



MALT GASTRIC LYMPHOMA: AN UPDATE OF PATHOGENETIC FEATURES

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Abstract – Extranodal marginal zone B-cell lymphoma of mucosa-associated lymphoid tissue (MALT lymphoma) is a low-grade lymphoma comprising 7-8% of all B-cell non-Hodgkin lymphomas. Common sites of involvement include lung, head and neck, ocular adnexa, skin, thyroid and breast, but the gastrointestinal tract is by far the most common site and the stomach is involved in almost two-thirds of all cases. Infection and autoimmune diseases are commonly considered as etiopathogenetic factors, being related to chronic stimulation of B-cell proliferation. The association between *Helicobacter pylori* infection and gastric MALT lymphoma provides the best evidence of an etiopathogenetic link between lymphoma and infection. Indeed, successful eradication of this microorganism can be followed by lymphoma regression in most cases. In recent years the role of other pathogenetic factors including genetic predisposition, somatic genetic mutations and chemokines activity, has become more evident. Particularly specific genetic abnormalities have been observed in MALT lymphomas, with different distribution accordingly to the site of development.

This review, therefore, addresses the major findings obtained in the last few years about MALT lymphoma and summarizes recent advances in its molecular pathogenesis.

KEYWORDS: MALT, MALT lymphoma, Gastric lymphoma, Pathogenesis, *H. pylori*.

INTRODUCTION

Extra-nodal marginal zone B-cell lymphoma of mucosa-associated lymphoid tissue represents approximately 8% of all non-Hodgkin lymphomas^{1,2}. Extranodal low-grade lymphomas were described at different sites including the gastrointestinal tract, salivary glands, lung and thyroid, showed similar clinical and histological features and are grouped into the MALT (Mucosa Associated Lymphoid Tissue) lymphoma³⁻⁶. The most common sites of involvement of MALT lymphomas include the stomach (70%), lung (14%), ocular adnexa (12%), thyroid (4%), and small intestine (including immunoproliferative small intestinal disease; 1%)⁷. Thus, the stomach is involved in almost two-thirds of all cases⁸. In some geographic areas, such as north-eastern Italy, the frequency

of MALT gastric lymphoma is particularly high, with an incidence of 13.2 cases per 100,000 per year, significantly higher than in other European countries⁹. Gastric MALT lymphoma is an indolent disease, remaining confined to the stomach for long periods, with ten-year survival rate approximately of 90%^{10,11}. However, in some cases a diffuse large B-cell lymphoma (DLBCL) could develop in MALT lymphoma, reducing the ten-year survival rate drops to approximately 42%¹⁰.

HISTOPATHOLOGY AND IMMUNOHISTOCHEMISTRY

All tissues with native or acquired mucosa-associated lymphoid tissue can be involved by MALT lymphoma. Histologically MALT lymphoma is



characterized by marginal zone neoplastic cells diffusely infiltrating surrounding tissues, including reactive lymphoid tissue, a process known as follicular colonization¹². In addition, in epithelized tissue, the neoplastic lymphoid cells often infiltrate the epithelial structures resulting in the formation of lymphoepithelial lesions (LELs). Neoplastic cells are constituted by centrocyte-like, monocytoid or plasmacytoid cells, with an admixture of scattered large cells. Finally, immunophenotypical profile (CD20+, CD21+, CD35+, IgM+, and IgD-) is superimposable to normal marginal zone cells. DLBCL may be observed in MALT lymphoma, suggesting a derivation from MALT lymphoma. The demonstration of identically rearranged immunoglobulin (Ig) genes between the low- and high-grade components of the same cases seems to confirm this hypothesis¹³. Transformed MALT lymphomas are CD10- and BCL2- but, in contrast to MALT lymphoma, they usually express BCL6¹⁴. Rarely, DLBCL develops in extra-lymphoid tissues in the absence of a previous MALT lymphoma (de novo DLBCL), with no clinical difference with respect to ex MALT DLBCL¹⁰ (Figure 1).

PATHOGENESIS

The development of MALT gastric lymphoma has been related to certain *Helicobacter pylori* (*Hp*) strains affecting genetically predisposed patients, suggesting the need of a strain-host-organ specific

ic process for the definitive neoplastic transformation of acquired MALT in gastric mucosa¹⁵⁻¹⁸ (Figure 2).

***H. pylori* strains**

H. pylori is the prerequisite for gastric MALT lymphoma development. Indeed chronic antigenic stimulation causes genetic instability and clonal growth of MALT lymphoma. Additional mutations of tumor suppressor genes such as p53 and p16, could induce progression to DLBCL¹⁵⁻¹⁸.

The role of antigen-driven clonal expansion of MALT lymphoma has been demonstrated by ongoing somatic hypermutation in the Ig V genes¹⁹. Also, the Ig V gene selection in MALT lymphoma development could suggest selective pressure of an antigen to increase the affinity of the immunoglobulin for antigens²⁰. Thus, the early stages of gastric MALT lymphoma growth may be induced by antigen-driven T cells specific for the *H. pylori* and the cure rate after bacterial eradication is higher than 75%^{21,22}. However, the role of host immune response has been not well studied, but it could play a relevant function, being only a minority of infected patients affected by gastric MALT lymphoma²³. Thus each *H. pylori*-related gastritis patients could develop gastric MALT lymphoma, but considering the very high prevalence of *H. pylori* infection in the general population and the low incidence of gastric lymphoma, it is arguable that some particular conditions

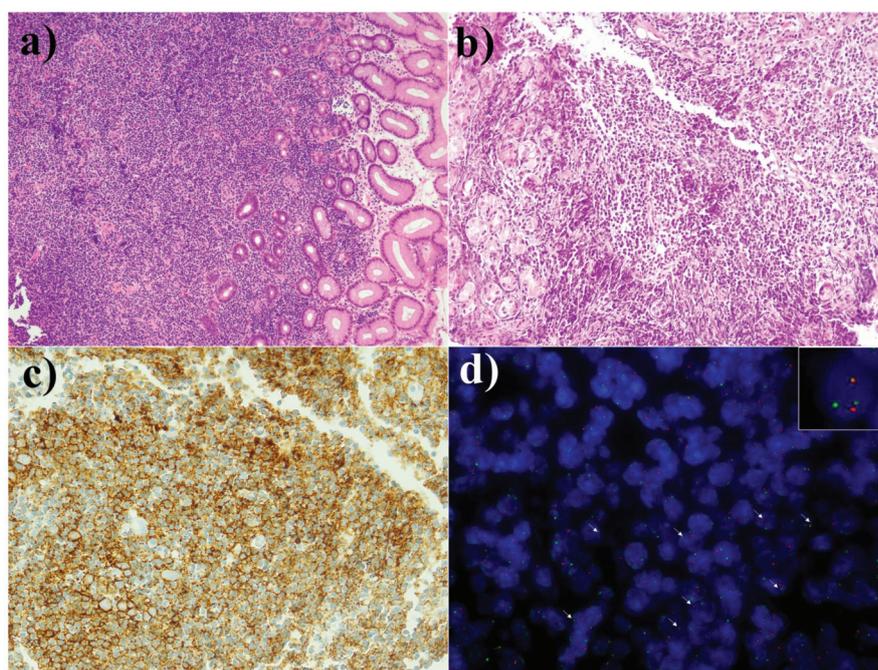
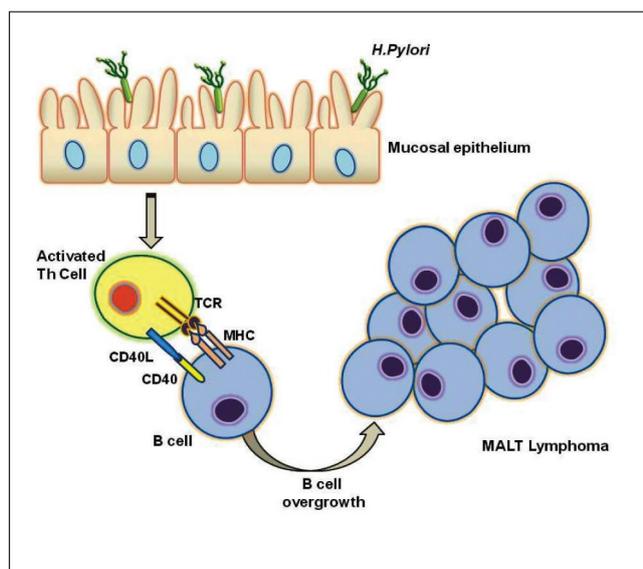


Figure 1. Histology, Immunohistochemistry and FISH for t(11;18). A-B, Haematoxylin and eosin-stained section of a stomach biopsy with a dense infiltrate of small lymphocytes (objective 20x and 40x). C, Immunohistochemical stain for the B-cell antigen CD20, demonstrating a dominance of the B-lymphocytic population (objective 40x). D, FISH positive analysis of chromosomal translocations t(11;18) (q21;q21), the most common structural chromosomal abnormality in gastric MALT lymphomas (objective 60x).

Figure 2. *H. pylori*-related gastric autoimmunity and MALT gastric lymphoma. *H. pylori* infection induces a strong gastric autoimmune response of Th-cells leading to B-cells proliferation through CD40-mediated signaling, as well as by Th2 cytokines. In a minority of infected patients *H. pylori*-specific Th-cells could have a deficient cytotoxic control resulting in impaired regulation of B-cell growth. The chronic proliferative state and the neoplastic transformation of these B-cells could induce the onset of gastric low-grade MALT lymphoma.



are needed for neoplasia development. Indeed, by co-culturing neoplastic lymphoid cells from gastric MALT-lymphoma patients and different inactivated *H. pylori* strains, a proliferation of B-cell expressing IL-2 receptors was observed, and IL-2 production by T cells in the supernatant was also detected²¹. Only 1 of the 13 different *H. pylori* strains tested could induce B-cell proliferation. The virulent factor of *H. pylori* does not impact on the development of MALT lymphomas as in gastric cancer and peptic ulcer disease²⁴. However, CagA positive strains have been found significantly more present in DLBCL than in low-grade MALT lymphoma²⁵. In addition, *H. pylori* may localize CagA protein into B-cells where it stimulates Bcl-2 expression, with consequent apoptosis inhibition²⁶.

Host organ features

GENETIC PREDISPOSITION

Genetic predisposition or development of MALT gastric lymphoma has been postulated, being the prevalence of *HLADQA1*0103* and *HLA-DQB1*0601* alleles and of *DQA1*0103-DQB1*0601* haplotypes higher in MALT-lymphoma patients as compared to controls²⁷. The allele frequencies of HLA-DQA1*0103 and HLA-DQB1*0601 in patients with gastric MALT lymphoma are about 41.6% and 36.1% respectively, resulting in the formation of the haplotype DQA1*0103-DQB1*0601 in approximately 55.5% of the patients²⁷. Also, the presence of *TNF-857 T* allele and the rare allele G of Toll-like receptor 4 (TLR4 Asp299Gly) were found approximately

in 10% of MALT-lymphoma patients, suggesting their possible role in the genetic susceptibility to gastric lymphoma^{28,29}. Finally, homozygous haplotypes for the rare allele G of *SNP3* (*rs12969413*) of the *MALT1* gene was identified approximately in 30% of patients and seems to protect patients from high- but not from low-grade gastric lymphoma³⁰.

CHEMOKINES ROLE

Lymphoepithelial lesions (LELs) are thought to be the origin of MALT lymphomas³¹. Indeed the close interaction among epithelial cells, T-cells, and B-cells induce survival in LELs with a reduced rate of apoptosis³². Gastric epithelial cells express high levels of HLA-DR during chronic *H. pylori* infection, with the recruitment of T-cells expressing CD40 ligand molecules. CD40 ligand interacts with CD40 molecule expressed on B-cells. Thus, B-cell stimulation is favored by CD40L-CD40 interaction associated to the action of various cytokines and chemokines. The transition from polyclonal to a monoclonal lesion is facilitated by chronic stimulation, causing B-cell proliferation with higher possibilities of acquiring genetic abnormalities³³⁻³⁵. Moreover, B-cell proliferation is sustained by cytokine APRIL, synthesized by macrophages, induced by *H. pylori* and *H. pylori*-specific T cells³⁶.

CHEMOKINE RECEPTORS IN MALT LYMPHOMAS

The large superfamily of chemokines includes peptides playing several biological functions. Indeed,



interaction between chemokines and chemokine receptors induces chemotaxis during inflammation³⁷⁻³⁹. CCR6, CCR7, CXCR3, CXCR4, and CXCR5 play the main role in B-cell homing process⁴⁰⁻⁴². Integrated analysis of chemokine receptors in extra-gastric MALT lymphomas respect to gastric MALT lymphomas demonstrated the up-regulation of CXCR1 and CXCR2 with down-regulation of CCR8 and CX3CR1 and loss of XCR1 expression⁴³. Also, CXCL12-receptor CXCR4 loss was documented in gastric MALT lymphomas when comparing to gastric extranodal DLBCL, nodal MZL, and nodal DLBCL⁴⁴ suggesting that CXCR4 expression is related to nodal lymphomas. Finally, another CXCL12 receptor, CXCR7, is overexpressed during the transformation of gastric MALT lymphomas into gastric DLBCL⁴⁴.

SOMATIC HYPERMUTATION AND GENETIC ABNORMALITIES

H. pylori infection increases activation-induced cytidine deaminase (AID) expression via NF- κ B in gastric cells both *in vitro* and *in vivo*, with subsequent accumulation of p53 mutation *in vitro*⁴⁵. AID is a key enzyme somatic hypermutation (SHM) and class switch recombination (CSR), immunological events acting to generate antibody diversity and maturity. Thus AID activity seems to play a role in lymphomagenesis through aberrant SHM (ASHM) of the 5 sequences of several protooncogenes, including PIM1, PAX5, RhoH/TTF, and cMYC and/or distinct genetic lesions, including chromosomal translocations⁴⁶⁻⁵⁰. ASHM has widely described in DLBCL, but it has also been found in 13 (76.5%) of 17 cases of MALT lymphomas and all 17 (100%) cases of extranodal DLBCL – still exhibiting a low-grade MALT lymphoma component (the so-called transformed MALT lymphoma) – were targeted by ASHM⁵⁰.

The main chromosomal and genetic abnormalities are reported in Table I.

Specific genetic abnormalities have been observed in MALT lymphomas, with different distribution accordingly to the site of MALT lymphomas development. Chromosome 3 and chromosome 18 trisomy have been described in up to 68% and 57% of patients, respectively⁵¹⁻⁵⁵.

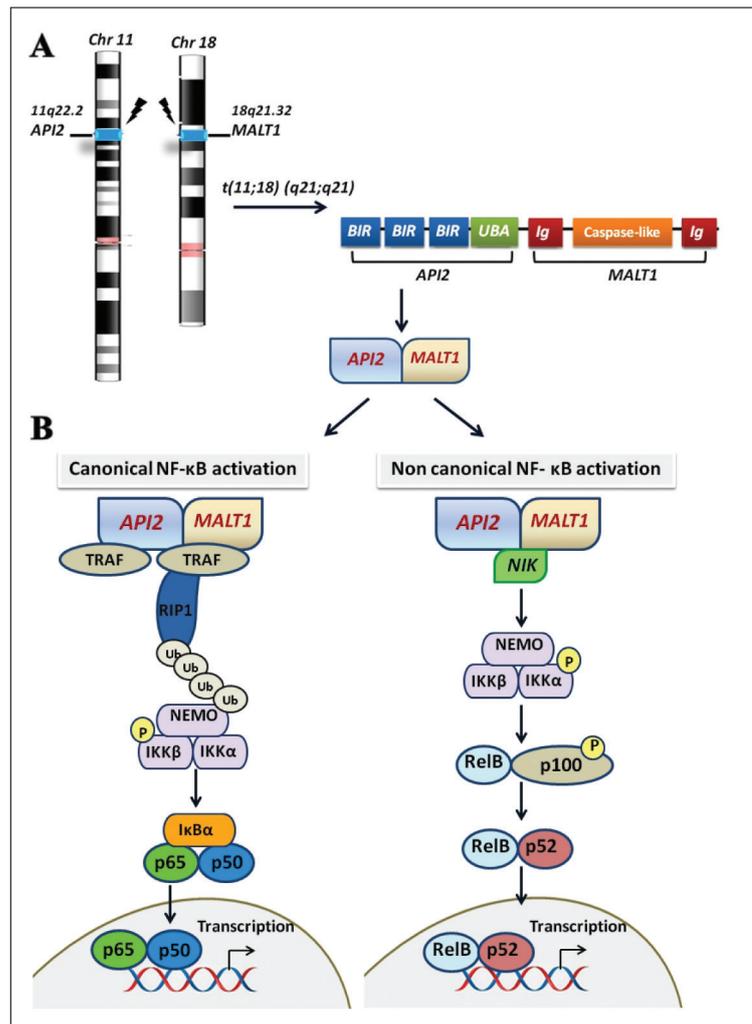
Particularly, trisomy of chromosome 3 has been mainly shown in orbital, than in lacrimal gland and conjunctival OAML⁵³. Trisomy of chromosome 18, instead, is more frequent in the conjunctival OAML and predominantly affects young women⁵⁵. A comparative genomic hybridization (CGH) carried out in 10 OAML cases showed recurrent chromosomal gains at 6p21 and 9q33-qter, in addition to trisomy 3, 12 and 18⁵⁶.

The mechanism through which these numerical aberrations are implicated in MALT lymphomagenesis has not been well studied, but some critical genes on chromosome 3 particularly have been proposed as related to lymphoma development, such as bcl6, FOXP1 and CCR4^{57,58}.

t(11;18) (q21;q21) is the most common chromosomal aberration observed in MALT lymphomas, mainly of gastric and pulmonary districts. Particularly it occurs in 10-50% of gastric MALT lymphomas⁵¹. The effect of translocation is the fusion of the N-terminal region of the BIRC2 (API2-apoptosis inhibitor 2) gene (located on chromosome 11) and the C-terminal region of the MALT1 gene (located on chromosome 18), with the formation of the API2-MALT1 chimeric fusion protein, able to activate the NF- κ B pathway⁵⁹⁻⁶⁴. Of note, it has been found that the prevalence of CagA-positive *H. pylori* strains was significantly higher in gastric MALT-lymphoma patients with the t(11;18) (q21;q21) compared to those without such a translocation⁶⁵ (Figure 3).

Mutation	Affected genes	Genetic alteration	Frequency	Main MALT lymphoma localization
Trisomy 3	FOXP1, BCL6, CCR4	Trisomy	68%	Gastrointestinal
Trisomy 12	Unkown	Trisomy	57%	Gastrointestinal
Trisomy 18	Unknown	Trisomy	20%	Gastrointestinal; mainly high grade
t(11;18)(q21;q21)	BIRC2(API2), MALT1	Translocation	10-50%	Stomach and lung
t(14;18)(q32;q21)	MALT1	Translocation	10-20%	Ocular adnexa, orbit, skin, and salivary glands
t(1;14)(p22;q32)	BCL10	Translocation	1-2%	Stomach, lung, skin; mainly high grade
t(3;14)(p14;q32)	FOXP1, IGH	Translocation	10%	Orbit, thyroid, skin
17p-	P53	Deletion	10-30%	Mainly high grade
6q23-	TNFAIP3	Deletion	Unknown	Ocular adnexal, salivary gland, thyroid,
cMYC	cMYC	Mutation	10-15%	Gastrointestinal, lung, ocular adnexa
P16	P16/INK4A	Hypermethylation	40-60%	Lung; mainly high grade
P57	P57(KIP2)	Hypermethylation	20-30%	Stomach; mainly high grade

Figure 3. API2-MALT1 chimeric fusion protein and Nuclear Factor-kappa B (NF-κB) pathway activation in gastric MALT lymphomas. *A*, The translocation $t(11;18)(q21;q21)$ leads to the formation of API2-MALT1 fusion protein that contains regardless of different breakpoints the N-terminal of API2 and the C-terminal of MALT1 including the following domains: BIR: Baculovirus inhibitor of apoptosis repeat, UBA: Ubiquitin-associated domain, Ig: Immunoglobulin-like, Caspase-like domain. *B*, API2-MALT1 fusion protein induces NF-κB activation through canonical and non-canonical pathway. In the canonical signaling, API2-MALT1 binding of TNF receptor associated factor 2 (TRAF2) induces RIP1 ubiquitination, promoting activation of the IKK complex, which consists of catalytic kinase subunits IKKα and IKKβ and a regulatory scaffold protein called NF-κB essential modulator (NEMO; also called IKKγ). IKK complex stimulates directly NF-κB, subsequently p65 and p50 translocate to the nucleus leading to the transcription of several genes. In the case of non-canonical signaling, API2-MALT1 fusion protein induces the proteolytic cleavage of NF-κB-inducing kinase (NIK), resulting in non-canonical NF-κB activation with the simulation of RelB and p52.



$t(14;18)(q32;q21)$ occurs in 15-20% of MALT lymphomas, mainly in non-gastrointestinal districts. This aberration leads MALT1 gene under the control of the IGH enhancer.

In $t(1;14)(p22;q32)$ the entire coding region of the BCL10 gene on chromosome 1 is under the control of the enhancer region of IGH gene on chromosome 14, leading to uncontrolled expression of the BCL10 gene⁶⁶. It is rarely observed, being described in 1-2% of MALT lymphomas, mainly stomach, lung, and skin⁶⁷. BCL10 is an intracellular protein that is essential for both the development and function of mature B-cells and T-cells. Recent studies show that BCL10 specifically links antigen receptor signaling in B and T cells to NF-κB activation^{68,69}. In MALT lymphomas with $t(11;18)(q21;q21)$, $t(14;18)(q32;q21)$ or $t(1;14)(p22;q32)$ MALT1, with or without BCL10 cooperation, activates the phosphorylation cascade leading to IκB-α phosphorylation. IκB-α links NF-κB in the cytoplasm. IκB-α phosphorylation enables the release NF-κB, which shuttles into the nucleus, playing its transcriptional role

with up-regulation of the cell cycle regulators expression anti-apoptotic proteins, growth factors, negative regulators of the NF-κB pathway and immunoregulatory cytokines⁷⁰⁻⁷⁵.

The translocations could be demonstrated through Fluorescent In Situ Hybridization (FISH) on neoplastic cells. Alternatively, BCL10 immunohistochemical expression could be used as a good surrogate marker of translocations in MALT lymphomas. Thus, the nuclear BCL10 expression suggests NF-κB activation after $t(11;18)(q21;q21)$ or $t(1;14)(p22;q32)$, while strong cytoplasmic perinuclear expression is related to $t(14;18)(q32;q21)$ [70, 76-79]. However, it has been noticed that MALT lymphomas lacking both $t(11;18)$ or $t(1;14)$ showed a moderate nuclear BCL10 expression, related to a poor prognosis^{80,81}. Moreover, an association between weak cytoplasmic BCL10 expression and translocation (14;18) has been found in only 3 cases⁸⁰.

Recently, FOXP1 (located at 3p14) was identified as a new translocation partner of IGH (q32) at low frequency in MALT lymphomas and DLBCL^{82,83}.



Overexpression of FOX1P in lymphoma cells demonstrates that FOX1P is a powerful transcriptional repressor of multiple pro-apoptotic genes⁸⁴.

The neoplastic growth-dependence from *H. pylori* has been associated to specific genetic status. Thus, *H. pylori*-dependent MALT lymphoma carrying trisomies 3, 12, or 18 could become *H. pylori*-independent and the transformation into high-grade tumors occurs through *P53* inactivation, *P16* gene deletion or chromosomal translocation of *cMYC* and *BCL6*^{5,85-88}. On the other hand MALT lymphomas with t(11;18)(q21;q21) are definitively *H. pylori*-independent but it rarely has the ability to transform into aggressive lymphomas⁷.

Recently, another possible mechanism for uncontrolled NF- κ B activation in MALT lymphoma, but not observed in gastric MALT lymphomas, is generated by homozygous deletion of the chromosomal band 6q23 with subsequent loss of the tumor necrosis factor alpha-induced protein 3 (TNFAIP3, A20)⁸⁹, an essential global NF- κ B inhibitor. In OAML, A20 inactivation is associated with poor lymphoma-free survival⁸⁹⁻⁹² and with a range of chronic inflammatory disorders⁹³⁻⁹⁷. A20 is also inactivated frequently by somatic mutations^{90,98,99}.

CONCLUSIONS

MALT lymphomas include a heterogeneous group of B-cell lymphomas, with different localizations and different genetic anomalies¹⁰⁰⁻¹⁰⁴. Infection and autoimmune disease are commonly considered as etiopathogenetic factors, being related to chronic stimulation of B-cell proliferation^{80,105-107}. Thus eradication of bacterial pathogens, in the early stage of disease, could be the cause of MALT lymphoma regression, particularly in gastric and ocular adnexa B-cell lymphomas [108,109]. In more advanced stages some genetic alterations could occur in neoplastic B-cells. All the described genetic abnormalities concur to deregulate NF- κ B signal pathway^{61,63,110-112}. In this view, a complete remission in a large portion of MALT lymphoma patients has been obtained by the use of bortezomib^{113,114} – a proteasome inhibitor inhibiting the NF- κ B signal pathway [115]. Also, the deregulation of NF- κ B has also been found in MALT lymphoma patients without known genetic abnormalities.

In this view, the therapy targeting NF- κ B may open new prospective in the treatment of this neoplasia.

CONFLICT OF INTERESTS:

The Authors declare that they have no conflict of interests.

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