

REVIEW

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Host immune response in B-cell lymphomas: friend or foe?

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Abstract

The interaction of B-cell malignancies with the host immune system is a dynamic and bilateral process. Certain lymphomas more commonly arise within a background of autoimmunity or chronic infection. Initiation of these tumors is commonly reliant on antigenic stimulation and/or T-cell help. Apart from its tumor-fueling role, the host immune response plays a critical role in cancer immunosurveillance and immunoediting. The concept of immunoediting holds that the immune system sculpts the tumor's immunogenicity in a dynamic process that involves three essential phases: elimination, equilibrium, and escape. Data obtained by studying gene-targeted animals and human lymphomas that support the critical role of the immune response in the initiation, progression, and immunoediting of lymphoid malignancies are summarized here. A thorough understanding of this interaction will lead to the identification of more rational treatment targets and improved immunotherapies in B-cell lymphomas.

Key words: lymphoma, immune escape, immunoediting.

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INTRODUCTION

Interaction between tumor and the reactive infiltrate was originally conceived as the process leading to tumor elimination and/or control of its progression. Recent studies have extensively redefined the role of the interaction between the host immune response and tumor, demonstrating that it is a bilateral and multistep process playing a more complex role in the etiology and progression of cancer. According to these findings, the host immune response shapes the immunogenicity of spontaneous or carcinogen-induced solid tumors, leading to the emergence and outgrowth of more aggressive, less immunogenic clones [21–24, 78]. This dynamic process, known as immunoediting, involves three essential phases: elimination, equilibrium, and escape. In the elimination phase the newly transformed cells are recognized and eliminated by the innate and adaptive immune responses. Incomplete elimination leads to a subclinical equilibrium phase in which tumor persists, but is restrained by the host immune pressure, ultimately leading to the emergence of less immunogenic clones. The expansion of these clones and subsequent acquisition of

additional lesions tilts the balance toward the tumor, which enters the escape phase.

B-cell lymphomas present as tumors with a variable inflammatory infiltrate that includes effector and regulatory T cells, macrophages, and dendritic cells. Recent studies demonstrate that the dual role of the host immune response leading from immunosurveillance to immune escape is not limited to solid tumors only, but also shapes the biological behavior of B-cell lymphomas. However, the interactions between host immune response and lymphoma involve additional levels of complexity, as the emergence of these tumors is often associated with certain underlying chronic inflammatory disorders. In this review, the role of the host immune response in the pathogenesis of B-cell tumors will be discussed. First, the role of chronic inflammation and associated molecular mechanisms leading to the initiation of lymphomagenesis will be addressed. The following sections will focus on the role of the immune response and key effector molecules in the progression of the established lymphoma from immune surveillance to immune escape.

IMMUNE RESPONSE AND LYMPHOMAGENESIS: THE ROLE OF INFECTIOUS AGENTS AND CHRONIC INFLAMMATION

Chronic activation of the lymphoid system and sustained proliferation of lymphocytes can be observed in several infectious and autoimmune diseases which are associated with the more common B-cell malignancies [26, 45, 74]. Lymphomagenesis associated with chronic infections by pathogens that are not lymphotropic and not directly oncogenic or with autoimmunity involves chronic stimulation of effector B-cells by pathogen-derived antigens or autoantigens. Lymphomas that arise according to this model commonly appear to originate from marginal-zone B cells [3, 17]. Chronic inflammation either at the site of infection or at the site of the autoimmune response elicits a polyclonal B-cell response and leads to the formation of extranodal lymphoid tissue, which is a prerequisite for lymphomagenesis (Fig. 1) [62]. Suggestive of antigen-driven selection, B cells in these lesions commonly exhibit a biased immunoglobulin (Ig) V gene usage and somatic hypermutation (SHM) [7, 16, 19, 20, 52, 56, 89]. Consistently, in mucosa-associated lymphoid tissue (MALT) lymphomas arising within the background of these lesions, CDR3 sequences of Ig receptor genes suggest a common specificity of surface B-cell receptors to the relevant pathogen or to autoantigens [7, 15]. For sustained B-cell proliferation, costimulatory signals and cytokines are provided by primed T cells and/or by dendritic cells. T cells from patients with gastric MALT lymphomas are able to support the proliferation of autologous B cells in the presence of *Helicobacter pylori* (*H. pylori*) extracts in a CD40-dependent manner, underscoring their pathogenic role [35]. A critical role of chronic T-cell help was also suggested in mouse models. *H. pylori* does not induce gastritis in SCID mice, but gastritis is induced by adoptive transfer of naïve CD4⁺ T cells to these mice [25]. *H. pylori* elimination is also impaired in MHC class

II-deficient mice, underscoring the role of CD4⁺ T helper cells [69]. Consistently, inherited genetic polymorphisms in the *CTLA4* gene are associated with increased risk of gastric MALT lymphoma in patients with *H. pylori* infection, suggesting that a defective negative signal and prolonged T-cell activation may be a predisposing factor for this malignancy [10].

Most lymphomas, however, develop in the absence of any known chronic antigenic stimulation. An alternative signal recruiting T cells fueling chronic lymphoproliferation can be elicited by superantigens. Several mouse strains that harbor endogenous retroviruses encoding superantigens develop tumors resembling human lymphomas. These tumors fail to grow in γ -irradiated or athymic mice except when simultaneously injected with normal syngeneic lymphoid cells, suggesting their dependence on T cell-derived costimulation [41, 51]. This costimulatory signal is obtained from activated interleukin (IL)-5-secreting superantigen-specific CD4⁺V β 16⁺ T cells [46, 90, 91]. A superantigen-dependent mechanism may also be involved in human Epstein-Barr virus (EBV)-related lymphomas. EBV transactivates superantigen encoded by the human endogenous retrovirus K18, which strongly and rapidly stimulates T cells [33, 88]. The response is initiated by oligoclonal superantigen-specific T-cell receptor (TCR) V β 13 T cells [33, 88]. Since CD4⁺ T cells greatly increase the development of EBV lymphomas, this mechanism may play at least a partial role in EBV-induced lymphomagenesis.

In a recent study, Zangani et al. [99] have shown that B cell-unique variable-region-derived idiotype (Id) peptides presented in the context of MHC II to T cells may serve as a chronic antigenic stimulus promoting lymphomagenesis [63, 99]. Transgenic Id⁺ B cells chronically helped by Id-specific Th2 cells developed into diffuse large B-cell lymphomas (DLBCLs). The phenotype of the lymphoma cells suggested that they were selected for potent interaction with T cells. They expressed high levels of MHC class II as well as costimulatory

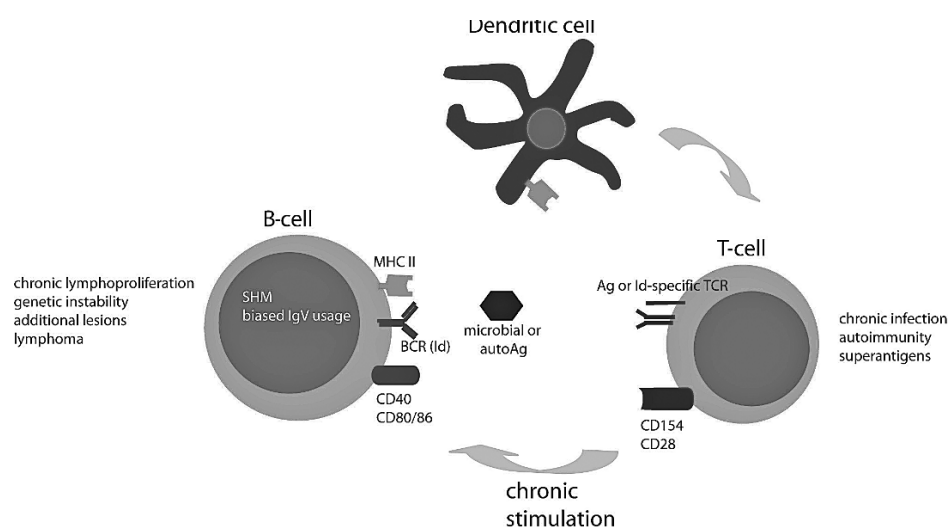


Fig. 1. Role of chronic stimulation in the initiation of lymphomagenesis. Polyclonal B cells specific to certain microbial or autoantigens are chronically helped by activated T cells and undergo prolonged activation, proliferation and form extranodal lymphoid tissue. B cells in these lesions exhibit a biased immunoglobulin V gene (IgV) usage and somatic hypermutation (SHM). Protracted antigen-dependent lymphoproliferation, sustained by costimulatory signals may lead to acquisition of additional lesions, genetic instability that renders B cells lymphoproliferation antigen-independent. See text for further details.

CD80/CD86 molecules and the $\lambda 2$ Id⁺ light-chain antigen [99]. These cells also expressed high levels of CD40, suggesting their dependence on activated T cell-derived signals. These results suggest that chronic Id-driven collaboration between T and B cells could represent a novel mechanism for lymphomagenesis. However, when Id⁺ B cells were transferred to transgenic mice expressing Id-specific TCR, lymphomas were uniformly rejected, likely due to the mounting of an anti-Id Th1 response, suggesting a dual role of the immune response in Id-mediated lymphomagenesis [54, 55]. These observations suggest that, apart from a tumor-fueling role in certain B-cell lymphomas, the host immune response plays a critical role in cancer immunosurveillance and immunoediting.

EPIDEMIOLOGIC EVIDENCE FOR LYMPHOMA IMMUNE SURVEILLANCE IN HUMANS

Indirect evidence suggesting that the host immune response is involved in lymphomagenesis is provided by population and epidemiologic studies demonstrating that lymphoid malignancies arise more frequently in immunocompromised individuals. In a recent meta-analysis of human immunodeficiency virus (HIV)-infected patients (n=444,172) and transplant recipients (n=31,977), the incidences of both non-Hodgkin's lymphoma (NHL) and Hodgkin's lymphoma (HL) were highly elevated [30]. Consistently, patients with certain congenital immune deficiency syndromes with loss of T-cell control (Wiskott-Aldrich syndrome) or abnormal T/B-cell interactions (hyper-IgM syndrome) are also at risk of developing lymphoma [26]. The clinical features shared by the majority of immunodeficiency-related lymphomas are DLBCL histology, aggressive clinical course, and an association with EBV or human herpesvirus 8 (HHV-8). These data suggest that in the absence of an effective immune response and lack of infection control, infected B cells are more likely to persist, expand, and acquire additional lesions. However, EBV- and HHV-8-negative lymphomas also occur in transplant recipients and patients with HIV, suggesting that factors other than uncontrolled infection account for the higher risk of lymphoma in these cases.

MOUSE MODELS OF LYMPHOMA IMMUNOEDITION

The hypothesis of cancer immune surveillance and immunoediting was rigorously examined and validated using gene-knockout mouse lymphoma models. Interferon (IFN)- γ sensitivity is crucial for successful immunoelimination of spontaneous or carcinogen-induced solid tumors and thus established the paradigm of immune surveillance and immunoediting [58, 78, 87]. Subsequent studies raised the role of this

cytokine in immunoediting of lymphoid tumors as well. IFN- γ and granulocyte-macrophage colony-stimulating factor double-deficient mice developed spontaneous lymphomas within a background of persistent infection and inflammation, highlighting the synergism between chronic inflammation and impaired immune surveillance [28]. Tumor formation was delayed or prevented by antimicrobial therapy, demonstrating that the interplay of infectious agents with cytokine-mediated regulation of immune homeostasis is an important determinant of lymphomagenesis [28].

A similar mechanism, involving ineffective elimination of chronically activated/transformed cells, was proposed for *lpr/lpr* or *gld/gld* mice [103]. These mice, mutant in *Fas* (CD95) or *Fas* ligand (CD95L), respectively, accumulate memory-like B cells and plasma cells [11, 14]. FAS is a proapoptotic protein expressed within germinal centers where it plays an important role in the negative selection of B cells [64]. FAS ligand cross-links the transmembrane FAS death receptor, leading to the assembly of a death-inducing signaling complex and initiating caspase-mediated apoptosis. FAS ligand-receptor system mutations greatly increase the risk of B-cell malignancies arising within the background of systemic immunity in both mice and humans. Dysregulation of the FAS system may also occur due to physiological or aberrant SHM [64], which likely extends the lifespan of B cells, increasing the likelihood of secondary genetic abnormalities and/or favor the outgrowth of lymphomas not susceptible to FAS ligand-mediated apoptosis [14, 85].

Defects in another death-inducing molecule, TNF-related apoptosis-inducing ligand (TRAIL) are also associated with increased incidence of late onset murine B-cell lymphomas [102]. Consistently, deletions of the chromosome 8p21.3 region including the TRAIL receptor 1 and 2 loci are a recurrent genetic abnormality in human B-cell NHL associated with the down-regulation of either receptor expression and impaired TRAIL-induced apoptosis [75].

Increased incidence of spontaneous B-cell lymphomas was also noted in perforin (*pfp*^{-/-}) mice and was further enhanced upon crossing with *Ifng*^{-/-}, $\beta 2$ -microglobulin ($\beta 2m$)^{-/-}, or *p53*^{-/-} animals [81, 86, 87]. Perforin is a pore-forming protein expressed exclusively by natural killer (NK) and cytotoxic T lymphocytes (CTLs) and is essential for NK- and CTL-mediated cytolytic activity [42, 80]. When transplanted to wild-type recipients, B-cell lymphomas formed in *pfp*^{-/-}*p53*^{-/-} mice were rejected in a CTL-mediated manner but grew progressively when transplanted to *pfp*^{-/-} mice, suggesting that loss of perforin resulted in an "unedited", highly immunogenic phenotype [81]. Similarly, lymphomas formed in *pfp*^{-/-} $\beta 2m$ ^{-/-} mice effectively primed cell-mediated cytotoxicity in an NK/ $\gamma\delta$ TCR⁺-dependent fashion and were rejected when transplanted to syngeneic control wild-type mice, but not by *pfp*^{-/-} animals [86]. Of note, lymphomas arising in mice with isolated IFN- γ deficiency were nonimmunogenic, suggesting weaker immunoselection pressure by IFN- γ [87].

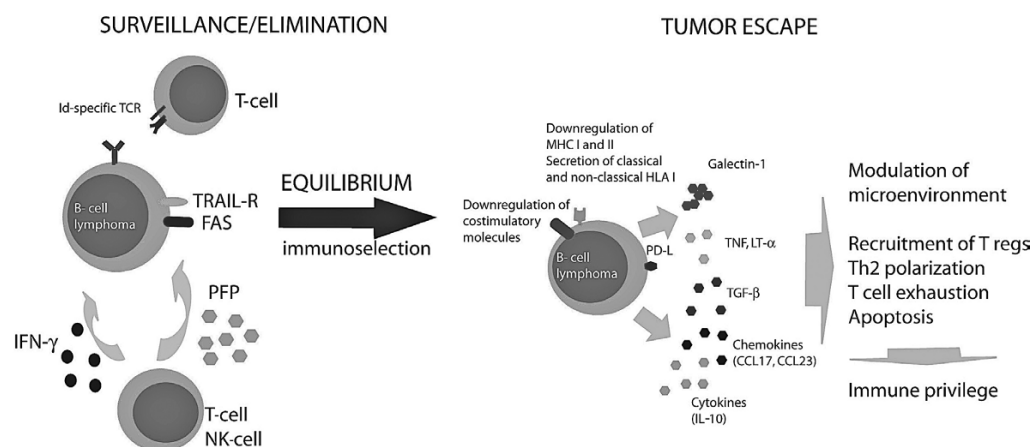


Fig. 2. Proposed scenario of immunoediting of B-cell lymphomas. During the elimination phase, the newly transformed cells are recognized and eliminated by the innate and adaptive immune responses. Tumor formation is facilitated by experimental gene targeting (*Ifng*^{-/-}, *Pfp*^{-/-}, *Fas*^{-/-}, *Fast*^{-/-}) or spontaneous mutations/deletions or SHMs occurring in humans (FAS, TRAIL-R). Incomplete elimination leads to a sub-clinical equilibrium phase in which tumor persists, but is it restrained by the host immune pressure, ultimately leading to the emergence of less immunogenic clones. The expansion of these clones and subsequent acquisition of additional lesions tilts the balance toward the tumor, which enters the escape phase. In the escape phase, cells utilize potent mechanisms to evade recognition (abnormalities in MHC expression, downregulation of costimulatory molecules) and create an immunoprivileged environment by secretion of certain mediators (e.g. Gal-1, IL-10, chemokines, TGF- β , TNF superfamily cytokines, PD-ligands).

Taken together, these results suggest that specific immunodeficiencies in mice are associated with increased incidence and/or accelerated onset of lymphoid tumors that exhibit reduced immunogenicity. The different immunogenic potentials of tumors arising in animals with different deficiencies suggest that the transition between “fully immunogenic, rejectable” to “non-immunogenic, transplantable” tumor involves an additional dynamic equilibrium stage during which the tumor is challenged by the immune system and loses its immunogenic potential (Fig. 2). Genetic instability and immune selection occurring during this phase finally result in the outgrowth of edited clones and the formation of clinically detectable tumors.

LYMPHOMA IMMUNE ESCAPE

As part of their response to selection pressure, lymphoma cells may exploit several different immunosuppressive strategies and immunological checkpoints to inhibit tumor-specific immune responses (Table 1 and Fig. 2). Tumor cells become resistant to proapoptotic signals from reactive cells or passively evade recognition or shape their microenvironment by producing immunoregulatory molecules that hijack or disarm the host immune response.

Role of HLA

An effective adaptive immune response requires interaction and cooperation between B and T cells. These interactions involve TCR-mediated recognition of an antigenic peptide presented on the MHC molecule

and costimulatory signals. The immunological synapse formation is further enhanced by adhesion molecules which dock B and T cells, facilitating the recognition and exchange of costimulatory signals. Therefore, abnormalities in the expressions of the molecules involved in this process on lymphoma cells will result in immunological ignorance and derange the immune response to the tumor. Loss of either class I or class II HLA expression is associated with fewer infiltrating CD8⁺ CTLs and inferior freedom from progression (FFP) and overall survival (OS) in patients with DLBCL [6, 71, 72]. Decreased expression of CD86 costimulatory molecule was also associated with lower tumoral infiltration by CTLs, suggesting that in the absence of costimulatory signal, T cells undergo apoptosis at the tumor site [84].

Given the complexity of antigen-processing and -presentation pathways, various molecular mechanisms responsible for complete or partial HLA loss have been reported, including abnormalities in transporter associated with antigen processing, β 2m, hemizygous deletions, and loss of heterozygosity [6, 18]. Alternative splicing or proteolytic cleavage and shedding likely account for the loss of membrane-anchored HLA and increased levels of soluble forms of these molecules (sHLA-I) [1, 2, 100]. Given the proapoptotic function of sHLA-I to cytotoxic T and NK cells in the absence of costimulatory signal, it is likely that the shedding of these molecules from the tumor surface provides an immune escape mechanism [12, 82, 101]. Consistently, elevated sHLA-I molecules are associated with inferior survival in NHL patients. Importantly, this association was independent of β 2m concentrations, suggesting mechanisms unrelated to tumor burden and cellular turnover [2].

Apart from complete or partial loss of surface HLA in lymphoma cells, certain inherited HLA repertoires are associated with inferior outcome in DLBCL and chronic lymphocytic leukemia (CLL) patients. The absence of the the HLA-DRB*02 and presence of the DRB*01 allele were related to adverse outcome of NHL and CLL, respectively [38, 49]. In an extended haplotype analysis, HLA A*01 and B*08 components of 8.1 HLA ancestral haplotype exhibited the strongest associations with shorter FFP and OS in DLBCL patients [65, 66].

Expression of the non-classical HLA molecule HLA-G has also been implicated in lymphoma immune escape. Non-classical HLA-I molecules include an oligomorphic family of molecules that predominantly function as inhibitors of the T and NK cells [36, 43, 44, 61]. HLA-G interaction with immunoglobulin-like transcript-family inhibitory receptors on T cells inhibits the proliferation of CD4⁺ cells and induces anergy and differentiation into suppressive cells [50, 53]. Production of soluble isoforms in B-cell lymphomas is likely driven by the interaction with normal constituents of the microenvironment, resulting in frequently elevated plasma levels of these isoforms [77]. Soluble HLA-G purified from patients' plasma inhibited T-cell alloproliferation at the concentrations encountered *in vivo*, suggesting that sHLA-G may be a functional immune escape mechanism. In line with this, in patients with CLL, HLA-G expression is associated with an unfavorable outcome and immunodeficiency [67].

Tumor-derived factors

B-cell lymphomas express a variety of soluble or

membrane-anchored factors that influence the immunopathology of host immune responses, shaping the microenvironment that fosters lymphoma's immune privilege. Local production of proapoptotic mediators by lymphoma cells eliminates potentially tumor-reactive effector cells, leading to underrepresentation of certain components of the immune response at the tumor site. At the same time, lymphomas produce chemokines, cytokines, and other substances that attract or induce the network of immunosuppressive cells, fostering tumor immune privilege.

One of the key components of the inhibitory network in B-cell lymphomas are regulatory T cells (Tregs) capable of suppressing anti-tumor CD4⁺ and CD8⁺ T-cell responses. This population of immunosuppressive CD4⁺CD25^{high}FOXP3⁺ T cells is frequently over-represented in the reactive infiltrate of NHL and HL in humans [27, 32, 57, 97, 98]. Tregs isolated from tumor biopsies are capable of suppressing proliferation and cytokine or granule production of CD4⁺ and CD8⁺ T cells [32, 57, 97, 98]. Intratumoral Tregs express the chemokine receptor CCR4, suggesting that they can be recruited to the tumor site by the chemotactic factors CCL17 (thymus- and activation-regulated chemokine) and CCL22 secreted by malignant B cells or may differentiate from naïve T cells at the tumor site under the influence of transforming growth factor (TGF)- β , a Treg-inducing cytokine produced by tumor cells [34, 37, 68, 70]. An additional potential mechanism explaining Treg infiltration in HL has been identified recently. In a screening for T cell-inhibitory molecules in classical HL (cHL), Reed-Sternberg (RS) cells were shown to

Table 1. Molecules and pathways involved in the immunopathogenesis of B-cell lymphomas

Molecule	Evidence	Proposed phase of immunoediting	References
BCR	Anti-idiotypic response in mouse models	elimination	54, 55, 63
<i>Ifng</i> ^{-/-}	Spontaneous lymphomas (strain dependent)	elimination	87
<i>Ifng</i> ^{-/-} <i>Gmcsf</i> ^{-/-}	Increased lymphomagenesis associated with chronic inflammation	elimination	28
<i>Pfp</i> ^{-/-}	Spontaneous "edited" lymphomas (augmented against a <i>p53</i> ^{-/-} and <i>Ifng</i> ^{-/-} background)	elimination	81
<i>Pfp</i> ^{-/-} <i>Ifng</i> ^{-/-}	Spontaneous "edited" lymphomas	elimination	87
<i>Pfp</i> ^{-/-} β 2m ^{-/-}	Spontaneous "edited" lymphomas	elimination	86
HLA	Loss of HLA in aggressive tumors	escape	2, 6, 38, 49, 67, 71, 72
	Increased sHLA in poor-outcome patients		
	Increased HLA-G plasma levels in poor-outcome patients		
	HLA polymorphisms associated with outcome		
TNF	Increased TNF and TNF-R levels in poor-outcome patients	escape	92–95
Fas/Fas ligand	Lymphoproliferative disorder in <i>Fas</i> ^{-/-} mice and humans	elimination	14, 103
	Somatic hypermutations		
TRAIL	Late-onset mouse lymphoma	elimination	75, 102
	Recurrent genetic abnormality in human lymphoma		
Gal-1	Th2/Treg-skewed microenvironment in cHL	escape	40
PD-1	T-cell exhaustion in cHL	escape	9, 73, 96
IL-10	Th2 polarization	escape	8, 47, 48, 83
CCL17, CCL22	Treg chemoattractants in cHL	escape	37, 68
TGF- β	Increased expression in cHL; T-cell suppression	escape	34

Abbreviations: BCR – B-cell receptor; IFN – interferon; β 2m – β 2-microglobulin; TNF – tumor necrosis factor; IL-10 – interleukin 10; TGF- β – transforming growth factor beta.

selectively overexpress the immunoregulatory lectin galectin-1 (Gal1) through an AP1-dependent enhancer [40]. In cocultures of activated T cells and HL cell lines, blockade of Gal1 expression in RS cells increased T-cell viability and restored the Th1/Th2 balance. In contrast, rGal1 treatment of activated T cells favored the secretion of Th2 cytokines and increased the relative abundance of CD4⁺CD25^{high}FOXP3⁺ Treg cells [40]. These data directly implicate RS cell Gal1 in the development and maintenance of an immunosuppressive Th2/Treg-skewed microenvironment in cHL.

In other B-cell malignancies, skewing and suppression of the host immune response is frequently mediated by local and/or systemic secretion of certain cytokines. IL-10 is a Th2 cytokine with pleiotropic effects in the immune system that include induction of peripheral T-cell anergy, induction of regulatory Tr-1 cells, and inhibition of dendritic-cell function [59]. In DLBCL, the immune response shift towards Th2-biased immunity is likely mediated by IL-10 secreted by malignant B cells. Increased serum levels of this critical Th2 cytokine were associated with poor prognosis and shorter survival of patients with DLBCL [8, 47, 48, 83].

A tumor's "counterattack" may also be mediated by the expression of certain tumor necrosis factor (TNF) family members, including TNF, lymphotoxin (LT) α , LT β , and Fas ligand. TNF, LT α , LT β , and their receptors are secreted by lymphoma cells and their elevated plasma levels are associated with larger tumor burden, disease dissemination, and B-symptoms [76, 92, 94, 95]. Prolonged local TNF production at the tumor site likely influences the reactive infiltrating cells, decreasing NK cell activity and participating in T-cell apoptosis induction (AICD – activation-induced T-cell death). These detrimental effects of excessive TNF production are more likely to occur in patients with genetic polymorphisms within the TNF promoter, associated with increased production of this cytokine [93]. Other lymphomas, including cHL and multiple myelomas, may utilize similar escape mechanisms involving FasL expression [70].

Another likely escape mechanism is mediated by programmed death (PD)-1 interaction with its ligands, including PD-L1 and PD-L2. PD-1 is a 55-kDa transmembrane receptor first identified in a murine hybridoma T-cell line undergoing AICD. PD-1 ligation in T cells induces phosphorylation of its ITIM motifs and recruitment of SHP-2, leading to inhibition of T-cell activation [79]. PD ligand's messenger RNA is overexpressed in primary mediastinal large B-cell lymphomas (PMBCLs) and cHL [73]. Genomic amplifications of PD ligand locus are present in over a half of PMBCLs and in HL cell lines, suggesting the likely mechanism of PD-L overexpression in these diseases [73]. PD-1 pathway engagement in these malignancies may lead to "T-cell exhaustion" and deficient cellular immunity. Blockade of the PD-1 signaling pathway in cHL-infiltrating T cells inhibited SHP-2 phosphorylation and restored the IFN- γ -producing function of T cells [96].

Functional consequences of this T-cell inhibitory interaction have also been documented in primary tumor biopsies from cHL patients analyzed by the genome-wide transcriptional approach, in which cHL-infiltrating T cells exhibited a specific profile of gene expression related to PD-1 engagement [9].

TRANSCRIPTIONAL AND HISTOLOGICAL FEATURES OF LYMPHOMA IMMUNE ESCAPE

These complex communication networks between malignant, stromal, and reactive cells lead to the formation of an inflammatory infiltrate with specific histological features. The variability in the composition of the infiltrate has led to several attempts to associate its specific components quantitatively with the efficacy of the immune response and patient survival. However, these attempts resulted in very conflicting results, related largely to inconsistent methodological criteria [4, 29, 31]. In addition, evaluation of a single component of the immune infiltrate in dissociation from the rest of its environment and its functional status may not be appropriate. These limitations can be circumvented using genome-wide transcriptional approaches in conjunction with immunohistochemical analyses. Using this approach, a DLBCL subtype with a brisk host immune/inflammatory response has been identified [60]. The DLBCLs in this category, termed host response (HR), exhibit increased expression of T/NK cell-receptor and activation-pathway components, complement cascade members, and macrophage/dendritic cell markers. Consistent with this signature, primary HR DLBCLs contain significantly higher numbers of morphologically distinct tumor-infiltrating lymphocytes and interdigitating dendritic cells [60]. The T-cell and dendritic-cell infiltrates in HR tumors resemble those of a histologically defined provisional World Health Organization subtype of DLBCL, namely T-cell/histiocyte-rich B-cell lymphoma (T/HRBCL). In spite of the brisk inflammatory infiltrates in HR (and T/HRBCL) tumors, patients with these DLBCLs do not have a more favorable outcome. In a screening for genes associated with prognosis, HR tumors were found to express a risk-related transcriptional modulator BAL1 and its binding partner BBAP (B-lymphoma- and BAL-associated protein) [39]. Expression of these genes was induced by host-derived IFN- γ , highlighting the dynamic interplay between the inflammatory infiltrate and malignant B cells in these tumors.

More recently, Dave et al. [13] identified distinct expression profiles associated with different outcomes in follicular lymphomas (FLs). The genes that best defined the prognostic signatures in FL were expressed primarily by T cells, macrophages, or dendritic cells, but not by the tumor cells themselves. Importantly, these signatures were not solely a surrogate for the number of infiltrating T cells, since many classical T-cell genes were not associated with either outcome, highlighting

the role of the functional status of infiltrate components in anti-lymphoma immune response. Consistent with this, in an immunohistochemical analysis of FL biopsies, two patterns of immune response were observed in which cellular localization and composition were directly associated with the clinical and biological features of the disease [5].

CONCLUDING REMARKS

Abundant experimental and clinical evidence supports the role of the immune system in the development and progression of B-cell lymphomas. The relationship between the host and the tumor is a complex and dynamic sequence of networked interactions that cannot be arbitrarily qualified as antagonistic or protagonic. Therefore, the immune system is neither lymphoma's friend nor its foe. It is a uniquely dynamic component of the tumor's microenvironment that, depending on the individual tumor's features, phase of the disease, underlying conditions, and genetic predispositions, may promote or inhibit tumor growth. Understanding the role, dynamics, and the factors that participate in orchestrating the different components of the immune system at different phases may lead to more successful interventions in the host immune system to augment cancer elimination and avoid unexpected immunotherapy-induced editing of the tumor.

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