

Prognostic Factors in Follicular Lymphoma

Thomas Relander, Nathalie A. Johnson, Pedro Farinha, Joseph M. Connors, Laurie H. Sehn, and Randy D. Gascoyne

From the Departments of Pathology & Laboratory Medicine and the Division of Medical Oncology, British Columbia Cancer Agency and the University of British Columbia, Vancouver, British Columbia, Canada.

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Corresponding author: Randy D. Gascoyne, MD, FRCPC, Department of Pathology, British Columbia Cancer Agency, 600 W 10th Ave, Vancouver, British Columbia V5Z 4E6, Canada; e-mail: rgascoyn@bccancer.bc.ca.

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ABSTRACT

Follicular lymphoma (FL) is one of the most common types of non-Hodgkin's lymphoma. It is usually diagnosed at an advanced stage, for which many treatment options exist, however, no curative standard therapy has been identified. The outcome is highly variable with a median survival of approximately 10 years. The life expectancy of patients with FL has been extended with the use of rituximab, a monoclonal antibody targeting the CD20 antigen on FL cells, but there remains a group of patients who fail to respond to chemoimmunotherapy and die early of their disease. Transformation of FL to an aggressive histology is an important event with high morbidity and mortality. The Follicular Lymphoma International Prognostic Index has become the clinically useful prognostic tool, but gives only a rough estimate of expected outcome. There is a need for useful biomarkers for prediction of the disease course of single patients to individualize therapy, especially in the new era of chemoimmunotherapy.

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INTRODUCTION

Follicular lymphoma (FL) constitutes approximately 20% of all newly diagnosed lymphoma cases,¹ making it the second most common subtype of non-Hodgkin's lymphoma worldwide and the most common subtype seen in North America.² It is characterized by an indolent clinical course, typical morphology, and the presence of a chromosomal translocation, t(14;18)(q32;q21) or variant in 85% of patients. This chromosomal aberration results in the juxtaposition of the immunoglobulin heavy chain gene (*IGH*) on chromosome 14 with the *BCL2* oncogene on chromosome 18 leading to constitutive, and therefore inappropriate, expression of the *BCL2* protein. Overexpression of *BCL2* confers relative resistance to apoptosis, thus giving the cells a survival advantage that may facilitate the acquisition and retention of secondary genetic abnormalities.

FL is a heterogeneous entity with some patients developing progressive or transformed disease early and 15% dying within 2 years from diagnosis, while others remain alive for decades without need for treatment. This variability in outcome underscores the necessity to gain further insight into the biology and clinical behavior of the disease to enable individualized therapy.

TREATMENT AND CLINICAL COURSE

The median age at diagnosis of FL is 59 years with a male to female ratio of 1:1.7.³ FL is typically diag-

nosed in the advanced stages, with only 26% to 33% of patients presenting with stage I to II disease.^{3,4} With conventional chemotherapy, even if combined with radiotherapy, advanced-stage FL is incurable. It is characterized by an indolent course with patients developing slowly progressive lymphadenopathy over many years, with or without constitutional B symptoms (eg, fever, weight loss > 10%, drenching night sweats). Temporary, spontaneous regressions occur in 20% of patients managed without initial therapy.⁵ Historically, median survival has ranged from 6 to 10 years.⁴⁻⁷

Transformation to an aggressive lymphoma occurs at a rate of 3% per year and is associated with substantial morbidity and mortality.^{8,9} Transformation is defined as the development of a more aggressive histology lymphoma, most commonly diffuse large B-cell lymphoma (DLBCL), that is thought to be clonally related to the original FL.

Limited-stage FL treated with external-beam radiotherapy results in prolonged remission in 30% to 50% of patients and an apparent plateau on the disease-free survival curve after 15 to 20 years.^{10,11} Two randomized studies showed that deferred initial treatment in asymptomatic advanced-stage patients does not compromise long-term outcome or risk of transformation.^{7,12} FL is highly sensitive to antineoplastic agents early, but grows increasingly resistant with successive lines of therapy.⁴

The chimeric anti-CD20 monoclonal antibody rituximab has significant activity alone¹³ and in combination with chemotherapy.¹⁴ The addition of

rituximab to chemotherapy has resulted in a higher rate of complete remission (CR) and prolonged remission duration without increasing clinically relevant toxicity.¹⁵ Several studies have confirmed an improvement in overall survival (OS) with immunochemotherapy as the initial treatment for FL.¹⁵⁻¹⁷ Furthermore, rituximab as maintenance therapy after induction therapy for relapse improves progression-free survival (PFS) and OS.¹⁸ However, an improved survival for patients diagnosed with FL has been noted over the past 25 years,¹⁹ an effect at least in part predating the introduction of rituximab, likely explained by improved diagnosis and supportive care.

CLINICAL PARAMETERS

Multiparameter Indices

The International Prognostic Index (IPI), originally developed for aggressive lymphoma, identifies four risk groups based on age, tumor stage, serum lactate dehydrogenase (LDH) level, performance status, and number of extranodal sites of disease.²⁰ The IPI also reliably identifies risk groups among FL²¹⁻²³; however, it only classifies a small proportion of patients into the highest-risk category.

Three prognostic indices have been developed specifically for FL. The Italian Lymphoma Intergroup (ILI) index identifies three risk groups with 10-year survival rates of 65%, 54%, and 11% based on six clinical parameters (advanced age, male sex, number of extranodal sites of disease, B symptoms, serum LDH level, and erythrocyte sedimentation rate).²⁴

In 2004, the Follicular Lymphoma International Prognostic Index (FLIPI) was published resulting from a multicenter effort.²⁵ It includes five parameters: age (> 60 v ≤ 60 years), stage (III-IV v I-II), anemia (hemoglobin < 120 v ≥ 120 g/L), number of involved nodal areas (> 4 v ≤ 4), and serum LDH (elevated v normal), and classifies patients into three groups with 10-year OS rates of 71%, 51%, and 36%, respectively. The FLIPI is predictive in patients treated with immunochemotherapy,²⁶ can be applied in first relapse,²⁷ and predicts transformation.²⁸ The IPI, FLIPI, and ILI indices have been directly compared, all identifying somewhat different risk groups.²⁹ Recently, the FLIPI-2 index was published, incorporating beta-2 microglobulin, lymph node size larger than 6 cm, bone marrow involvement, anemia, and age older than 60 years (Table 1).^{25,30,36} All of these clinical indices are robust, easy to use in clinical practice, and of value for stratification in clinical trials; however, marked variations in outcome remain within each risk group.

Biomarkers in Blood and Bone Marrow

There are conflicting reports regarding the prognostic impact of bone marrow (BM) involvement by FL. BM involvement was associ-

Table 1. Adverse Factors in the FLIPI and the FLIPI2 Indices

FLIPI ²⁵	FLIPI2 ³⁰
Age > 60 years	Age > 60 years
Stage III-IV	Bone marrow involvement
Anemia (Hb < 120g/L)	Anemia (Hb < 120 g/L)
Number of involved nodal areas > 4	Nodes > 6 cm
LDH > ULN	β2-microglobulin > ULN

Abbreviations: FLIPI, Follicular Lymphoma International Prognostic Index; Hb, hemoglobin; LDH, lactate dehydrogenase; ULN, upper level of normal.

ated with decreased survival in several investigations including those of the ILI and the FLIPI.^{24,25,32,33} In contrast, others have not found BM involvement in itself to affect survival,³⁴ but rather the histologic pattern³⁵ or degree of marrow involvement.³⁶ Importantly, BM status at the time of diagnosis has been included in the FLIPI-2.³⁰

The characteristic t(14;18)(q32;q21) generates a *BCL2-IGH* fusion gene, which can be used as a marker of disease detectable by polymerase chain reaction (PCR).³⁷ This technique is highly sensitive and can routinely detect one translocation-positive cell in 10⁶ cells in peripheral blood (PB) or BM. PCR has been used for detecting minimal residual disease (MRD) after therapy.³⁸ Three different break points within the *BCL2* gene have been identified in FL.³⁹⁻⁴¹ However, the value of molecular monitoring in FL has not yet been established. Despite attaining a CR after chemotherapy, the BM remained positive by PCR in all or most patients without clear prognostic impact in some reports,⁴²⁻⁴⁴ whereas others have found molecular CRs to be common.⁴⁵ Rambaldi et al⁴⁶ reported that the degree of BM involvement by lymphoma by quantitative real-time PCR before rituximab plus cyclophosphamide, doxorubicin, vincristine, and prednisone (R-CHOP) therapy was predictive of outcome and that patients attaining molecular CR experienced a prolonged freedom from relapse.

Currently, the implication of the presence of t(14;18)-positive cells detected by PCR remains unknown. Not all PCR-positive patients relapse, and some convert to PCR negativity without therapy.⁴⁷ Furthermore, t(14;18)-positive cells have been found in patients in long-term remission after therapy for FL^{48,49} and *BCL2* translocations have been detected by PCR in PB from healthy individuals and from autopsies from patients without lymphoma.^{50,51}

Other Biomarkers in Blood

Biomarkers readily measurable from the PB that have been correlated with outcome in FL are summarized in Table 2.⁵²⁻⁶⁷ Beta-2 microglobulin has reached wide acceptance as a prognostic marker and is included in FLIPI-2,³¹ but is not universally available in retrospective cohorts.^{24,25} LDH is a robust prognostic factor in several types of lymphoma; however, in FL it is elevated in only 20% of patients.^{24,25} Serum angiogenic factors have been analyzed in heterogeneous groups of patients with lymphoma with partly conflicting results.^{59,60,61,63,68} Interestingly, polymorphisms leading to high expression of tumor necrosis factor may influence outcome in non-Hodgkin's lymphoma, pointing to the importance of host factors.^{62,64-66}

PATHOLOGIC PARAMETERS

FL is a neoplasm of germinal center B cells that mimic the architecture of normal secondary lymphoid follicles. Benign and malignant follicles contain a heterogeneous mixture of non-neoplastic cells including T cells, benign B cells, follicular dendritic cells (FDC), and macrophages. The majority of patients with FL manifest two major types of neoplastic B cells: small centrocytes and larger centroblasts. Histologic grading of FL is based on the relative proportions of these two cell types.

Histologic Grade

The current WHO classification recognizes three histologic grades (grades 1 to 3) of FL.⁶⁹ Grading of FL is poorly reproducible

Table 2. Peripheral Blood Biomarkers and Prognosis in FL

Biomarker	Effect on OS	Other Effects	Comment
Absolute lymphocyte count	Longer if ↑ ⁵²		
Beta-2 microglobulin	Shorter if ↑ ⁵⁴ Shorter if ↑ ⁵⁵ Shorter if ↑ ⁵⁶	Poor response and short TTF if ↑ ^{15,53} Shorter FFP if ↑ Shorter FFP in first relapse if ↑ ⁵⁷	FL grade 3 FL grade 3
LDH	Shorter if ↑ ^{24,25,33} No effect ⁵⁸		Stage I-II
Albumin Serum Urine	Shorter if ↓ ^{24,25}	Poor response and short PFS if ↑ ⁵⁸	
VEGF	Shorter if ↑ ⁵⁹	Associated with other poor prognosis factors	Only 13% FL
FGF	Shorter if ↑ ⁶⁰	Strong prognostic factor	Only 14% FL
VEGF + FGF	Shorter if ↑ ⁶¹ No effect ⁶²	Combination independent of IPI	Only 14% FL 30% FL
Endostatin	Shorter if ↑ ⁶³	Associated with VEGF ↑	Only 16% FL
TNF	Shorter if ↑ ^{64,65}	Shorter PFS if ↑	Combined with receptor levels; 40% indolent lymphoma
TNF + sCD23		Poor response if ↑ ⁶⁶	Indolent lymphoma
sICAM-1	Shorter if ↑ ⁶⁷	Correlated to advanced disease and B-symptoms	Minority FL

Abbreviations: FL, follicular lymphoma; OS, overall survival; TTF, time-to-treatment failure; FFP, freedom from progression; LDH, lactate dehydrogenase; PFS, progression-free survival; VEGF, vascular endothelial growth factor; FGF, fibroblast growth factor; IPI, International Prognostic Index; TNF, tumor necrosis factor; sICAM-1, soluble inter-cellular adhesion molecule-1.

among pathologists, calling into question studies that report prognostic impact based solely on this variable. Similarly, subtle architectural variations, such as the presence of diffuse areas, have not been well annotated in most FL studies. Immunostaining for FDCs has been infrequently performed, making it difficult to accurately determine true follicle formation in most reported studies.^{70,71} Several studies have suggested a correlation between grade and survival in FL.^{23,69,72,73} Although there is no OS difference between patients with grade 1 or 2 FL, there remains controversy about an inferior OS correlating with FL grade 3. This may reflect that grade 3 FL itself is heterogeneous. Anthracycline-based therapy has been claimed to be beneficial when treating patients with grade 3 FL⁶⁹ and to have a potential for cure; however, this remains controversial.^{23,55,56,74,75} Miller et al⁷⁶ found no plateau in the survival curve or difference in OS between patients receiving aggressive therapy for FL of different grades. In a retrospective analysis, Chau et al⁷³ found no difference in survival among FL grades 1 to 3. Patients with FL grade 3 were similarly at risk for late relapses as for grades 1 and 2.

The WHO classification subdivides FL grade 3 into FL grade 3A, made up of a mixture of centroblasts and centrocytes, and FL grade 3B, in which the centroblasts are distributed in confluent sheets.⁶⁹ Potentially, FL grade 3A may lie within the spectrum of disease with FL grades 1 to 2, while FL grade 3B may behave similarly to de novo DLBCL. Similar to FL grades 1 to 2, FL grade 3A is more likely to be CD10 positive and t(14;18) positive compared with FL grade 3B.⁷¹ Furthermore, chromosomal aberrations involving 3q27 (*BCL6*) occur in a similar frequency in FL grade 3B and DLBCL.^{71,77} However, in one report comprising 190 patients with FL grade 3, no difference in event-free survival or OS was found between patients classified as grade 3A and grade 3B,⁷⁰ which is supported by Chau et al.⁷³ Thus, the

relevance of distinguishing between FL grade 3A and 3B remains unclear. Identifying areas of diffuse disease,⁷⁰ likely a harbinger of transformation, may be more clinically relevant.

Immunophenotype: Neoplastic Cells

Proliferation index. The proliferation index has prognostic value in FL.^{23,78} It correlates with the number of large cells and thus with histologic grade and with OS in univariate analysis but not in multivariate analysis.⁷⁹

BCL2 and BCL2 family proteins. The family of BCL2-related proteins plays a central role in the surveillance of mitochondrial integrity by balancing between pro- and antiapoptotic members. Only a few of these proteins have been studied in relationship to prognosis in FL and no consistent correlation has been found.⁸⁰ As a possible exception, a high number of MCL1-positive centroblasts has been correlated with poor OS.⁸¹ Similarly, expression of the long RNA isoform of *BCLX_L* has been correlated with prognosis in FL,⁸² however, expression of the protein did not.⁸³

Using reverse-phase protein microarrays, when microdissected follicles from reactive lymph nodes were compared with follicles with FL, most proapoptotic and antiapoptotic proteins except for BCL2 were present at comparable levels in BCL2-positive and BCL2-negative tumors with activation of the AKT/BAD signaling pathway.⁸⁴ Gulmann et al⁸⁵ also used a proteomic approach to analyze apoptotic pathways in FL. They found phosphorylation of AKT to be frequent in FL suggesting that it may act as an antiapoptotic agent along with BCL2. High ratios of BCL2/BAK and BCL2/BAX were associated with early death from disease. The expression patterns of other proapoptotic members of the BCL2 family have largely unknown clinical impact.⁸⁶ Future studies on the role of BCL2 family proteins in FL are

needed as they may identify patients who will benefit from novel BCL2 mimetics, small molecules that specifically target BCL2 proteins.^{87,88}

Germinal center–related markers. *BCL6* encodes a zinc finger transcription factor involved in germinal center formation. CD10 is a membrane metalloendopeptidase expressed in the germinal center. In FL, these two markers of germinal center origin are expressed in more than 95% and 75% of cases, respectively.⁸⁹ Although their prognostic significance is established in DLBCL,⁹⁰ their relevance in FL is less clear. Using immunohistochemical scoring systems to combine the percentage of positive malignant cells and their intensity of expression, the expression level of *BCL6* has been correlated with favorable prognosis in FL.⁹¹ PU.1 is an ETS-domain transcription factor essential for the development of myeloid and B lymphoid cells. Constitutive PU.1 expression inhibits the earliest B-cell development, and low levels of PU.1 expression in hematopoietic progenitor cells are instrumental in promoting B-cell fate determination.⁹² Torlakovic et al⁹³ studied the clinical impact of proteins associated with the germinal center in FL and found PU.1 protein expression, but not CD10 or *BCL6*, to be a favorable marker of OS independent of the FLIPI.

Cell cycle regulators. *TP53* mutations have been reported in FL at diagnosis and are associated with an inferior survival.⁹⁴ The presence of mutations leading to overexpression of the *TP53* protein has been associated with transformation.^{95,96} Expression of *TP53* protein is only moderately correlated with the presence of mutations (64%) and similarly with the expression of key regulators of *TP53*, such as *CDKN1A* or *MDM2*.⁹⁷ The latter have also been shown to correlate with transformation.^{97,98} A gene expression profiling study of 57 patients with FL established a set of 14 genes that were highly expressed in patients with a favorable response to CHOP; however, only expression of *CYCLIN B1* mRNA and protein level had prognostic impact independent of the FLIPI.⁹⁹

Others. *SOCS3* is a cytokine suppressor that inhibits cytokine signaling by Janus kinase (ie, the JAK-STAT pathway). Overexpres-

sion of *SOCS3* has been reported to be an independent unfavorable prognostic factor in FL.¹⁰⁰ Overexpression of Ying-Yang 1, a zinc-finger protein regulating *IL4* gene expression, has also been linked with shorter survival in FL.¹⁰¹

Cytogenetics and Molecular Genetics

Classical karyotyping. Cytogenetic analysis of FL reveals a wide range of recurrent, nonrandom chromosomal alterations. FL is characterized by the overexpression of the antiapoptotic protein *BCL2* as a result of the t(14;18)(q32;q21) or its rare variants t(2;18) and t(18;22). t(14;18) is present in approximately 85% of grade 1 and 2 FL and although it is considered insufficient on its own to cause FL, it provides these B cells with a survival advantage leaving them prone to accumulate additional genomic abnormalities.¹⁰² However, in a study of FL cases lacking the t(14;18), Horsman et al¹⁰³ found distinct patterns of recurrent chromosomal alterations. In another report, FLs lacking the t(14;18) were less likely to express CD10 or *BCL2*, were more likely to arise at extranodal sites and had a better OS. Recently, Katzenberger et al¹⁰⁴ described t(14;18)-negative FL characterized by a predominantly diffuse growth pattern, presenting clinically with large but localized inguinal tumors. The majority of FL patients without a t(14;18) have a deletion in 1p36.

The malignant cells in FL have an average of four to six different cytogenetic changes in addition to the *BCL2* translocation.^{105,106} Only 5% of FL have t(14;18) as the sole detectable abnormality. The most common abnormalities are break points in chromosome 1, deletions in the long arm of chromosome 6 (6q-), trisomy 7 (+7), trisomy 12 (+12), presence of a derivative of chromosome 18 (der(18), and duplication of X (+X).¹⁰⁶

Early studies suggested that the number of abnormalities and presence of certain alterations (6q-, +7, +X, +21) were associated with an inferior survival.¹⁰⁷ However, as karyotypic complexity increases after therapy,¹⁰⁸ there is an inherent selection bias if biopsies

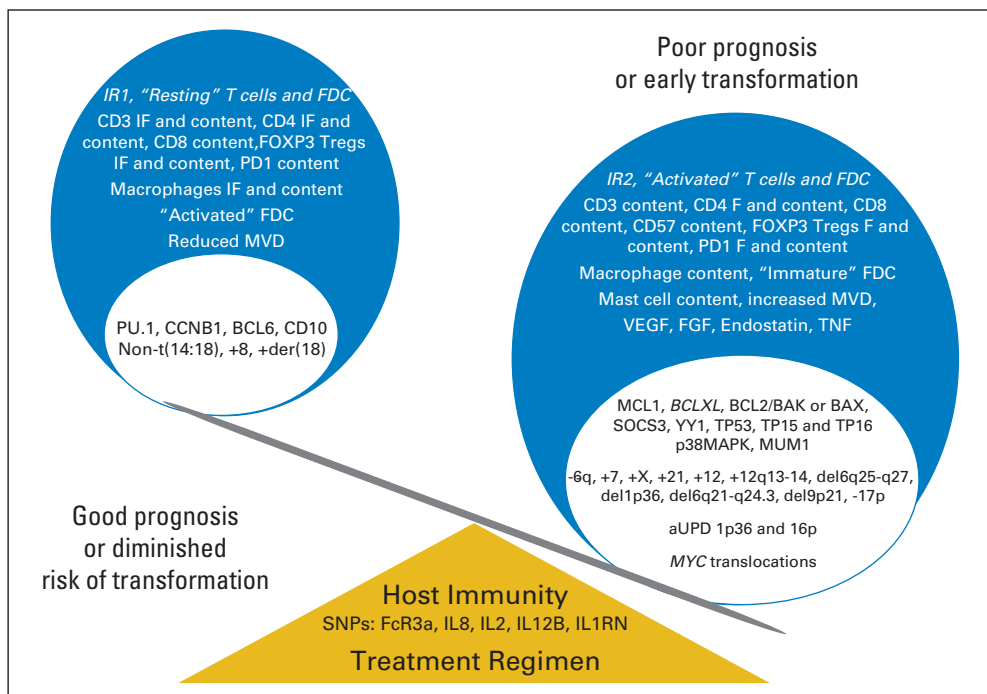


Fig 1. Biomarkers impacting survival or transformation in follicular lymphoma (FL). Some biomarkers are controversial, resulting from treatment heterogeneity. Larger circle: features of nonmalignant cells. Inner circle: tumor cells. IR, immune response; FDC, follicular dendritic cells; IF, interfollicular; F, follicular; MVD, microvessel density; VEGF, vascular endothelial growth factor; EGF, endothelial growth factor; TNF, tumor necrosis factor; aUPD, acquired uniparental disomy; SNPs, single nucleotide polymorphisms.

taken at the time of progression or relapse are used for analysis. Tilly et al¹⁰⁹ reviewed 66 FL biopsies taken at the time of diagnosis and found deletion 6q to be associated with an inferior survival. Höglund et al¹¹⁰ reviewed the karyotypes of 336 cases of FL and, using principle components analysis, postulated distinct pathways of clonal evolution of chromosomal changes arising in a temporal order with early changes being 1q+, +7, +8, +12, and +der(18) and later 2p-, 10p-, -15, 17p-, and 17q-. Based on the clinical data on 165 patients, +12 and 17p- were correlated with an adverse outcome. In contrast, we recently reviewed 210 karyotypes from FL biopsies taken at diagnosis and found no association between the number or type of cytogenetic abnormalities with clinical outcome.¹¹¹

Comparative genomic hybridization. Comparative genomic hybridization (CGH) can be performed by hybridizing tumor DNA against normal chromosomes (chromosomal CGH) or by using microarray platforms with spotted DNA probes (array CGH).¹¹² Viardot and colleagues¹¹³ analyzed 124 samples of FL using chromosomal CGH and reported a number of recurrent alterations. In a subset analysis of 82 patients, loss of chromosomal material at 6q25-27 was a strong independent predictor of inferior survival. Cheung et al¹¹⁴ identified two genomic regions, deletions in 1p36.22-p36.33 and 6q21-q24.3, to be highly associated with transformation and inferior OS in patients with FL using array CGH. Recently, Schwaenen et al¹¹⁵

reported a large number of recurring genomic aberrations in FL as analyzed by array CGH, of which deletions in 9p21 (*CDKN2A/B*), 6q25, and 6q26 were associated with inferior survival.

Single nucleotide polymorphism arrays. Copy-neutral loss of heterozygosity, undetectable by previously available methods, can be identified using single nucleotide polymorphism (SNP) arrays. This phenomenon, termed acquired uniparental disomy (aUPD), results from mitotic recombination or nondisjunction and has been described in FL.^{112,116} In a recent report, a number of recurring aUPDs were described in FL, of which aUPD on 1p36 correlated with shortened OS and aUPD on chromosome 16 was predictive of transformation.¹¹⁷

Host Constitutional Genetics

SNPs are changes in the DNA sequence by one base pair. Recent studies have suggested that SNPs in the *FcγR* genes may significantly alter the binding affinity between the Fc portion of rituximab and the Fc receptors on macrophages.^{118,119} Cartron et al¹²⁰ found a correlation between the *FcRIIIA* genotype and response to single-agent rituximab in untreated FL. Patients homozygous for -158VV *FcRIIIA* polymorphism did significantly better than the heterozygotes -158VF. In a study of recurrent FL, Weng and

Table 3. Morphologic, Immunophenotypic, and Gene Expression Biomarkers in FL

Biomarker	Impact on Survival	Risk of Transformation
Morphology		
Tumor cells		
Histologic grade ^{70,74}	Therapy-dependent, increasing grade associated with worse OS; effect possibly mitigated by doxorubicin-containing regimens	No effect
Grade 3A v 3B ^{22,55,70,71,76,77}	No effect	Typically already present in grade 3B
Architecture (diffuse) ^{26,71}	Controversial	Increased
Proliferative rate ^{22,78,79,133,174,175}	Controversial	No effect
Microenvironment		
Microvessel density ¹²⁹⁻¹³¹	Controversial	Not studied
Macrophages ^{83,127,135-137}	Unfavorable	No effect
FDC ^{102,135,176}	Unfavorable if immature phenotype of FDCs	Increased; associated with FDC disruption
CD4 ⁺ T cells ^{83,102,136,140,142,149,177-179}	Controversial	No effect
CD8 ⁺ T cells ^{136,142,146,147}	Controversial	Controversial
Regulatory T cells ^{136,140-142,177}	Controversial	Not studied
Single gene (RNA and/or protein)		
<i>BCL6</i> and <i>CD10</i> ⁹¹	Favorable	Not studied
<i>BCL2</i> and <i>BCL2/BAX</i> or <i>BAK</i> ^{80,86}	High ratio favoring <i>BCL-2</i> associated with early death	Not studied
<i>MCL1</i> ⁸¹	High <i>MCL-1</i> associated with worse outcome	Not studied
<i>BCLX_L</i> ⁸²	High <i>BCL-X_L</i> associated with inferior survival	Not studied
<i>MUM1</i> ^{180,181}	Expression of <i>MUM1</i> may be associated with inferior survival	Not studied
<i>PU.1</i> ⁹³	Favorable	Not studied
<i>SOCS3</i> ¹⁰⁰	Unfavorable	Not studied
<i>YY.1</i> ¹⁰¹	Unfavorable	Not studied
Multigene		
<i>IR-1</i> and <i>IR-2</i> ¹²⁷	Variable; <i>IR-1</i> associated with favorable OS, while <i>IR-2</i> predicts for inferior OS	Not studied
81-gene predictor ¹²⁸	No effect; strongly predictive of immediate clinical behavior	No effect

Abbreviations: FL, follicular lymphoma; OS, overall survival; FDC, follicular dendritic cells; IR, immune response signature.

colleagues¹²¹ confirmed these findings and identified a second polymorphic site related to the duration of response (*FcRIIA* 131 histidine/arginine). Similarly, Ghielmini et al¹²² reported that *FcRIIA* V/V was a predictive factor for event-free survival in rituximab monotherapy in FL. In contrast, Maloney et al and others^{123,124} did not find that *FcRIIA* or *RIIA* polymorphisms correlated with outcome in a study of R-CHOP.

Recently, Cerhan et al¹²⁵ analyzed the impact of immune response SNPs in FL. Germline DNA was analyzed from patients with FL and a final set of four prognostically relevant immune response SNPs was identified (interleukin [*IL*] -8, *IL2*, *IL12B*, and *IL1RN*). An outcome predictor was built using clinical and demographic factors combined with the four deleterious SNPs, which identified three risk groups with 5-year OS estimates of 96%, 72%, and 58%, respectively. These patients were treated in an era before the use of rituximab. Although these four genes strongly predict outcome in patients with FL, none of them has been shown to be associated with the risk of developing FL.^{125,126} Together with the gene expression profiling (GEP) data below,¹²⁷ these results suggest that the composition and functional status of the immune cells in the tumor microenvironment of FL may largely be driven by the genetics of the host.

Non-Neoplastic Cells of the Microenvironment

Lymph nodes involved with FL contain an admixture of non-neoplastic T cells, FDCs, macrophages, and other cells. A renewed interest in the microenvironment in FL followed the Leukemia Lymphoma Molecular Profiling Project (LLMPP) study in 2004¹²⁷ in which GEP of whole-section frozen lymph nodes from 191 cases of FL demonstrated that the tumor microenvironment was the most important predictor of patient outcome. Two signatures of gene expression were identified that best correlated with survival prediction. The immune-response 1 (IR-1) signature included genes encoding for T-cell markers and some genes that are highly expressed in mono-

cytes/macrophages, and predicted a favorable outcome. The IR-2 signature included genes preferentially expressed in macrophages or dendritic cells, and predicted an unfavorable outcome. When patients were grouped into quartiles based on their survival-predictor scores, median survival rates ranged from 3.9 years to 13.6 years. These data highlighted the dominant prognostic role of the microenvironment in FL and suggested that the critical determinants of outcome might already be present at diagnosis.

After the LLMPP study, Glas et al¹²⁸ performed GEP in a series of patients with FL who were grouped according to outcome and transformation. They defined an 81-gene predictor that correlated with immediate clinical behavior but not with long-term survival or risk of transformation. Interestingly, the genetic profile of patients with early transformation exhibited an activated status of T cells, FDCs, and macrophages characterized by genes that were present in the favorable IR-1 signature of the LLMPP study. Differences in experimental design, patient selection, gene expression platforms, and data analysis may explain the different conclusions between these two studies.

Microvessel density. Despite evidence for a vital role of angiogenesis in supporting tumorigenesis,¹²⁹ some reports have suggested that increased vessel density correlates with better prognosis in FL.¹³⁰ Intriguing results by Streubel et al¹³¹ demonstrated that endothelial cells of the microvasculature share the *BCL2* rearrangement characteristic of FL, implying an intimate relationship between the two.

FDC meshwork “immaturity.” In addition to presenting antigens, FDCs comprise the scaffolding of both benign and malignant follicles, their dendritic processes providing structural support for B cells and non-neoplastic cells. An immature FDC phenotype is typified by expression of low-affinity nerve growth factor and CNA42, accompanied by absence of mature FDC markers such as CD21, CD35, CD23, and CXCL13. This phenotype typifies undifferentiated fibroblastic cells and has been reported to correlate with progression

Table 4. Molecular Genetic Biomarkers in FL

Gene	Impact on Survival	Risk of Transformation
<i>BCL2</i> ^{165,182-186}	No clear survival difference between t(14;18)-positive FL and t(14;18) negative; suggestion that <i>BCL2</i> breakpoint may affect survival, but unconfirmed by later studies	Somatic mutations of <i>BCL2</i> gene on the translocated allele may rarely underlie transformation
<i>MYC</i> ^{161-163,170}	Translocations of <i>MYC</i> rarely encountered at diagnosis; tend to confer an inferior survival	Infrequently associated with transformation, but when found they are associated with markedly inferior post-transformation survival
<i>CDKN2A/B</i> ^{160,187}	Tumor suppressor genes on chromosome 9p21; only rarely found at diagnosis and not definitively associated with survival	Paired sample studies clearly show loss of <i>CDKN2A/B</i> through deletion, mutation, or hypermethylation is associated with histologic transformation
<i>TP53</i> ⁹⁵⁻⁹⁷	Loss of <i>TP53</i> tumor suppressor only rarely seen at diagnosis; mutation is closely correlated with protein expression in FL	Loss of <i>TP53</i> was the first gene implicated in transformation of FL; LOH not typically associated with 17p13 deletion
<i>MDM2</i> ^{97,99}	None	Expression correlated with transformation, but not obviously correlated with TP53 gene status; found within the amplified region of chromosome 12q13-14 frequently associated with transformation
<i>BCL6</i> ^{164,184,188}	No clear affect on survival in FL	Postulated to increase risk of transformation, but studies documenting the presence of translocations were based exclusively on inverse LD-PCR
<i>CCNB1</i> ⁹⁹	Increased expression of cyclin B1 associated with improved survival after CHOP chemotherapy	

Abbreviations: FL, follicular lymphoma; LOH, loss of heterozygosity; LD, long-distance; PCR, polymerase chain reaction; CHOP, cyclophosphamide, doxorubicin, vincristine, and prednisone.

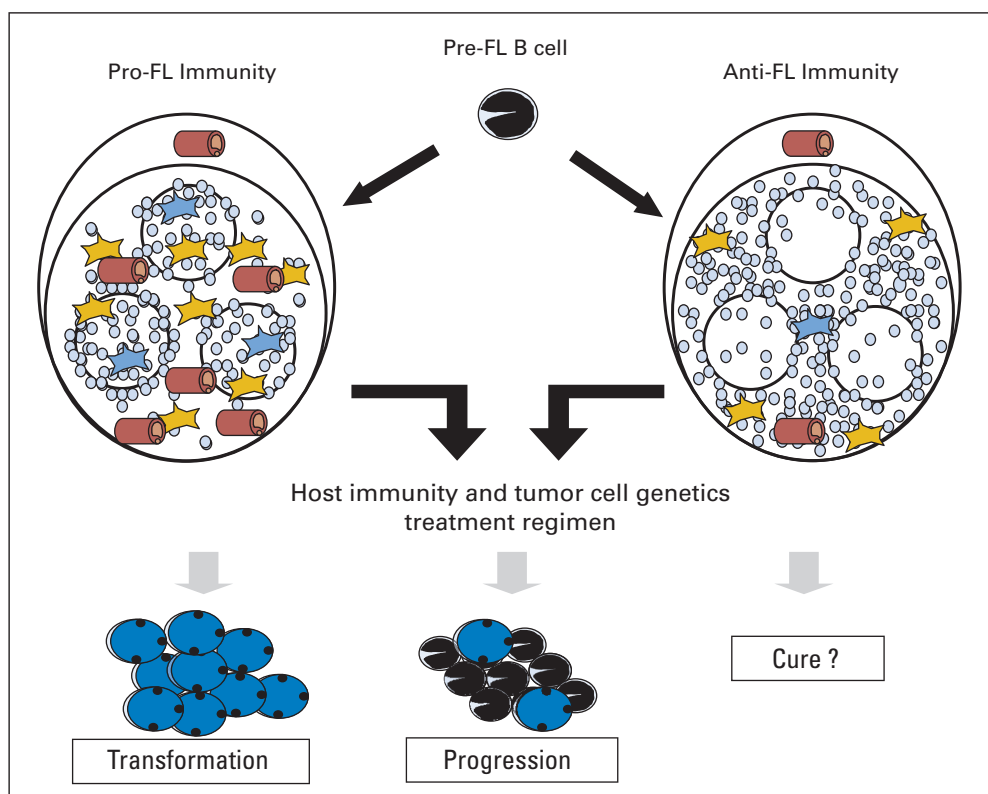


Fig 2. Model of how non-neoplastic cells in the microenvironment might impact survival and transformation in follicular lymphoma (FL). Left: follicular polarization of CD4+ cells, especially forkhead box protein P3–positive regulatory T cells (blue circles), increased numbers of vessels (red tubes), mast cells (blue stars), or macrophages (gold stars): local immunity supports tumor growth. Right: an antilymphoma immune response.

and/or transformation,¹³² but not in all studies.⁸³ These changes correlate with loss of normal T-cell infiltration within follicles and might reflect a reduced cross-talk between these two cell types. Disruption of the tight FDC meshwork that characterizes FL has been associated with early transformation.¹³³

Macrophages. Tumor-associated macrophages have been described in a number of cancers, with increased numbers of benign macrophages typically associated with inferior survival. Farinha and colleagues⁸³ demonstrated that the small subset of FL cases with high macrophage content experienced markedly decreased OS and PFS independent of the IPI. These data appear consistent with the LLMPP GEP study, with high macrophage content being a surrogate for the IR-2 signature.¹²⁷ Alvaro et al¹³⁴ reported opposite results finding that increased macrophages were associated with indolent clinical behavior. In a related study, these same authors found that 30% of macrophages express STAT1 protein and that presence of this subset of cells was associated with inferior survival.¹³⁵ In two recent trials, a high macrophage content was associated with poor survival after chemotherapy, but not if combined with rituximab.^{136,137}

Macrophage plasticity has been well described, as these cells can be broadly separated into helper (M1) and healer (M2 or activated) cell types.¹³⁸ In most tumors, tumor-associated macrophages are polarized to a M2 phenotype and appear to create a trophic environment that favors the tumor cells.¹³⁹ A pan-macrophage marker (CD68) cannot capture these distinctions and may explain the discordant results.

T-cell subsets. T cells comprise a majority of the non-neoplastic cells in FL biopsies and play an important role in FL. Subsets include helper CD4-positive T cells, cytotoxic CD8-positive T cells, CD57-positive follicular helper T cells, and immunosuppressive regulatory T

cells (Treg), but the exact role played by these subsets is not completely understood. Studies investigating the roles of CD4-positive and CD8-positive T cells in FL utilize different methodologies and have conflicting results.^{133,134,140-144} Tregs are a subset mostly with a CD4-positive CD25-positive forkhead box protein P3-positive¹⁴⁵ immunophenotype that serve a critical role in regulating CD4 and CD8 effector functions by suppressing proliferation and cytokine production of these cells.¹⁴⁶ In epithelial malignancies, Tregs have been implicated in creating an immunosuppressed microenvironment that allows the tumor cells to escape the host immune response.¹⁴⁷ Some investigators have reported that an increased number of Tregs was associated with favorable clinical behavior in FL,^{134,141} while others claim that the T-cell distribution may be more relevant.^{143,148} Recently, a low number of tumor-infiltrating programmed cell death 1–positive was associated with transformation and with inferior survival.¹⁴⁹ Still, the precise role of T-cell subsets in FL biology remains unclear. The clinical impact of these cells in the microenvironment may be largely influenced by the characteristics of the patient and the treatments received.¹⁴⁵ Specific therapies may have different effects on neoplastic cells versus cells within the microenvironment. Moreover, the role of host genetics influencing the immune microenvironment has only recently been explored.¹²⁵

Transformation

Histologic transformation is often heralded by a sudden change in clinical behavior, such as a rise in serum LDH or development of unusual extranodal sites of disease. It is a dominant clinical event, associated with shortened survival and relative resistance to therapy. The reported frequency varies dramatically ranging from 5% to 60%

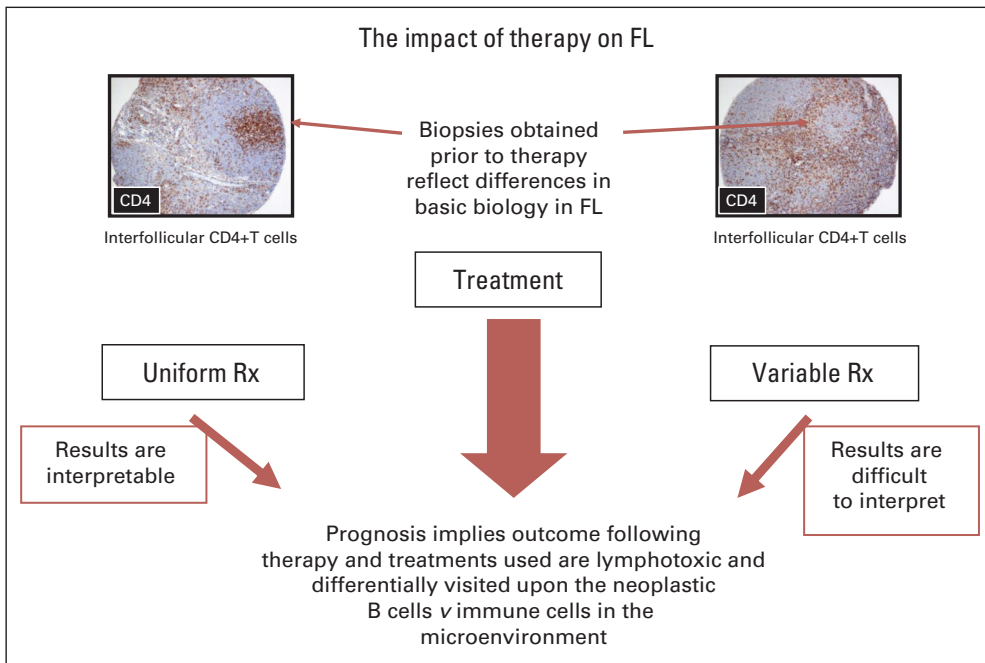


Fig 3. Treatment influences prognostic markers. Biopsies stained for CD4. Left, T cells within neoplastic follicles; right, in the interfollicular region. Importantly, treatments differentially visit toxicity on tumor cells versus cells in the microenvironment. The prognostic role of any factor must be interpreted with caution if treatment varies. FL, follicular lymphoma; Rx, therapeutic regimens.

of patients with FL.^{5,8,150-156} Since risk of transformation is time dependent, approximately 3% per year, this variation probably reflects differing durations of follow-up. The length of time that patients are followed and the rigor with which biopsies are obtained at progression heavily affect the reported frequency. Biomarkers that predict for survival do not necessarily correlate with those that predict risk of transformation.

An association between increased FLIPI score and frequency of transformation has been noted.^{9,28} Morphologic features associated with transformation risk include the presence of diffuse areas and disruption of the FDC meshwork.^{132,157} The presence of grade 3B FL and increased intrafollicular CD4-positive T cells have also been linked to early transformation.¹³³

Studies using paired samples (FL and subsequent DLBCL) have demonstrated that transformation is a molecularly heterogeneous event, including loss of *TP53*, loss of the *CDKN2A* tumor suppressor, or acquisition of *MYC* translocations, leading to upregulation of *MYC* or its target genes.^{95,96,98,158-163} Other molecular alterations include mutations of the coding region of *BCL2* and translocations involving *BCL6*.^{164,165} Cytogenetic studies of paired samples have revealed candidate chromosomal alterations, including +7, +12q13-14, and -6q16-21.¹⁶⁶⁻¹⁷⁰ Lastly, a number of small studies using gene expression profiling of paired samples have been published.^{160,170-173} These demonstrate the molecular heterogeneity underlying transformation, implicating upregulation of *p38 MAP KINASE*, upregulation of *MYC* and its target genes, and a generic increase in the mitotic machinery.

Recent data suggest that FL may comprise two major patient subgroups; those destined to develop transformation and those who will not.⁹ Distinguishing between these two clinical risk groups might have major implications for therapy.

Translation Into the Clinic

A summary of factors associated with outcome in FL is shown in Figure 1. As presented in Tables 2, 3, and 4,¹⁷⁴⁻¹⁸⁸ consensus on

which biomarkers to use in clinical practice and how these might impact treatment decisions is still lacking. Most prognostic markers were studied before the introduction of rituximab and require validation in the current era of chemoimmunotherapy. At this time, disease behavior and robust indices, such as the FLIPI and FLIPI-2, remain the basis for clinical decision making. The key elements in the interaction of host immunogenetics, tumor microenvironment, and therapy in FL are still not well understood (Fig 2). The inclusion of correlative science into clinical trials should help to determine the precise role of biomarkers in predicting survival and transformation risk in FL. Prospective randomized clinical trials will be instrumental in defining future prognostic factors in FL, as uniform treatment groups can be compared (Fig 3). If patients who respond poorly to standard therapy can be identified and the mechanism(s) underlying their inferior outcome determined, these patients could reasonably be considered candidates for novel therapies with the potential for improved outcome avoiding toxicity from ineffective therapy.

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AUTHOR CONTRIBUTIONS

Conception and design: Thomas Relander, Pedro Farinha, Randy D. Gascoyne

Administrative support: Randy D. Gascoyne

Provision of study materials or patients: Randy D. Gascoyne

Collection and assembly of data: Randy D. Gascoyne

Data analysis and interpretation: Thomas Relander, Nathalie A. Johnson, Pedro Farinha, Joseph M. Connors, Laurie H. Sehn, Randy D. Gascoyne

Manuscript writing: Thomas Relander, Nathalie A. Johnson, Pedro Farinha, Joseph M. Connors, Laurie H. Sehn, Randy D. Gascoyne

Final approval of manuscript: Thomas Relander, Nathalie A. Johnson, Pedro Farinha, Joseph M. Connors, Laurie H. Sehn, Randy D. Gascoyne

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CORRECTIONS

Author Corrections

The January 10, 2010, article by Oktay et al, entitled, "Association of *BRCA1* Mutations With Occult Primary Ovarian Insufficiency: A Possible Explanation for the Link Between Infertility and Breast/Ovarian Cancer Risks" (J Clin Oncol 28:240-244, 2010), contained an error.

The primary institutional affiliation for David Barad was inadvertently omitted and should have been listed as The Center for Human Reproduction, New York, NY.

The authors apologize to the readers for the mistake.

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The July 10, 2010, article by Sargent et al, entitled, "Defective Mismatch Repair As a Predictive Marker for Lack of Efficacy of Fluorouracil-Based Adjuvant Therapy in Colon Cancer" (J Clin Oncol 28:3219-3226, 2010), contained errors.

presented for dMMR and pMMR patients who were not treated, whereas they should have been given for patients who were treated.

The authors apologize to the readers for the mistakes.

In Table 2 and Table 4, the univariate and multivariate results (HR, 95% CI, and *P* values) for DFS and OS were

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Journal Corrections

The June 10, 2010, article by Thurlow et al, entitled, "Spectral Clustering of Microarray Data Elucidates the Roles of Microenvironment Remodeling and Immune Responses in Survival of Head and Neck Squamous Cell Carcinoma" (J Clin Oncol 28:2881-2888, 2010), contained an error.

Journal of Clinical Oncology apologizes to the authors and readers for the mistake.

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In Table 1, under Primary Tumors, the value for FA (KEGG) in the column "*P* Reduced Multivariate" was inadvertently omitted and should have been $< .001$.

The June 10, 2010, review article by Relander et al, entitled, "Prognostic Factors in Follicular Lymphoma" (J Clin Oncol 28:2902-2913, 2010), contained an error.

Journal of Clinical Oncology apologizes to the authors and readers for the mistake.

The left-hand image in Figure 3 was identified as "Interfollicular CD4+T cells," whereas it should have been "Intrafollicular CD4+T cells."

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