=154), newly diagnosed CLL (n=174), and adult patients seen in the general medicine clinic (n=689). After a median follow-up of 4 years for patients with MBL and CLL and 3 years for controls, hospitalization owing to serious infections was noted to occur more among patients with MBL (16%) and CLL (18%) than among controls (2.6%). In a Cox proportional hazard analysis of all 1017 patients (controls, MBL, and CLL), male sex (hazard ratio [HR], 2.3), major comorbid health problems (HR, 1.7), the presence of CLL (HR, 3.2), treatment for progressive CLL (HR, 2.4), and the presence of MBL (HR, 3.0) were independently associated with risk of hospitalization for infection.<sup>57</sup> In contrast, separate studies of individuals with low-count MBL suggest that these patients do not have a higher risk for developing infections when compared with the general population.<sup>47</sup>

**MBL and Secondary Malignancy** An association between CLL and increased risk of secondary cancers has long been recognized. In a large retrospective study of 16,367 CLL patients enrolled in the SEER program who were followed for 5.2 years, 11% of patients developed a second solid tumor. This rate was significantly higher than that of the general population (odds ratio, 1.20).<sup>58</sup> In a more recent study of more than 2.3 million patients with various solid malignancies enrolled in the SEER database, overall

survival was compared in patients with and without preexisting CLL. After adjusting for age, sex, race, and disease stage, patients with cancers of the breast, colorectum, kidney, prostate, and lung had an inferior overall survival if they had preexisting CLL, compared with patients without a diagnosis of CLL.<sup>59</sup>

Multiple studies suggest an approximate 2-fold increase in the incidence of second cancers among CLL patients.<sup>60,61</sup> Whether patients with high-count MBL are at an increased risk for secondary malignancies has also been explored. A recent study evaluated the risk of secondary nonhematologic cancers among locally-dwelling patients with MBL (n=125), CLL (n=153), and controls (n=596) seen in the general medicine clinic at the Mayo Clinic from 2004 to 2009.62 After a median follow-up of 4.2 years, 16% of patients with MBL developed nonhematologic malignancies, compared with 4% of controls (HR, 5.0). The MBL cohort had a higher incidence of cancer of the breast, lung, and nervous system than the control cohort. In contrast to these findings in patients with high-count MBL, 78 individuals with low-count MBL identified in a hospital outpatient clinic did not appear to have a higher risk of developing a secondary nonhematologic malignancy.47

Collectively, these observations regarding risk for serious infection and secondary malignancy suggest that there is a clinical phenotype to high-count MBL that goes beyond the risk for progression to CLL. Indeed, the findings suggest that the risk of hospitalization for infection and/or risk of secondary malignancy may be higher than the likelihood of progression to CLL requiring treatment. Further follow-up and validation of these preliminary findings will hopefully allow us to derive more insight into the risk of nonhematologic malignancy and infection among patients with both high-count MBL and low-count MBL.

#### Can Patients With MBL Serve as Stem Cell Transplant Donors?

Allogeneic transplant is now a well-established therapy for patients with CLL. For CLL patients who meet the international consensus criteria for transplantation,<sup>63</sup> a matched sibling is the preferred donor source. As previously discussed, CLL has a strong genetic predisposition, with approximately 10% of patients having 1 or more first-degree relative affected by CLL. Moreover, approximately 15% to 18% of patients from CLL families<sup>19-21</sup> as well as up to 15% of older relatives of patients with sporadic (ie, nonfamilial) CLL have MBL.<sup>22</sup> Accordingly, approximately 1 out of every 7 relatives undergoing human leukocyte antigen typing to serve as a sibling donor may have unrecognized MBL if evaluated using sensitive screening assays.<sup>64</sup> A number of cases of transfer of MBL donor clones to CLL patients undergoing transplant have been reported.<sup>65-67</sup> The identification of an MBL clone in a potential sibling donor is a challenging situation. If the patient has more than 1 sibling who is a match and is considered a suitable donor, the donor without MBL may be prioritized. However, in the case of a patient who has only 1 matched sibling, whether an unrelated donor should be chosen for transplantation remains an unanswered question. Cases of transfer of CLL-like MBL from unrelated donors to children undergoing stem cell transplant have also been documented, thus raising the broader question of whether all patients preparing to donate stem cells (including unrelated donors) should be screened for MBL.<sup>68</sup>

#### Conclusion

The formal recognition of MBL as a separate diagnostic entity in the 2008 IWCLL guidelines has made it important for practicing hematologists/oncologists to be familiar with MBL. Two distinct types of MBL exist: one that is detected using highly sensitive flow cytometry assays in population screenings (low-count MBL) and the other detected in a healthcare setting owing to lymphocytosis (high-count MBL). New evidence suggests that the clonal B-cell biologic characteristics (eg, IGHV mutation status, chromosomal abnormalities detected by FISH, and IGHV gene usage) of high-count MBL closely mirror those of Rai stage 0 CLL, whereas low-count MBL has a distinct clinical and biologic profile. Patients with high-count MBL progress at a rate of 1% to 2% per year to CLL requiring therapy, whereas individuals with low-count MBL have a very low risk of progression. Recent studies suggest that the risks of serious infection and/or secondary malignancy among patients with high-count MBL are greater than the likelihood that they will progress to CLL requiring treatment. Additional studies are needed in order to better understand the risks of infection, secondary malignancies, and appropriate clinical management of patients with MBL.

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