

## Molecular mechanisms of the antitumor effects of anti-CD20 antibodies

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### 1. ABSTRACT

Anti-CD20 monoclonal antibodies (mAbs) have become the mainstay in the treatment of non-Hodgkin's lymphomas and have shown significant activity in patients with B-cell chronic lymphocytic leukemia. Antitumor action of these antibodies results from triggering of indirect effector mechanisms of the immune system that include activation of complement-dependent cytotoxicity (CDC), antibody-dependent cellular cytotoxicity (ADCC), or phagocytosis. Moreover, some studies indicate direct influence of anti-CD20 mAbs on tumor cells that leads to induction of various types of cell death. Despite the wealth of data on the mechanisms of cytotoxicity that accumulated over the last two decades their relative contribution to the therapeutic outcome is still difficult to predict in individual patients. Elucidation of molecular mechanisms of anti-

CD20 mAbs action is necessary to deliver their maximal activity in rationally designed combinations with other therapeutic approaches and to design next generation anti-CD20 mAb with improved ability to eliminate tumor cells.

### 2. INTRODUCTION

The idea of using antibodies as antitumor therapeutics is not new. The original Paul Ehrlich's concept of "magic bullet" that would eliminate diseased cells while sparing normal tissues inspired many generations of researchers looking for disease-selective therapeutics. "Magic bullets" became feasible with the development of hybridoma technology that enabled production of monoclonal antibodies (mAbs) in quantities sufficient for

**Table 1.** Monoclonal antibodies approved for clinical use in oncology

mAb name	Target antigen	Used to treat	Clinical approval
Rituximab	CD20	Non-hodgkin lymphoma	1997
Ibritumomab tiuxetan	CD20	Non-hodgkin lymphoma	2002
Tositumomab	CD20	Non-hodgkin lymphoma	2003
Ofatumumab	CD20	Chronic lymphocytic leukemia	2009
Alemtuzumab	CD52	Chronic lymphocytic leukemia	2001
Gemtuzumab ozogamicin	CD33	Acute myelogenous leukemia	2000
Bevacizumab	VEGF	Colorectal cancer Non-small cell lung cancer Breast cancer Glioblastoma Kidney cancer	2004 2006 2008 2009 2009
Panitumumab	EGFR	Colorectal cancer	2006
Cetuximab	EGFR	Colorectal cancer Head & neck cancers	2004 2006
Trastuzumab	HER2	Breast cancer	1998

**Table 2.** Anti-CD20 monoclonal antibodies

Antibody	Clinical status	Characteristics			effector mechanisms (compared with rituximab)		
		Origin	Type	Isotype	CDC	ADCC	Apoptosis
Rituximab	Approved	Chimeric	I	IgG1	=	=	=
Tositumomab*	Approved	Murine	II	IgG2a	-	=	+++
Ofatumumab	Approved	Human	I	IgG1	+++	=	=
Ibritumomab**	Approved	Murine	***	IgG1	***	***	***
Ocrelizumab	Phase 3	Humanized	I	IgG1	=	+	=
Veltuzumab	Phase 2	Humanized	I	IgG1	+	=	=
Obinutuzumab	Phase 2	Humanized	II	IgG1	-	+++	+++
PRO131921	Phase 2	Humanized	I	IgG1	+	++	=
AME-133	Phase 2	Humanized	I	IgG1	=	+	=
LFB-R603/EMAB-6	Phase 1	Chimeric	I	IgG1	=	+++	=

\* radioimmunoconjugate bound to <sup>131</sup>I, \*\* radioimmunoconjugate bound to <sup>90</sup>Y, \*\*\* no data available

clinical use (1). MAb themselves proved to be the tools that enabled identification of numerous tumor-associated antigens that served as targets for "magic bullet". Moreover, mAbs are used in diagnostic procedures that are currently employed to delineate the antigenic profile of tumor cells thereby determining treatment to be utilized in a particular situation.

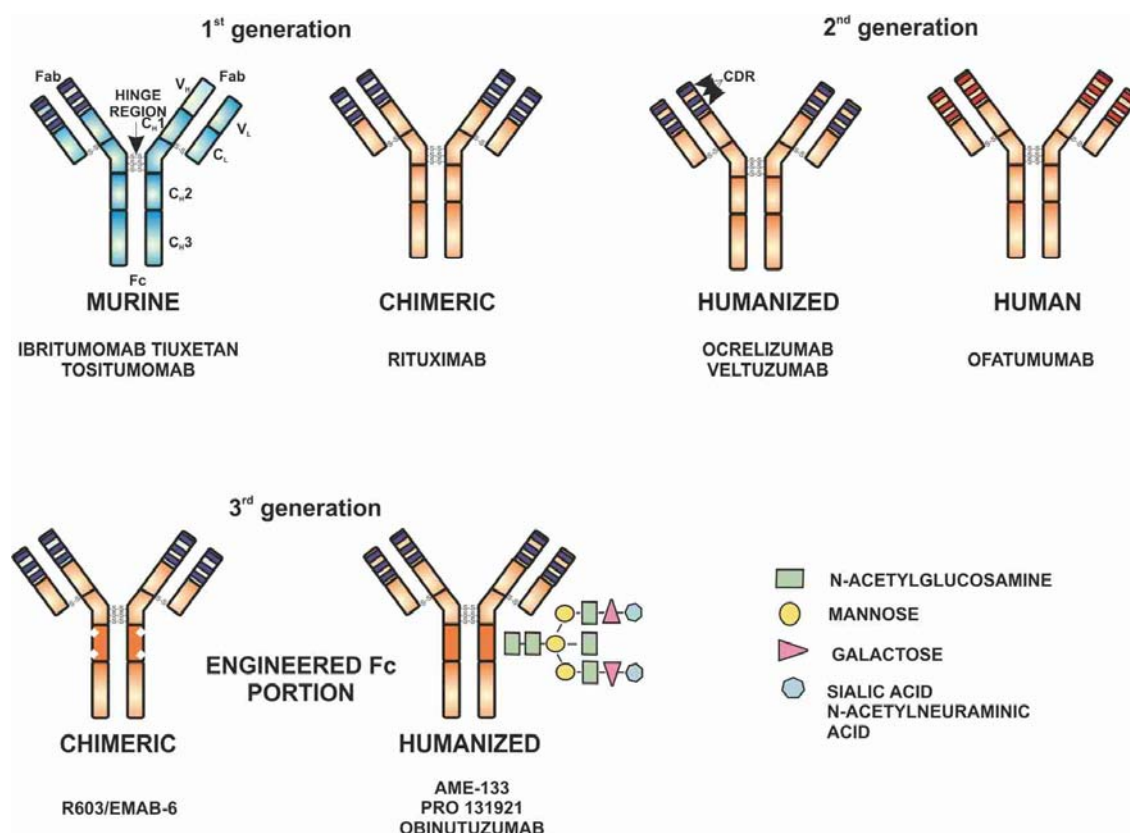
Currently 10 mAbs have been approved for clinical use in oncology (Table 1). Four of these target a single antigen - a CD20 molecule expressed by normal B cells and several types of tumor cells. CD20 became the first identified molecule targeted by a clinically approved mAb - rituximab. At least 6 additional anti-CD20 antibodies are either approved for clinical use or are in various stages of clinical development (Table 2).

During the 13 years since its clinical approval in 1997 rituximab has significantly improved response rates and patients survival in a variety of lymphoid malignancies. In developed countries almost all patients diagnosed with CD20-positive B cell non-Hodgkin's lymphoma (NHL) are treated with anti-CD20 mAbs. Initial clinical studies indicated that rituximab alone can induce objective, albeit mainly partial antitumor responses in approximately 50% of patients. Complete responses and long-term survival is observed more frequently in patients treated with rituximab and conventional chemotherapeutics in several combination schedules, such as R-CHOP (rituximab + cyclophosphamide, doxorubicin, vincristine and prednisone) or R-CVP (rituximab + cyclophosphamide, vincristine and prednisone). In addition, rituximab proved to be effective and safe in the management of a number of

autoimmune diseases and demonstrated utility in transplantation (2-3). Because of all these favorable effects in multiple different diseases rituximab has been coined a nickname of "vitamin R" (4). However, despite continued progress in dissecting the molecular mechanisms of action of rituximab and other anti-CD20 mAbs we still face a number of unanswered questions. Elucidation of these mechanisms is vital for improving currently used therapeutic regimens.

### 3. WHY ANTI-CD20 MABS ARE SO EFFECTIVE?

It is widely accepted that rituximab as well as other anti-CD20 mAbs can trigger antibody-dependent cellular cytotoxicity (ADCC), complement-mediated cytotoxicity (CDC), and direct induction of cell death but the relative contribution of these effector mechanisms has so far been difficult to pinpoint. Additionally, sensitization of tumor cells to conventional chemotherapeutics and induction of delayed vaccinal effects contribute to the clinical efficacy of these antibodies. CD20 molecules are very abundant in the plasma membrane of NHL cells, frequently exceeding 25 x 10<sup>4</sup> molecules per cell (which is 2-10-fold higher than CD19 (5)), allowing clustered opsonization of tumor cells by mAbs. Tight association of CD20 with plasma membrane results in binding of mAbs in a close proximity to the cell surface, which is important in deposition of C3/C5 convertases of the complement system and formation of the membrane attack complex (MAC) (6). Moreover, CD20 molecules tend to form complexes of at least 4 molecules (tetramers), which might facilitate formation of supramolecular clusters of mAbs that can stably bind C1q components of complement system (7-8).



**Figure 1.** Three generations anti-CD20 monoclonal antibodies.

It appears that no CD20 ligand, which might interfere with anti-CD20 mAb binding, exists. CD20 is usually described as an antigen resistant to internalization or shedding even after mAb binding, thereby allowing for extended (up to several days) binding of mAb, a time which is more than enough for triggering effector mechanisms of Fc $\gamma$ R-bearing cells of the immune system. Intriguingly, an increasing number of studies indicate that this is not always the case and several mechanisms of CD20 modulation exist that affect clinical efficacy of anti-CD20 mAbs (see below).

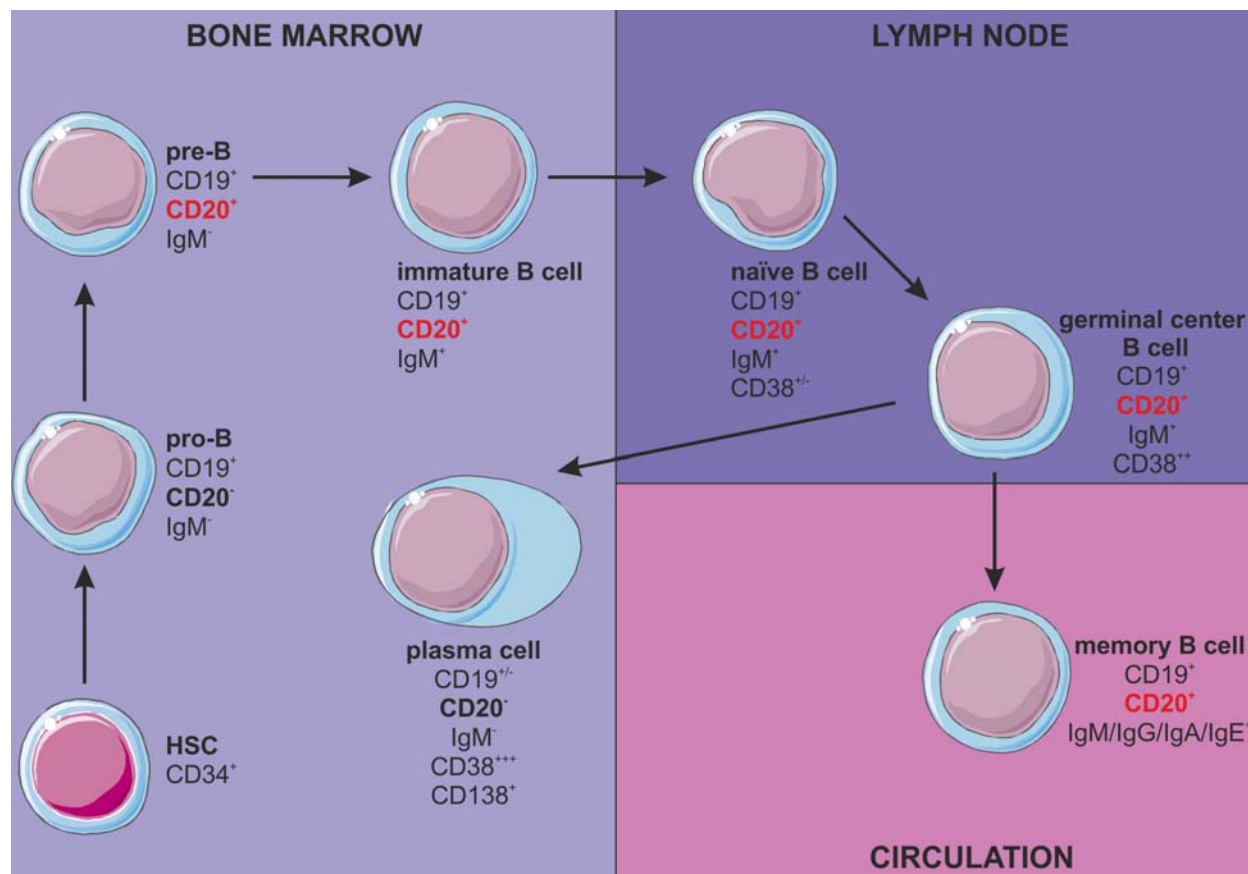
#### 4. ANTIBODIES AND MOLECULES TARGETING CD20

The clinical success of rituximab, tositumomab and ibritumomab tiuxetan, which constitute a first generation of anti-CD20 mAbs, led to a design and evaluation of a number of other anti-CD20 therapeutics. These antibodies, classified as a second or a third generation anti-CD20 mAbs, can bind to distinct epitopes within CD20, have different pharmacokinetics and may trigger stronger effector mechanisms as compared with rituximab (Figure 1). Second generation antibodies have a humanized (ocrelizumab, veltuzumab) or a completely human (ofatumumab) IgG1 constant fragments, while third generation antibodies (PRO131921, AME-133, obinutuzumab, LFB-R603/EMAB-6) have humanized tails, additionally adjusted by genetic engineering to outperform rituximab in triggering effector mechanisms (9-12).

Additionally, TRU-015, a small modular immunopharmaceutical composed of single chain anti-CD20 Fv fragment linked to human IgG1 CH2 and CH3 domains, which is undergoing clinical evaluation in the treatment of rheumatoid arthritis, has been shown to exert antitumor activity (13). The only second generation mAb approved for clinical use so far is ofatumumab, which is a more potent complement activator than rituximab (14). The likely reason for this is that ofatumumab binds to a distinct epitope than rituximab, which is located even closer to a B cell membrane. Moreover, ofatumumab seems to be more effective in triggering NK cell-mediated ADCC, which is independent of Fc $\gamma$ RIIIa polymorphism (see below).

#### 5. CD20 - A TARGET FOR RITUXIMAB

CD20 is an integral membrane molecule broadly expressed during B-cell ontogeny. It is present on the surface of numerous developmental stages of B cells from the early pre-B to the mature B cell stage (Figure 2). Its expression is ceased in normal as well as in malignant plasma cells, although one study reported that IFN- $\gamma$  can induce CD20 expression in multiple myeloma cells (15). This restricted profile of CD20 expression ensures that neither B-cell precursors nor other cell lineages are endangered during anti-CD20 mAb treatment (16). Lack of significant influence on plasma cells should not lead to impaired immunoglobulin production against pathogens. CD20 is a non-glycosylated phosphoprotein expressed in



**Figure 2.** Structure of CD20 molecule.

three isoforms of 33, 35 or 37 kDa, depending on the degree of phosphorylation (17). It was initially described as a human B-lymphocyte specific antigen and was initially referred to as B-lymphocyte surface antigen B1 (18). Later studies indicated that not only B lymphocytes but also other types of cells including normal and malignant T cells (19-21) as well as melanoma stem cells (22) or blood-derived CD133-positive stem cells (23) are able to express CD20, although to a much lower levels than cells of the B-cell lineage.

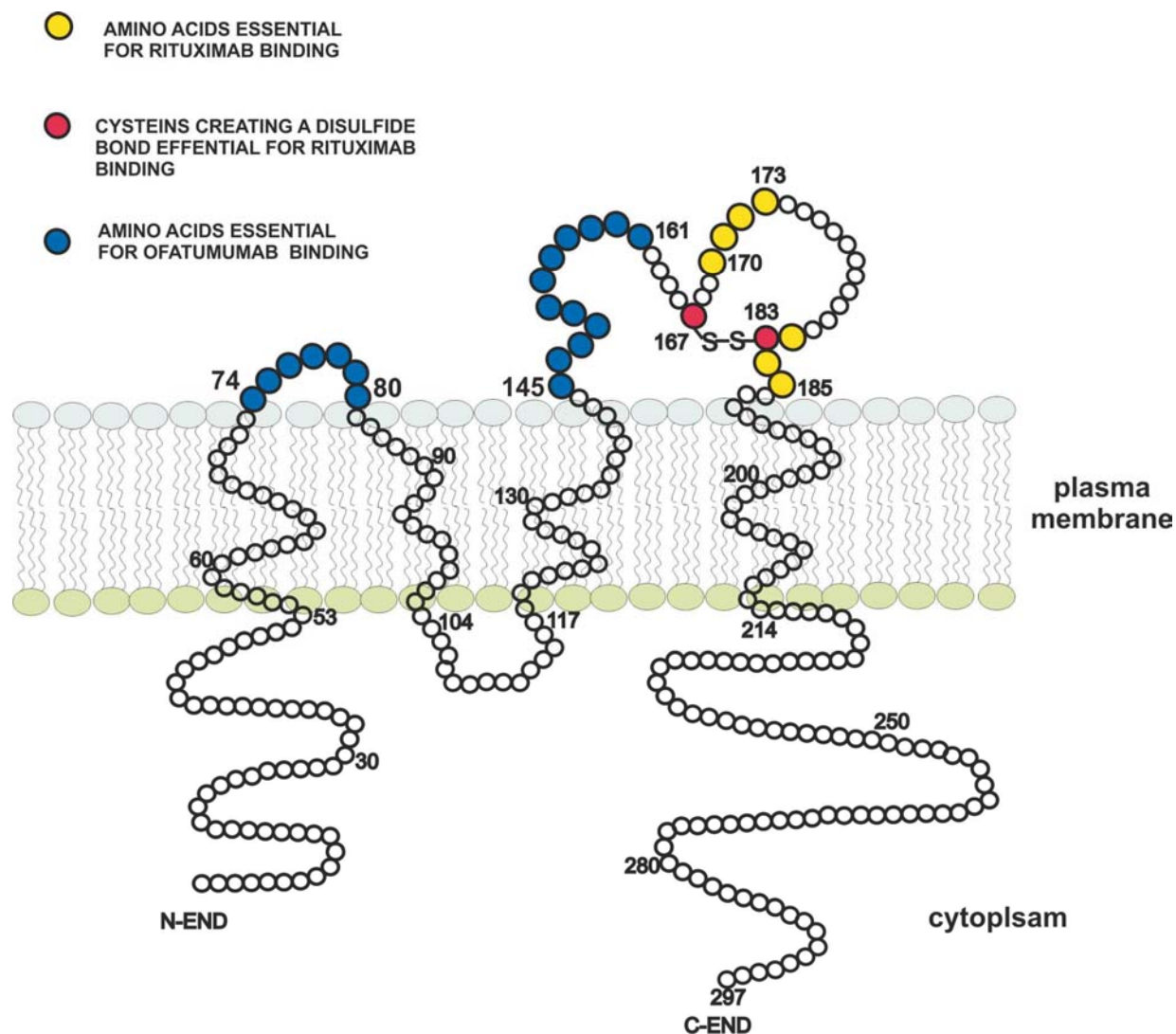
### 5.1. Gene structure and expression

CD20 was the first identified and is the best studied member of the membrane-spanning 4A gene family (MS4A). The members of this family consisting of more than 25 proteins, such as high affinity IgE receptor FcεRIβ (MS4A2) and hematopoietic cell-specific protein (HTm4, MS4A3) are characterized by common structural features and similar gene structure with 20-40% amino acid homology (24). In 1988 Tedder *et al.* completely cloned the genes for human (25) and murine (26) CD20. Human 16-kb gene, consisting of 8 exons, is located on chromosome 11q12-q13, mapping to the same chromosomal location as the genes for 8 other members of MS4A family.

The CD20 gene does not contain a classical TATA box but has several minor transcription initiation sites. Consequently, the transcription may start at several

points in exon 1 and 2 resulting in production of few different mRNAs, varying in length from 2.6 to 3.4 kb (25). Recently, a novel ΔCD20 mRNA transcript has been described that encodes a truncated protein of 15-17 kDa (27). This protein apparently associates with intracellular domains of normal CD20 and its levels increase in rituximab-resistant cells. It is possible that association with ΔCD20 can modulate the levels of CD20 in the plasma membrane or may affect translocation to lipid rafts.

CD20 expression is regulated by several transcription factors. The major region responsible for promoter activity is estimated to be located between -40 and -450 bp, containing at least four regulatory regions. The early studies led to the identification of several positive and negative regulatory *cis* elements in the sequence of the cloned gene (28). Subsequently, a BAT box containing an octamer binding site for commonly expressed Oct-1 and B-cell specific Oct-2 transcription factors at -255 to -201 was identified (29-30). As mutations of this site do not completely ablate CD20 expression (30), the involvement of other regions and transcription factors was suspected. Later on, it was shown that PU.1/Pip, important regulators of B-cell specific genes encoding such proteins as CD72 and immunoglobulin light chain, are able to bind to the CD20 promoter at -160 position and are involved in CD20 expression regulation (31). Additionally, a binding site for basic helix-loop-helix-zipper (bHLHZ) family of



**Figure 3.** Expression of CD20 during B-cell development.

transcription factors, that bind ubiquitously expressed transcription factors and include TFE3 (transcription factor E3) and USF (upstream stimulatory factor) was found (31). Finally, another regulatory site in CD20 promoter containing a sequence for binding of the B cell-specific activator protein (BSAP), a regulatory protein encoded by Pax5 gene, was described (32).

The mechanisms underlying the regulation of CD20 expression still remain poorly understood. Several studies demonstrated that some cytokines, including interleukin-4 (IL-4) (33-34), granulocyte-macrophage colony stimulating unit (GM-CSF) (34), tumor necrosis factor (TNF) (34-35), interferon  $\alpha$  (IFN- $\alpha$ ) (36), and IFN- $\gamma$  (15) are able to induce CD20 expression. Reactive oxygen species (ROS) may also influence CD20 expression (37). In CD20-positive cell lines irradiation or administration of hydrogen peroxide as a source of ROS has been reported to increase CD20 expression, while administration of antioxidants reversed this process (37).

## 5.2. Protein structure and localization

CD20 contains four membrane spanning domains with both termini in the cytoplasm (Figure 3) (38). Apart from the membrane-spanning domains, the protein contains two extracellular loops: a short (7 amino acids) loop localized between the first and the second transmembrane domains, that is highly conserved among the other MS4A family members, and a longer one (44 amino acids) localized between the third and the fourth transmembrane domains (39). Tight association with the plasma membrane protects the antigen from shedding.

As a hydrophobic, transmembrane protein, CD20 is constitutively associated with low affinity to lipid rafts (40-42). Binding of some (but not all) antibodies to CD20 increases its association with lipid rafts, favoring translocation of the molecule from the border to a centre of a raft area and facilitating oligomerization of CD20 molecules (42). At least in some cells CD20 appears to be localized to membrane protrusions known as microvilli

(43). Although CD20 co-localizes with BCR within lipid rafts on the surface of B-cells these molecules dissociate rapidly before BCR internalization (43). Additionally, CD20 has been shown to co-localize with CD40, MHC class I and II molecules, other tetraspan molecules (CD53, CD81 and CD82), and a transmembrane adapter protein p75/80 (also known as C-terminal Src kinase-binding protein, Cbp) (44-46). It is still not clear how CD20 interacts with these molecules.

### 5.3. CD20 function

Despite extensive ongoing research a natural ligand for CD20 has not been identified and the detailed function of the molecule remains to be elucidated. CD20 seems to be involved in B-cell development, activation and proliferation at least to some extent through regulation of intracellular calcium concentration and redistribution (7, 47). The majority of knowledge on the biological function of CD20 is based on studies with knockout animals, genetically modified cells or various monoclonal antibodies that ligate CD20 on normal or malignant B cells. The results of these studies, depending on the type of antibody used, have demonstrated that CD20 engagement may lead to increased B-cell survival (48) and proliferation (49) or, just the opposite, to cell cycle arrest (50) and induction of apoptosis (51-53).

The oligomeric structure and close homology to FcεRIβ, which is involved in Ca<sup>2+</sup> conductance, suggest that CD20 may form a membrane channel involved in the regulation of ion transport. Indeed, initial studies revealed that transfection of CD20-negative cells with *cd20* gene increases cytoplasmic Ca<sup>2+</sup> concentrations (7). However, these studies involved whole cell patch clamp analyses rather than cytosolic Ca<sup>2+</sup> measurements, and more recent studies clearly indicated that CD20 is not a Ca<sup>2+</sup> channel in transfected cells (54). Subsequently, Li *et al.* (55) have reported that human CD20 is responsible for calcium flux during BCR signaling. They suggested that CD20 is involved in extracellular calcium influx required during B-cell activation and works as store- or capacitance-operated calcium channel. These observations have been extended by Walshe *et al.*, who demonstrated that binding of rituximab to CD20 leads to its clustering with BCR followed by "borrowing" of the BCR signaling pathways that trigger Ca<sup>2+</sup> release from intracellular stores (54). Even though the data presented above is convincing the relatively mild phenotype of CD20 knockout mice suggest that apart from CD20 also some other calcium channels may participate in B-cell activation.

Although the studies in CD20 knockout mice have surprisingly shown no significant impairment in humoral response (56), a recent report on the patient with CD20 deficiency has changed the general view on the function of CD20. The authors demonstrated that despite normal development of naïve B-cells, the absence of CD20 expression leads to immunodeficiency with severely impaired antibody formation, development of hypogammaglobulinemia, and impaired responses against polysaccharides after vaccination (57).

### 5.4. The epitopes recognized by anti-CD20 mAbs

The specific epitope for rituximab is encoded by sequences found in exon 5 of the MS4A1 gene, corresponding to a large extracellular domain comprising amino acids 165 to 184. Two amino acid sequences: ANPS and YCYSI at positions 170 to 173 and 182 to 185 are critical for rituximab binding (8, 58-59) (Figure 3). Therefore, the epitope is discontinuous and a disulfide bond between C167 and C183 is necessary to hold the two fragments in steric proximity (39). Different but overlapping epitopes are bound by ocrelizumab and other humanized antibodies. On the other hand ofatumumab binds to a completely different but also discontinuous epitope formed by sequences in a shorter (residues 74-80) and a longer loop (residues 145-161) of CD20 (60). The epitope for tositumomab has not been characterized in detail, but seems to be different than those recognized by rituximab and ofatumumab (61).

## 6. EFFECTOR MECHANISMS OF ANTI-CD20 MABS

Anti-CD20 mAbs can be divided into two types (62-63). Type I antibodies (rituximab and ofatumumab) redistribute CD20 to lipid rafts and are efficient activators of the complement cascade, but are relatively poor inducers of apoptosis, unless cross-linked by secondary anti-IgG antibodies (see below). Type II antibodies (tositumomab) are ineffective in complement activation, but readily activate homotypic adhesion of tumor cells and trigger a apoptotic or non-apoptotic cell death. Both types of antibodies can engage immune cells in ADCC or immunophagocytosis (62-64). The reasons for the differential engagement of effector mechanisms most likely lies in the unique specificities of type I vs. type II antibodies. This was most clearly demonstrated in studies that compared activation of CDC, phagocytosis or the capacity to induce cell death by engineered type I and II antibodies that had exactly the same Fc fragments of murine IgG2a subclass (61). The engineered mAbs retained the properties of original antibodies.

It is possible that it is the ability of type I antibodies to redistribute CD20 molecules to lipid rafts that makes these antibodies so effective in complement activation (62-63, 65). Lipid rafts are small (10-200 nm) membrane domains rich in cholesterol and glycosphingolipids, which facilitate the assembly of signaling molecules (66). It is conceivable that by concentrating multiple copies of CD20-mAb complexes within a clustered area of plasma membrane facilitates juxtaposition of Fc fragments allowing facile binding of C1q globular heads. Also the high cholesterol content within lipid rafts might contribute to efficient incorporation of MAC in the plasma membranes as has been demonstrated for erythrocytes (67).

For several reasons the relative contribution of each of these mechanism is difficult to predict. Most of the mechanistic studies have been done in *in vitro* systems, which do not include multiple variables affecting their efficacy in a living organism, including hyperoxia, which is

inherent to *in vitro* studies, lack of donor-derived serum, changes in the temperature during cell manipulation etc. Effector cells used in these experiments are not syngeneic, and the polymorphic differences between different donors are usually not considered. Moreover, the effector cells are obtained from normal, and not tumor-bearing individuals. Finally, the experimental assays usually take hours to days, but not weeks as is the case of anti-CD20 therapy in patients. Therefore, it is difficult if not even impossible to directly compare effector mechanisms in cell culture assays. Another important question is whether these assays should not consider simultaneous activation of all potential effector mechanisms that never act separately in patients.

Animal studies with anti-CD20 mAbs provide more valuable information, but there are additional variables inherent to species-specificities that affect interpretation of experimental data. For example, rituximab cannot be used in studies with normal mice since it does not bind to murine CD20 (68). This obstacle can be obviated by using either transgenic mice with human CD20, syngeneic models with murine tumor cells transfected with human CD20, or immunodeficient mice transplanted with human tumor cells. However, it is hard to predict an extent of species-dependent specificity in binding of chimeric or humanized antibodies to murine C1q or Fc $\gamma$ R as the contact sites for C1q in murine IgG2b and human IgG1 are different (69), and binding of human Fc to murine FcR is not optimal. Moreover, xenotransplantation studies suffer from additional drawbacks. For example, the impact of murine microenvironment on the expression levels of CD20 molecules or complement regulatory proteins is unknown. What is the influence of human MHC class I molecules on NK cells activity in mice? Is there a role for damage-associated molecular patterns (DAMPs) in recognition of human cells? These studies do not allow to measure distant vaccinal effects due to a lack of adaptive immunity. The last variable can be eliminated by using mouse anti-CD20 mAbs, but murine CD20 lacks typical redistribution motifs, which are present in the human antigen (70). Therefore, murine cells do not respond to mAb ligation in the same way as human. Studies in animals transplanted with murine tumor cells transfected with human CD20 gene and treated with rituximab suffer from the same species-compatibility problem (human Abs may not interact efficiently with mouse effector cells) and the results are confounded by the possibility of inducing an immune response against xenogeneic CD20 antigen. All these limitations do not invalidate the results obtained in *in vitro* or *in vivo* studies but need to be considered during interpretation of experimental data.

Another important issue is that tumor development is a long-term process associated with suppression of effector mechanisms of the immune system. Moreover, rituximab is most effective in combination with chemotherapeutics that exert immunosuppressive effects and lead to development of leucopenia. All these effects are likely to affect mechanisms associated with cell-mediated effector functions to a higher degree than activation of the complement cascade.

### 6.1. Complement-dependent cytotoxicity

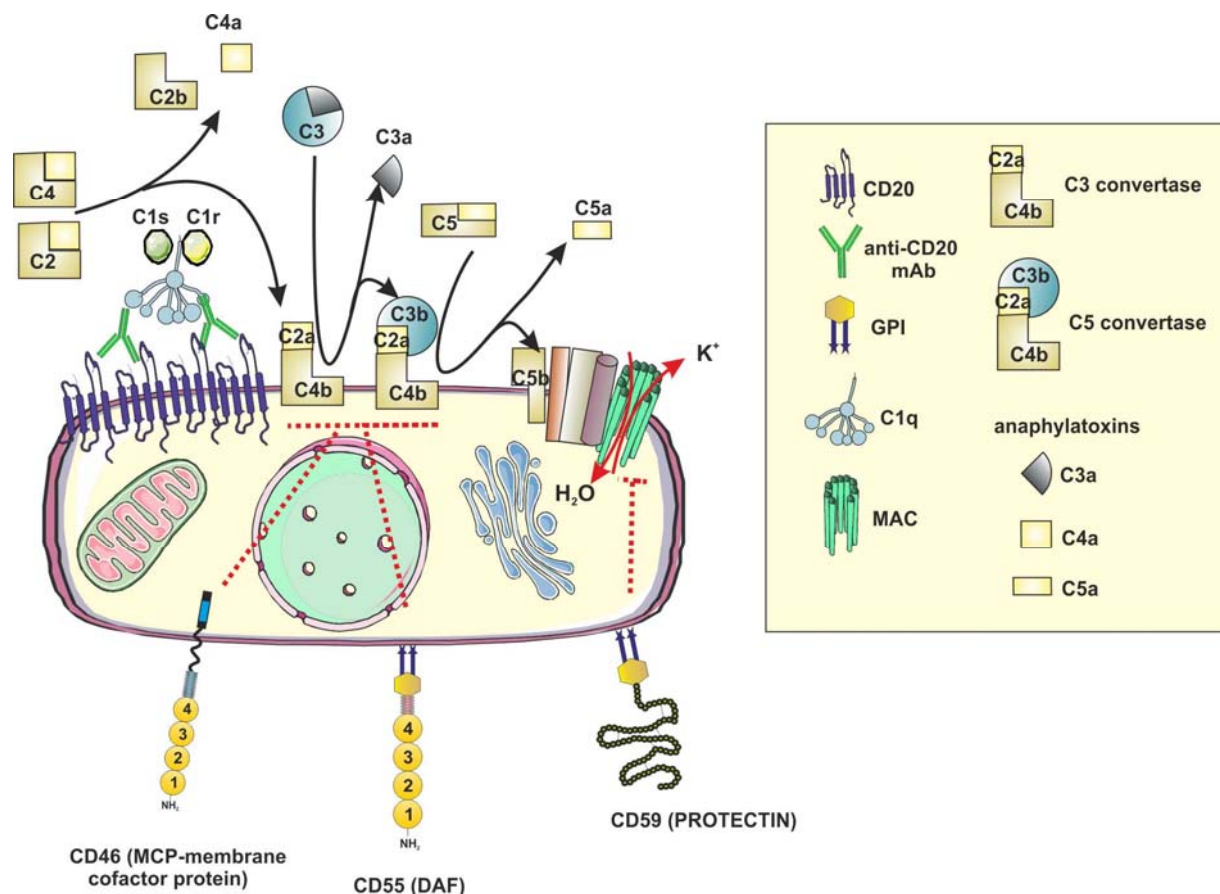
CDC is an innate effector mechanism that participates in elimination of extracellular microorganisms or infected cells. It can be triggered in a spontaneous, so called alternative pathway or following recognition of target cells by opsonins such as lectins or antibodies. The first step of immunoglobulin-mediated i.e. classical pathway of complement activation is binding of C1q component to Fc portions of antigen-bound IgG or IgM antibodies, which triggers a cascade of proteolytic events leading to formation of a membrane-attack complex (MAC, C5b-9) (71). Activation of the complement cascade may also trigger several immune-mediated mechanisms in addition to direct cytotoxicity. Byproducts of the complement activation, including C1q, C3b, iC3b, and C4b are effective opsonins that facilitate removal of immune complexes and dead tumor cell debris by phagocytic cells. Opsonizing C3b molecules that bind to complement receptors (CR) strongly enhance Fc $\gamma$ R-mediated phagocytosis of IgG-opsonized cells by macrophages and neutrophils (72). Small complement fragments released during the activation cascade (C3a, C4a and C5a), collectively referred to as anaphylatoxins are potent chemoattractants for leukocytes, also capable of triggering basophil and mast cell degranulation, increasing vascular permeability or smooth muscle constriction (73). Moreover, C5a can increase expression of Fc $\gamma$ RIII and suppress expression of inhibitory Fc $\gamma$ RIIb in macrophages (see below) (74).

#### 6.1.1. CDC - *in vitro* studies

The degree of complement activation depends on several factors that include a tumor subtype, CD20 expression level, the presence of complement regulatory proteins (CRP), or the class or type of antibody (Figure 4). Type I anti-CD20 mAbs can activate the classical pathway of complement cascade and a number of observations indicate that CDC participates in elimination of normal and malignant B cells *in vitro* (75-80). This is most straightforwardly shown in studies with primary and established B cell lines that undergo rapid lysis when co-cultured with type I mAbs and complement components (usually a serum). Follicular lymphoma (FL) and mantle cell lymphoma (MCL) cells are killed more effectively than cells of diffuse large B-cell lymphoma (DLBCL), or B-cell chronic lymphocytic leukemia (B-CLL) (79). A sigmoidal correlation exists between CD20 levels and rituximab-mediated killing via CDC, but not ADCC (80). Similarly, other studies indicate that the potency of CDC in anti-CD20 mAb therapy correlates to some extent with CD20 expression levels (77-78).

#### 6.1.2. CDC - *in vivo* studies

Depletion of complement components by cobra venom factor (CVF) significantly reduces antitumor activity of anti-CD20 mAb in severe combined immunodeficient (SCID) mice (62, 81-82). Similarly, studies with C1q-deficient mice revealed that in syngeneic mouse models (murine cells stably transfected with a human CD20 gene) activation of the classical complement pathway is fundamental for elicitation of therapeutic activity of anti-CD20 mAbs, whereas the activity of NK



**Figure 4.** Activation of complement cascade by anti-CD20 mAbs.

cell, neutrophils, macrophages or T cells is dispensable (83-84). Studies in cynomolgus monkeys revealed that administration of rituximab induces a rapid (within 2 minutes) C3b(i) deposition in the plasma membrane of B cells that co-localizes with rituximab (85), and that the ability to eradicate CD20-positive cells with IgG1 mAbs was completely lost by the exchange of Fc fragments into IgG4, which lack complement-binding activity (86). Similarly, infusion of rituximab leads to deposition of C3b(i) in the plasma membranes of normal B cells (87).

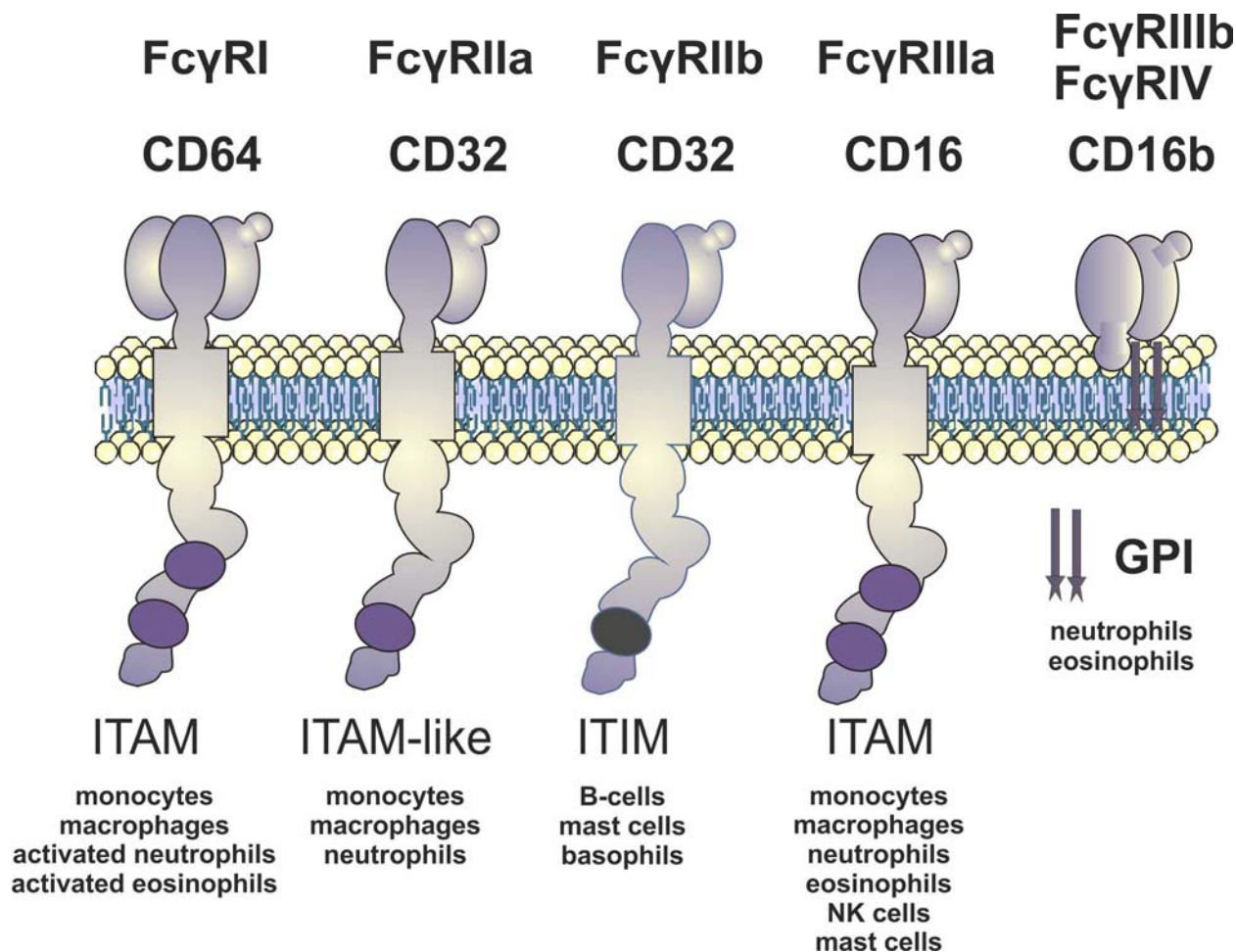
Clinical observations indirectly confirm the involvement of complement activation in rituximab-treated patients. Administration of rituximab to CLL patients is associated with a profound loss of complement activity (87) or in a decrease in C2, C3 and C4 concentrations (87-88), which most likely results from complement consumption. Likewise, administration of rituximab increases plasma concentrations of complement activation products C3b/c and C4b/c in NHL patients (89). Moreover, treatment with rituximab leads to selection of CD59-positive cells in some patients with B-CLL (90), a finding also supported by similar observations in SCID mice (82).

At odds with these observations Ushida *et al.* reported that in mice deficient in C1q (C1q<sup>-/-</sup>), C3 or C4 complement components anti-CD20 mAbs effectively

deplete normal B cells (91). Also, a recent study revealed that rituximab-mediated depletion of B cells in human CD20 transgenic mice was comparable in wild-type and C1q<sup>-/-</sup> and C3<sup>-/-</sup> mice (92). In another study performed in BUB mice, which have exceptionally potent complement hemolytic activity, antitumor effects of genetically modified anti-CD20 mAbs with at least 30-fold reduced affinity for C1q were unaffected (93).

Also clinical studies provide ambiguous results on the role of complement in the antitumor efficacy of anti-CD20 mAbs. While C1qA polymorphism associated with low C1q concentrations correlates with prolonged response to rituximab in patients with FL (94), other studies indicate that administration of a fresh frozen plasma, which is a source of complement, improves antitumor activity of this antibody in patients with B-CLL (95). A recent study involving real-time imaging technique of living cells obtained directly from rituximab-treated patients revealed a close relationship between CDC susceptibility and clinical response to rituximab-containing chemotherapy (96). CDC susceptibility in this study was also significantly correlated with the level of CD20 expression.

Complement activation can be responsible for infusion-related side effects, which are associated with a substantial increase in blood components of activated



**Figure 5.** Activation of antibody-dependent cellular cytotoxicity (ADCC) and phagocytosis by anti-CD20 mAbs.

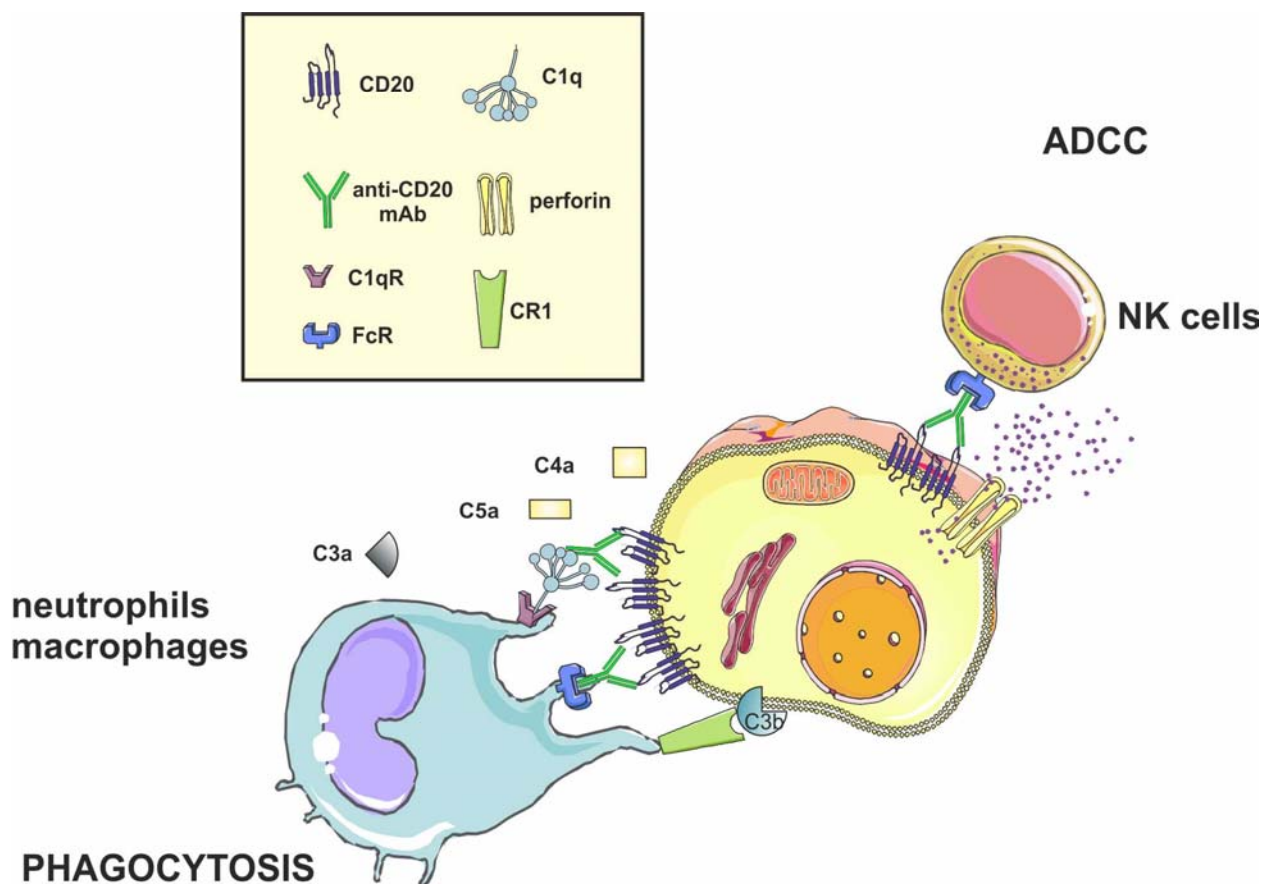
complement cascade, mainly C3b and C4b (89). Additionally, some observations indicate that complement activation may even have detrimental effects in the setting of anti-CD20 mAb treatment. For example, C3 has been shown to directly inhibit the activity of NK cells and C3b components opsonizing tumor cells can inhibit ADCC mediated by these cells (97-98). Moreover, iC3b components attached to apoptotic cells favor development of immune tolerance-inducing dendritic cells (99). Phagocytic cells may participate in "shaving" reaction, which leads to removal of immune complexes together with rituximab and CD20 molecules from circulating tumor cells (see below).

## 6.2. FcγR-mediated cytotoxicity

Activation of effector cells of the immune system seems to be the most universal mechanism of cytotoxic effects as it is induced by both type I and type II anti-CD20 mAbs. CD20 binding by these antibodies on target tumor cells activates monocytes, macrophages, neutrophils, NK cells or  $\gamma\delta$  T cells via receptors for the constant fragment of IgG (FcγR). These receptors can be broadly divided into activating or inhibitory (100). Human activating receptors include FcγRI (CD64), FcγRIIA

(CD32a), and FcγRIII (CD16). Activation of these receptors initiates signaling pathways through immunoreceptor tyrosine-based activation motifs (ITAM) found in cytoplasmic parts of FcγRIIA or in shared dimeric common  $\gamma$  chains that associate with FcγRI and FcγRIII. FcγRIIB (CD32b) is an inhibitory receptor that signals via immunoreceptor tyrosine-based inhibitory motifs (ITIM) (Figure 5).

Activation of effector cells via FcγR can result in various outcomes that depend on the type of FcγR engaged as well as the type and activation status of effector cells (Figure 6). Also the class and the type of anti-CD20 mAb, the presence of C3b or expression of MHC class I molecules in the target cells can influence the response of effector cells (101-103). Possible mechanisms of FcγR-mediated effects include: ADCC, immunophagocytosis, release of cytokines, proteases, reactive oxygen species (ROS) or crosslinking leading to induction of apoptosis (104). It still remains to be determined which cells and in which mechanisms participate in elimination of malignant B cells during anti-CD20 mAb treatment. These issues are difficult to address in a clinical setting. Studies in preclinical models are partly contradictory and it is formidable to interpret their results considering manifold



**Figure 6.** Direct induction of tumor cell death by anti-CD20 mAbs.

species incompatibilities between humanized (or human) antibodies and murine effector mechanisms (see above).

#### 6.2.1. FcγR-mediated cytotoxicity - *in vitro* studies

Rituximab can induce ADCC of CD20-positive tumor cells by human peripheral blood mononuclear cells (PBMC) (105-106). Most of the ADCC activity of PBMC can be attributed to NK cells. Freshly isolated NK cells can kill up to 3 rituximab-coated target cells within 16 h. This number can be increased 2-fold by addition of IL-2 (107). Some studies indicate that peripheral blood-derived monocytes show *in vitro* anti-CD20 mAbs-mediated ADCC cytotoxicity towards malignant B-cells (108-109), but other do not confirm this, but indicate that only M-CSF-stimulated macrophages differentiated from CD14<sup>+</sup> monocytes can mediate phagocytosis of rituximab-coated B-CLL cells (110). Neutrophils and γδ T cells are another population of cells that can exert cytotoxic effects towards rituximab-opsonized tumor cells (111-112).

Many variables affect susceptibility or resistance of tumor cells to anti-CD20 mAb-mediated cytotoxicity. These are associated with the presence or expression of molecules that regulate the activity of effector cells. For example, expression of ULBP molecules, which serve as ligands for activating NKG2D receptors increases susceptibility of NHL cells to NK cell-mediated ADCC

(113). On the other hand, a negative correlation with the expression of MHC class I molecules was found (113-114). Moreover, deposition of C3b on target cells impairs the interaction between the Fc fragment of rituximab and NK-cell receptor - FcγRIII (CD16), decreasing effector cell activation and ADCC (98). Also in mice C3 depletion enhanced NK-cell activation and improved the effectiveness of rituximab therapy (97).

#### 6.2.2. FcγR-mediated cytotoxicity - *in vivo* studies

Unambiguous role of the cell-mediated mechanisms participating in elimination of tumor cells was revealed in experiments done with *FcRγ*<sup>-/-</sup> mice, that do not have common γ chains associating with FcγRI, FcγRIII and FcγRIV (a mouse ortholog of human FcγRIIIa). Antitumor effects of anti-CD20 mAbs are nearly completely abolished in these animals indicating that FcR-dependent mechanisms significantly contribute to *in vivo* activity of these antibodies (93, 115). This conclusion is supported by a growing number of clinical reports showing superior antitumor effects of rituximab in patients with NHL or Waldenström's macroglobulinemia having FcγRIIIa allelic variants that bind IgG1 with higher affinity (116-118). Of interest, the influence of the *FCGR3A* polymorphism is completely lost when rituximab is combined with chemotherapy (119-121). No association between FcγR polymorphic variation and response to treatment in patients

with CLL has been found (122). This is especially intriguing considering that induction of CDC requires about 10-fold more Abs deposited on the cell surface than does ADCC (123). Therefore, at low CD20 expression levels, which is typical for CLL, ADCC mechanisms might be dominant. Similarly, an allelic variant of FcγRIIA that binds IgG with higher affinity has been independently associated with better response rates in patients with FL (117). Treatment with anti-CD20 mAbs of mice deficient in inhibitory FcγRIIB resulted in better antitumor responses (93, 115), but it seems that polymorphism of genes encoding an inhibitory FcγRIIB does not affect response to rituximab in patients with FL (124).

In contrast to complement-mediated lysis the efficiency of macrophage-mediated phagocytosis is not affected by CD20 expression levels (110). Although the polymorphism of CD16 seems to affect ADCC of rituximab-coated targets by NK cells it does not affect phagocytosis by macrophages (110). Several mechanistic studies in mice revealed that normal and malignant B-cell depletion with anti-CD20 mAbs requires monocyte/macrophage FcγR expression (91, 93, 125). Clinical studies support the positive correlation between tumor-associated macrophages (TAMs) and response to rituximab (126-127).

Neutrophils are another leukocyte population that can contribute to the antitumor effects of anti-CD20 mAbs. Resting neutrophils exhibit low levels of FcγRIIa and FcγRIIb. The latter is expressed exclusively by these cells and is involved in immunophagocytosis rather than ADCC. *In vitro* studies revealed that neutrophils participate in ADCC by using FcγRI, especially upon activation with G-CSF or IFN-γ and to a lesser degree by using FcγRIIa. However, these cells are far less potent in killing tumor cells as compared with NK cells (111, 128). Experiments in mice revealed that anti-lymphoma effects of rituximab are significantly reduced in neutrophil-depleted SCID mice and completely abrogated in neutrophil- and NK cells-depleted animals (129). However, murine, but not human, neutrophils mainly express FcγRIV, which can bind human IgG1, and clinical observations indicate that there is no association between polymorphism of FcγRIIb and response to rituximab (130).

### 6.3. Direct cell killing

Based on morphologic and biochemical criteria several types of programmed cell death processes have been identified. Apoptosis - a historically classical programmed cell death - is executed by either external or internal pathway (131-132). The former is initiated by stimulation of death receptors, such as Fas (CD95) or TRAIL-R, and results in caspase 8 or 10 activation followed by proteolytic activation of caspase 3. During the intrinsic pathway BH3-only members of the Bcl-2 family regulate the release of cytochrome c from mitochondria. Cytochrome c together with Apaf-1 activate caspase 9, which triggers activation of downstream caspases 3 and 7. Caspase 3 degrades poly-(ADP-ribose)-polymerase (PARP - one of the enzymes repairing DNA injuries), activates phospholipase C, and leads to proteolysis of DNaze

inhibitor, what results in DNA fragmentation. A type 2 or autophagic cell death is characterized by a massive vacuolization of the cytoplasm. Autophagic cytoplasmic degradation requires the formation of a double-membrane structure called the autophagosome, which sequesters cytoplasmic components as well as organelles and traffics them to the lysosomes (132). A third type of cell death is necrosis. Although it has long been described as a passive, accidental and unorganized way to die, recent evidence suggests that necrotic cell death can be actively propagated as part of signal transduction pathways (133).

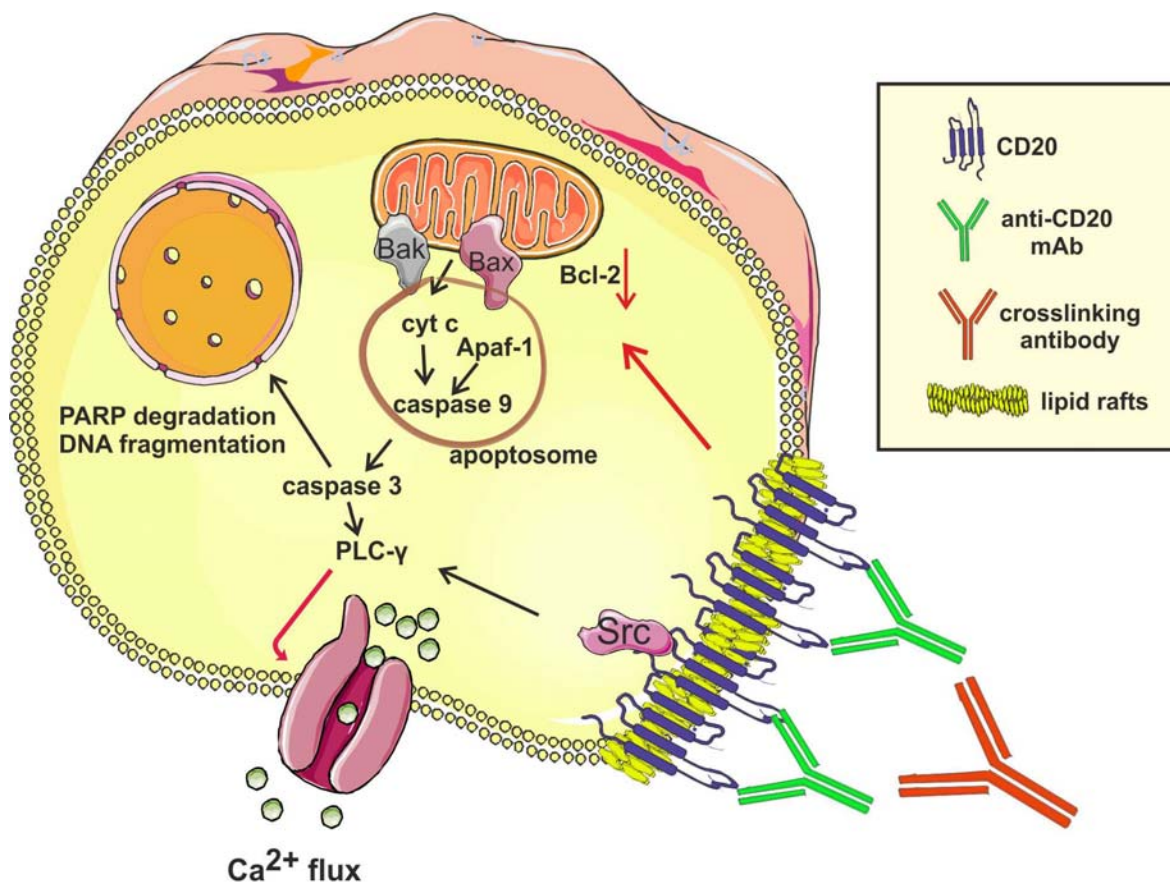
#### 6.3.1. Direct cell killing - *in vitro* studies

Anti-CD20 mAbs can induce death of malignant B cells (Figure 7) (51, 134). The mechanism of direct cytotoxic effects varies depending on the type of mAbs used. Type II mAbs, such as tositumomab more effectively induce direct killing of most B-cell tumor cell lines (52). In most studies crosslinking of rituximab or other type I mAbs with secondary antibodies is necessary to elicit apoptotic cell death. It is achieved by binding two molecules of rituximab by an antibody that recognizes their Fc fragments (crosslinking) (135), using a homodimerized rituximab (136), modified self-associating antibodies (137), or a dextran polymer of rituximab (138). However, the existence of *in vivo* crosslinking is controversial since the production of antibodies against rituximab is not observed in patients (139). It is hypothesized that crosslinking can be achieved by FcγR-bearing cells (135), but such possibility was recently ruled out (140). Although the existence of crosslinking has not been formally proven several authors report induction of caspase activation after rituximab administration *in vivo* or in patients with B-CLL (141-142).

After cross-linking rituximab can activate apoptosis via both external (143) and internal (41, 141, 144) pathways, as well as caspase-independent, in which there is no PARP degradation or chromatin condensation (145-146).

The involvement of death receptor-mediated apoptosis in anti-CD20 mAb-mediated cytotoxicity was hypothesized after observing that these antibodies induce homotypic adhesion of tumor cells. Clustering of tumor cells could enable direct interactions between cell surface molecules participating in extrinsic pathways of cell death. Indeed, in cells incubated with anti-CD20 mAbs an increased expression of Fas is observed (53, 147). Blocking anti-FasL antibodies decrease the percentage of tumor cells undergoing apoptosis (53) and anti-Fas antibodies synergize with rituximab in killing of CD20<sup>+</sup> tumor cells (147). Similarly, improved *in vitro* as well as *in vivo* effects of rituximab were observed in combination with anti-TRAIL-R mAbs (mapatumumab or lexatutumumab) or with recombinant human TRAIL (148-149).

In some studies rituximab was shown to directly induce cytotoxic effects towards tumor cells, without any crosslinking (135, 150). Intriguingly, this effect is observed in some but not all CD20<sup>+</sup> tumor cell lines (151). A recent study revealed that susceptibility to direct cytotoxicity correlates with the level of GM1 gangliosides (152), which



## DIRECT CELL KILLING

**Figure 7.** Structure and expression of human and mouse FcγRs.

are sialic acid-containing glycosphingolipids that participate in the formation and stabilization of lipid rafts. Based on these observations it is possible that type I antibodies can trigger death of CD20<sup>+</sup> cells only when CD20 molecules can be translocated to lipid rafts containing high levels of GM1 gangliosides or after crosslinking. In contrast, type II antibodies readily induce cytotoxic effects without the need for raft translocation. The mechanisms of these effects remain to be elucidated.

Cell death induced by type II mAbs is not a classic apoptosis. It does not lead to caspase processing or DNA fragmentation, seems to be independent of Bcl-2 activity, and does not involve autophagy (153-154). Instead, these antibodies induce homotypic adhesion of tumor cells associated with rapid and sustained actin redistribution that leads to structural changes in lysosomes that swell and release their contents, including cathepsin B, into the cytoplasm precipitating loss of plasma membrane integrity and cell death (154).

### 6.3.2. Direct cell killing - *in vivo* studies

Only few studies show direct induction of apoptosis by anti-CD20 mAbs. In xenografted human

lymphoma model rituximab treatment induces activation of caspases (142). Activation of caspase-3, caspase-9 and PARP cleavage have also been observed in some CLL patients treated with rituximab indicating that direct apoptosis might be involved in elimination of tumor cells (141). However, B cells transfected with Bcl-2 gene that are resistant to apoptosis-inducing agents are efficiently eliminated from mice (92). Clinical studies revealed that patients with CLL not responding to rituximab treatment have an increased ratio of anti-apoptotic Mcl-1 to pro-apoptotic Bax ratio, although the pretreatment levels of other anti-apoptotic proteins, such as Bcl-2 or XIAP had no influence on the treatment efficacy (90). Preclinical studies revealed that antisense Bcl-2 oligonucleotides or AT-101, a BH3 domain (Bcl-2 homology domain 3) mimetic, strongly potentiate rituximab-mediated effects in SCID mice transplanted with human lymphoma xenografts (155-156). Promising and beneficial effects of combination of rituximab with sodium oblimersen, a Bcl-2 antisense oligonucleotide, in patients with indolent NHL have also been observed (157).

Type II antibodies retain their full antitumor activity in NK cell-depleted or NK cell-deficient (Beige)

mice (62). F(ab')<sub>2</sub> fragments from these antibodies retained significant *in vivo* activity and both B1 and its F(ab')<sub>2</sub> fragments effectively induced apoptosis of CD20<sup>+</sup> lymphoma cells indicating that direct cytotoxic effects rather than CDC, ADCC or phagocytosis are responsible for their tumoricidal activity (62).

### 6.4. Vaccinal effects

Administration of anti-CD20 mAbs to patients with B-cell tumors most likely triggers all of the effector mechanisms at the same time. It should be emphasized that CDC, ADCC or induction of cell death are not interdependent or mutually exclusive but most likely interact and cooperate in elimination of malignant B cells. Delayed responses observed in some patients treated with rituximab led to suggestions that anti-CD20 mAbs might also favor development of adaptive immune responses. Tumor cells damage by complement or during ADCC might be associated with an increased availability of fragments of tumor cells opsonized by antibodies and/or complement fragments (158). Moreover, rituximab-binding to lymphoma cells can induce expression of CCL3 and CCL4 chemokines (81) that together with complement activation products (C3a, C5a) could participate in recruitment and activation of antigen presenting cells (APC) such as dendritic cells or macrophages. In transplantation, for example, C3a and C5a receptors on donor APC are critical for triggering T-cell-mediated rejection (159-160). Chemoattracted and activated APC might then effectively capture damaged tumor cells, process engulfed proteins and present tumor-associated antigens in association with major histocompatibility complex (MHC) molecules to T cells. *In vitro* studies confirmed that lymphoma cells undergoing rituximab-induced apoptosis can be taken up by immature dendritic cells, induce their maturation and promote cross-presentation to activate CD8<sup>+</sup> cytotoxic T cells (161). Although anti-CD20 antibody treatment or dendritic cell vaccination alone showed minimal antitumor effects in mice, the combined treatment resulted in significant long-term survival (162). A small exploratory clinical study revealed that in 4 out of 5 patients with follicular lymphoma rituximab treatment is capable of inducing idiotype-specific T-cell response (163). Also, a booster effect, i.e. a favorable and quick response to rituximab after the second infusion might indirectly confirm the possible existence of rituximab-induced "vaccinal" effects (164).

## 7. FACTORS AFFECTING THE ACTIVITY OF ANTI-CD20 MABS

Although rituximab is a critical monoclonal antibody in the treatment of CD20-positive B-cell malignancies the resistance to this treatment has been a considerable clinical problem. Unfortunately, a significant percentage (50%) of patients who initially respond to rituximab-based first line therapies eventually relapse (139, 165). Moreover, although more than 95% of patients with NHL express surface CD20 there are patients who demonstrate intrinsic resistance to initial therapy. There is mounting evidence supporting the existence of multiple mechanisms of antitumor rituximab action, but the

mechanisms of rituximab resistance are still poorly understood.

### 7.1. The expression of CD20

CD20 expression is quite heterogeneous in various lymphoma subtypes. Typically, CLL have a lower (dim) CD20 expression and this seems to be responsible for the lower response rates to rituximab treatment as compared with FL and MCL. Several studies have addressed whether the level of CD20 expression correlates with efficacy of rituximab and may be used to predict progression of disease and response to treatment. The results are to some extent conflicting. In some *in vitro* studies with cells derived from patients suffering from various B-cell malignancies a positive correlation between CD20 levels and rituximab sensitivity (R-CDC) was found (77-78). However, these observations were not corroborated by other studies (79). An elegant study by van Meerten *et al.* has demonstrated a sigmoidal correlation between CD20 expression level and rituximab-mediated CDC but not ADCC (80). In this *in vitro* experimental model the level of CD20 expression was the only variable and it was clearly shown that reduced CD20 expression leads to impaired CDC. A direct correlation between R-CDC and the number of CD20 molecules in primary NHL cells was also found by Bellosillo *et al.* (77). It has been established that the minimum level of  $5 \times 10^4$  CD20 molecules per cell is necessary for rituximab to induce CDC (77). It should be mentioned that MACs formation leads to rapid necrotic-type cell death only when multimers of MACs are assembled (166-167), which in turn depends on CD20 levels. Strategies that induce upregulation of CD20 expression may improve rituximab-mediated cell kill of low CD20-expressing cells and provide a rationale for overcoming rituximab-resistance.

On the contrary, all processes that cause CD20 decrease, downregulation, changes in epitope structures, or in CD20 localization within cellular membrane could potentially impair antitumor activity of rituximab-based therapies and lead to rituximab resistance

#### 7.1.1. Transcriptional regulation

It is still frequently taken for granted that CD20 expression levels in various B-cell tumors is relatively constant. However, accumulating evidence indicates that CD20 can be modulated at several levels, both transcriptional and posttranscriptional, and this can even lead to selection of antigen-loss variants of tumor cells. Several case or retrospective studies reported that CD20-negative relapses after rituximab treatment do occur (168-175). The prevalence and duration of CD20 loss are currently unknown. A number of mechanisms that account for modulation of CD20 levels have been proposed. Most likely their occurrence and significance varies depending on the type of malignancy. In CLL rituximab-mediated down-modulation of CD20 is associated with reduced levels of CD20 mRNA both *in vitro* (176) and *in vivo* (177) indicating that transcriptional regulation participates in this process. Indeed, a recent study with CLL cells indicated that Flt3

ligand (FL) activates signaling cascades that inhibit expression of PU.1, a transcription factor involved in the expression of *cd20* gene (178). Rituximab-mediated down-regulation of CD20 mRNA and protein levels in CLL was transient and did not lead to selection of antigen-loss variants (177).

Epigenetic mechanisms also play an emerging role in the regulation of CD20 levels. This was first reported in classic Hodgkin lymphomas that normally do not express CD20, but do so in response to a DNA demethylating agent 5-aza-deoxycytidine (5-aza-dC) (179). Downregulation of CD20 mRNA has been also observed in CD20-negative cells obtained from patients after relapse of rituximab-treated B-cell malignancies (175). Also in these cases 5-aza-dC restored CD20 mRNA expression, increased CD20 surface levels and sensitized tumor cells to rituximab-mediated ADCC (175). It is noteworthy that CpG islands are absent from the CD20 promoter region, located ~5 kb upstream of the transcription site, and CpG methylation of the CD20 promoter has not been observed in CD20-negative transformed cells (175, 180). Thus, it can be hypothesized that altered, epigenetically-regulated expression of transcription factors critical for CD20 gene expression may contribute to the aberrant CD20 transcriptional regulation.

Another epigenetic mechanism associated with modulation of CD20 expression is regulated by histone acetylation. Tomita *et al.* have established a CD20 negative lymphoma cell line (RRBL1) from a patient treated repeatedly with rituximab-containing chemotherapy. Decreased expression of CD20 has been observed at both protein and mRNA level and was completely reversed by trichostatin A, an epigenetic drug that modulates histone-acetylation status (181).

### 7.1.2. Posttranscriptional regulation

It is frequently underscored that CD20 molecules are not endocytosed from tumor cells after antibody binding. However, it was demonstrated that 1F5 (182-183) as well as rituximab (176, 184) can be internalized by malignant cells. Also stimulation of normal B cells through CD40 has been shown to down-regulate CD20 expression, which occurs by protein kinase C-dependent endocytosis (185). Internalization of CD20 can be also induced by lenalidomide (186). Recent studies indicate that only type I anti-CD20 mAbs induce CD20 internalization and that this mechanism, rather than shaving, is responsible for modulation of this antigen (92). It is uncanny that CD20 internalization has been overlooked so far. Detailed molecular mechanisms that are responsible for this process are urgently needed to design rational combination therapies allowing more effective management of B-cell tumors.

Even more enigmatic are mechanisms that might lead to shedding of CD20 molecules. The presence of soluble, circulating CD20 molecules has been demonstrated in patients with NHLs or CLL (187-189). Considering a tight association of tetraspanins with plasma membrane it is possible that CD20

molecules detected in the serum are released from B cells as exosomes or these are merely fragments of tumor cells released in response to damage induced by CDC or ADCC.

NHL cells chronically exposed to rituximab acquire a resistant phenotype associated with reduced surface CD20 levels and decreased sensitivity to rituximab-mediated CDC and ADCC (190). Microarray cDNA analysis revealed that rituximab-resistant cells reveal decreased surface CD20 levels and exhibit up-regulation of the components of the ubiquitin-proteasome system (190). Proteasome inhibition partially reversed rituximab resistance (190) indicating that CD20 might be a substrate of intracellular proteolytic degradation systems. Recent studies indicate that indeed CD20 can be ubiquitinated and proteasome inhibitors bimodally regulate surface CD20 levels - short-term inhibition of proteasome activity up-regulates CD20 levels, while prolonged inhibition leads to autophagic degradation of these molecules (191).

A novel splice variant of mRNA that encodes a truncated, non-anchored CD20 protein ( $\Delta$ CD20) selectively expressed in malignant, but not resting B cells was recently isolated from healthy donors (27). This protein apparently associates with intracellular domains of normal CD20 and its levels increase in rituximab-resistant cells. It is possible that association with  $\Delta$ CD20 can modulate the levels of CD20 in the plasma membrane or may affect its translocation to lipid rafts.

Finally, conformational changes or altered reorganization of CD20 within lipid rafts can be associated with reduced binding of anti-CD20 antibodies to discontinuous epitopes formed within the larger or between the extracellular loops of CD20 (33, 192).

### 7.1.3. CD20 mutations

CD20 mutations have been detected in 11 (22%) out of 50 patients with non-Hodgkin's B-cell lymphomas treated with rituximab-containing therapies (193). Especially C-terminal deletions have been strongly associated with decline or disappearance of CD20, a short time to progression, and early relapse of disease. In DLBCL CD20 mutations were shown to be extremely rare before rituximab treatment indicating that they do not account for primary resistance (194-195). However, of the rare samples available after R-CHOP almost 20% had been CD20-negative and one contained *cd20* mutation (194). Another study in Japan reported two initially CD20-positive patients with relapsed DLBCL, who transformed into CD20-negative tumors harboring *cd20* mutations (175).

### 7.1.4. Other mechanisms

Treatment with anti-CD20 mAbs may saturate or exhaust effector mechanisms responsible for elimination of tumor cells. Rituximab-mediated ADCC of NK cells leads to downregulation of Fc $\gamma$ RIIIa (196). Similar effects were observed with other mAbs, such as trastuzumab (197). Re-expression of Fc $\gamma$ RIIIa may take as many as 24 h (198). Similarly, the complement system can be exhausted as a result

of rituximab treatment, and restoration of complement components concentrations can take even longer, from a few days up to several weeks (87). Saturation of effector mechanisms may enable alternative processing pathway referred to as "shaving" (199). In this reaction the complexes of antibodies and their targets are extracted from tumor cells in a process of trogocytosis, a process of plasma membrane exchange within immunological synapse that forms between the tumor and FcγR-bearing cell (64, 200-201). Trogocytosis leads to removal of CD20 molecules from tumor cells and selects for cells resistant to anti-CD20 mAbs (199). Fractionated small dose or subcutaneous dosing schedules limit exhaustion of effector mechanisms and may be more effective than standard intravenous bolus rituximab injections in CLL patients (199, 202-203).

### 7.2. CD20 independent mechanisms of resistance to anti-CD20 mAbs

A number of complement regulatory proteins (CRP) protect normal cells from CDC. Three of them are believed to be the most important: CD46 (MCP – membrane cofactor protein that binds to and serves as a cofactor in the cleavage of C3b and C4b), CD55 (DAF – decay accelerating factor, which accelerates inactivation of C3 and C5 convertases) and CD59 (which impairs MAC formation). These inhibitors are also present on tumor cells, and might facilitate their escape from complement attack (204). Indeed, expression of CD55 and CD59 limits rituximab-mediated CDC in B-cell tumors (79, 205).

Furthermore, tumor cells may become refractory to R-ADCC in mechanism involving resistance to enzymatic activity of granzymes and perforin. It has been demonstrated that expression of protease inhibitor 9 (inhibitor of granzyme B) is used by tumor cells to escape their elimination by effector cells of the immune system (206).

## 8. APPROACHES TO IMPROVE ANTITUMOR EFFICACY OF ANTI-CD20 MABS

### 8.1. Complement-dependent cytotoxicity

Antibodies blocking complement regulatory proteins, the use of phospholipase C that cleaves off a GPI anchor from CD55 and CD59, or siRNA that knocks-down CRP expression facilitate rituximab-mediated cytotoxicity (77, 207-210). Also in a xenograft *in vivo* models it was shown that antibodies blocking the activity of CD55 and CD59 (211) or a recombinant adenoviral fiber knob protein that cross-links CD46 molecules (212) enhance therapeutic effects of rituximab. Fludarabine, the nucleoside analogue clinically active against CLL and indolent NHL has been shown to act synergistically with rituximab and to down-regulate the membrane expression of CD55 without significantly altering CD20 levels (213).

Recently, extracellular protein kinases have been shown to regulate activation of the complement cascade. One such ectokinase is casein kinase 2 (CK-2), which phosphorylates serine residues at the N-terminus of C9 component, impairing its joining to C5b-8 and formation of

the fully functional MAC (214). Inhibition of ecto-CK-2 activity may increase rituximab efficacy (215).

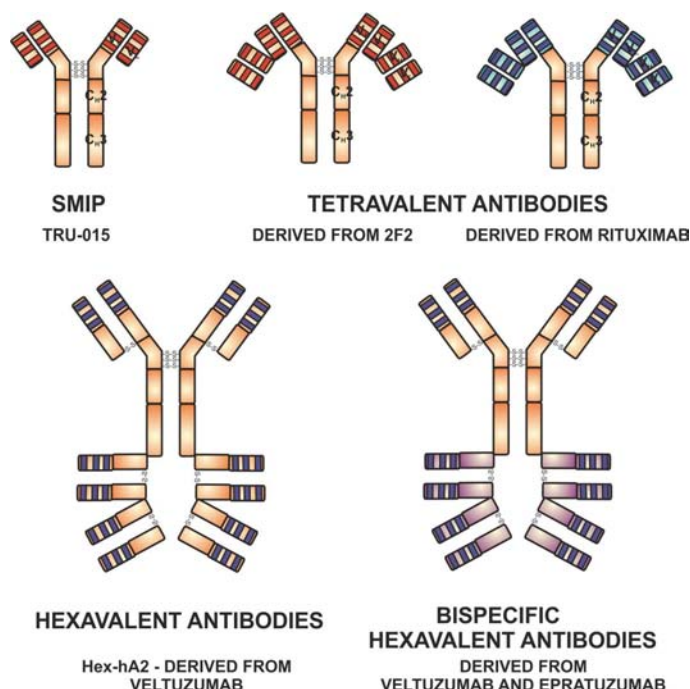
Another approach that exploits the ability of rituximab to trigger complement activation is based on administration of antibodies specific for C3b and iC3b, the cell-associated complement C3 cleavage products (216).

However, not all studies confirm the significant role played by CRP. For example, pretreatment levels of CD46, CD55 and CD59, or combinations of these proteins, did not predict clinical responses to rituximab in patients with FL (217). In B-CLL the expression levels of CD46, CD55 and CD59 did not correlate with R-CDC, but antibodies blocking CRPs increased lysis of tumor cells incubated with rituximab and complement (78).

### 8.2. Antibody-dependent cell-mediated cytotoxicity

Strategies to augment ADCC are usually directed at increasing the killing activity of effector cells. This is most easily achieved by activating the function of neutrophils, macrophages or NK cells with recombinant cytokines. A number of hematopoietic growth factors (G-CSF, GM-CSF, M-CSF), interleukins (IL-2, IL-12, IL-15, IL-21), chemokines (macrophage chemotactic protein-1), and interferons (IFN-α, IFN-γ) have been shown to potentiate R-ADCC *in vitro* (15, 109-111, 218-220). These studies were followed by clinical trials that indicated effectiveness of several approaches. For example, in a small study involving 15 patients with FL addition of G-CSF to a standard R-CHOP regimen resulted in 100% overall response rate with 12 patients achieving complete response (221). Combination of G-CSF with rituximab (no chemotherapy) also seems to prolong the duration of remission in patients with low-grade lymphomas (222). Similarly, GM-CSF enhances rituximab activity in patients with FL (223). Although in animal studies administration of IL-2 significantly potentiated anti-CD20 mAb-mediated antitumor effects (5), clinical studies did not show improved responses in patients concomitantly treated with rituximab and rhIL-2 (224). However, the clinical study included a rather small group of patients and no other factors such as FcγR polymorphism were evaluated that might influence the therapeutic outcome of the combination treatment. Additionally, recent clinical observations indicate that also high serum soluble interleukin-2 receptor levels might be associated with inferior prognosis and might affect responses to rituximab (225). Combination of rituximab with IL-12, a cytokine that strongly stimulates cell-mediated immunity (226), has so far been disappointing in clinical trials (227). Similarly, combination with IFN-α-2a has not lived up to its expectations (228).

Next to recombinant cytokines also other immunomodulatory drugs have been used to improve effector functions of immune cells in combination with rituximab. These include toll-like receptor 9 (TLR9) agonists - CpG oligonucleotides (229), β-1,3-glucan, which binds to the lectin domain of the leukocyte complement receptor CR3, and facilitates binding to iC3b thereby triggering cytotoxicity of iC3b-coated tumor cells (230), or lenalidomide, which stimulates cytotoxicity of NK cells,



**Figure 8.** Novel anti-CD20 mAbs.

increases production of IL-2, and inhibits angiogenesis (231).

## 8.3. Combination therapies

There are multiple reasons that substantiate combination of anti-CD20 mAbs with chemotherapeutics. These include independent mechanism of antitumor action, non-overlapping toxicities, antibody-mediated sensitization to cytostatic/cytotoxic effects of chemotherapeutics. Rituximab exhibits synergistic activity with many chemotherapeutics, e.g. antimetabolites (metotrexat (232), fludarabine (233)), anthracyclines (doxorubicin (234)), taxoids (paclitaxel (235)), lignans (etoposid (236)) and alkylating agents (cyclophosphamide (234), chlorambucil (237), cisplatin (238)). To achieve even greater effectiveness the above-mentioned drugs are joined into schemes. In clinical trials the addition of rituximab to standard schemes, like CHOP (cyclophosphamide, hydroxy-daunorubicin, Oncovin, prednisone) (239), EPOCH (etoposide, prednisone, Oncovin, cyclophosphamide, hydroxydaunorubicin) (240) or CVP (cyclophosphamide, vincristine, prednisone) (241) increased the treatment effectiveness, and the observed synergism allowed to use lower doses evoking less side effects. Cytostatics impair cell divisions and cause many sublethal injuries inducing apoptosis, and rituximab by decreasing Bcl-2 level sensitizes cells to their activity. As could be presumed it does not happen is a one peculiar mechanism, but as a result of several overlapping and complementary intracellular pathways (235, 242-245).

Moreover, rituximab acts synergistically not only with standard chemotherapeutics, but also with new drugs like bortezomib in patients with various B-cell

malignancies (246-248), thalidomide (249), lenalidomide, a thalidomide-derivative immunomodulator (250), everolimus (mTOR inhibitor) (251), tenesipimycin (Hsp90 inhibitor) (252) or anti-malarial artesunate (253). Also new antibodies are added to rituximab therapy, e.g. galiximab (anti-CD80) (254), alemtuzumab (anti-CD52) (255), bevacizumab (anti-VEGF) (256) or epratuzumab (anti-CD22) (257). By joining calicheamicin with rituximab an immunotoxin was obtained, which more effectively evokes apoptosis, simultaneously not impairing CDC or ADCC effectiveness (258).

## 9. CONCLUSIONS

A number of variables affecting the interactions between target and effector cells seems to influence the efficacy of mAbs. These include mAbs concentration, their affinity for target antigen, target antigen density, epitope specificity for target antigen, type of effector cells as well as mAbs affinity for FcR. Modifications of anti-CD20 mAbs fine-tuning all these variables are therefore expected to increase their therapeutic activity. Several studies have addressed this possibility. Oligonucleotide-directed mutagenesis of immunoglobulin genes led to design of anti-CD20 mAbs with higher affinity for CD20, FcγRIII or both, which were more potent in triggering ADCC against tumor cells (106). Removal of fucose from anti-CD20 IgG1 antibodies potentiates NK cell-mediated ADCC against tumor cells by increasing antibody affinity for FcγR (259). A growing number of additional anti-CD20 antibodies or anti-CD20-targeted therapeutics are being developed in pre-clinical setting (Figure 8). These include rituximab triple mutant with extremely potent apoptosis-inducing activity (260), autophylic (self-associating) DXL625

antibody specifically designed to trigger enhanced apoptosis (261), hexavalent antibodies (Hex-hA2), which comprise 6 Fab and one Fc fragment (262), tetravalent antibodies (DiMcAb) derived from two anti-CD20 mAbs (rituximab and 2F2) (263), bispecific anti-CD20/CD22 antibodies derived from veltuzumab and epratuzumab (anti-CD22 mAb) (264), or even engineered T cells expressing CD20-specific chimeric T-cell receptors (TCR) (265).

It is difficult to reconcile many discrepant observations addressing engagement of effector mechanisms of anti-CD20 mAbs described in this review. The obvious disparities in results of experimental and clinical studies arise from different numbers of target cells (low numbers of transplanted tumor cells vs. larger numbers in long-term established tumors in patients), CD20 expression levels, and the fact that malignant B cells are usually heavily passaged before transplantation. Maintenance of tumor cells in media containing heat-inactivated serum results in down-regulation of CRPs thereby increasing their susceptibility to CDC. Another possibility is that transplanted malignant B cells frequently localize to different body compartments.

Identification of the mechanisms of cytotoxic effects of anti-CD20 mAbs is necessary to establish assessable molecular and genetic predictive factors that can be used to plan tailored therapeutic approaches in individual patients. This would mean that mAb therapy of lymphoma has entered a new age.

## 10. ACKNOWLEDGEMENTS

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