

Fc γ Rs in Health and Disease

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Abstract Genetic defects affecting the humoral immune response and especially the production of antibodies of the immunoglobulin G (IgG) isotype result in a heightened susceptibility to infections. Studies over the last years have demonstrated the crucial role of Fc-receptors for IgG (Fc γ Rs) widely expressed on innate immune effector cells in mediating the protective function of IgG. During the last years, additional ligands interacting with Fc γ Rs as well as additional receptors binding to IgG glycosylation variants have been identified. In this review, we discuss how the interaction of these different ligands with classical and novel Fc γ -receptors influences the immune response and which strategies microorganisms have developed to prevent them.

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1 Introduction

Apart from physical barriers, cells of the innate immune system, including mast cells, neutrophils, monocytes, and macrophages represent one of the first lines of defense against pathogenic microorganisms. Armed with a multitude of receptors, such as the Toll-like receptor family, recognizing danger and pathogen associated molecular patterns (DAMPs and PAMPs), they are able to recognize microorganisms directly and thereby prevent an overwhelming infection (Iwasaki and Medzhitov 2010). In the absence of adaptive immunity, however, many infections cannot be cleared, emphasizing the importance of the interplay between the two arms of the immune system. Antibodies, the hallmark of the adaptive immune response, are essential in providing protection against recurrent infections (Ballow 2002). While low affinity antibodies of the IgM isotype are characteristic for the early immune response, antibodies of the IgG subclass dominate the later response and are typically of higher affinity and exquisite specificity for the respective target antigen. Genetic defects affecting the production of high affinity IgG antibodies often result in a heightened susceptibility to microbial infections emphasizing the protective role of this isotype (Ballow 2002). Studies performed in mouse model systems over the last decade have led to the conclusion that the underlying mechanism of this protective activity of IgG, which consists of four different subclasses in mice (IgG1, IgG2a/c, IgG2b, IgG3) and humans (IgG1–IgG4), is the recruitment and activation of innate immune effector cells via receptors specific for the IgG Fc (fragment crystallizable) domain (Fc γ -receptors, Fc γ R) (Hogarth 2002; Nimmerjahn and Ravetch 2008b; Takai 2002). Depending on the effector cell, crosslinking of these receptors results in cell degranulation, release of different cytokines/chemokines, phagocytosis, or antibody dependent cellular cytotoxicity (ADCC). Thus, Fc-receptors provide the link between the high specificity of the adaptive immune system and the powerful effector functions of cells of the innate immune system and target these proinflammatory activities to sites of infection or healthy tissues during autoimmune disease (Hogarth 2002; Nimmerjahn and Ravetch 2008b; Takai 2002). In contrast to the early IgM dominated immune response, which largely depends on the activation of the classical complement pathway, marking microorganisms for phagocytosis via complement receptors or initiation of bacterial lysis through the generation of lytic membrane attack complexes, activation of the complement pathway is not essential for IgG mediated effector functions, although it can enhance the activity of certain IgG subclasses (Azeredo da Silveira et al. 2002; Carroll 2004; Clynes and Ravetch 1995; Nimmerjahn and Ravetch 2005; Ravetch and Clynes 1998; Sylvestre et al. 1996; Uchida et al. 2004). While this proinflammatory activity of IgG is desirable in the case of an infection, it leads to severe tissue and organ damage if directed toward healthy tissues during autoimmune disease (Hogarth 2002; Nimmerjahn and Ravetch 2008b; Takai 2002). Several factors, including the individual IgG subclass and the antibody glycosylation pattern, can influence the quality and strength of this interaction (Nimmerjahn and Ravetch 2006). Besides IgG, other molecules such as members of the evolutionary conserved pentraxin family can bind to Fc γ Rs

(Marnell et al. 2005; Woof and Burton 2004). More recently, it was shown that certain antibody glycosylation variants can bind to other cell surface receptors belonging to the family of C-type lectins unrelated to the family of classical FcγRs (Anthony et al. 2008a, b; Kaneko et al. 2006b; Nimmerjahn and Ravetch 2008a). This review summarizes our current understanding of how the interaction of these different ligands with cellular FcγRs is regulated and how this might help develop novel therapeutic avenues for the optimization of antimicrobial and the amelioration of autoreactive antibody responses.

2 The Family of Canonical Fcγ-Receptors

FcγRs are a conserved family of glycoproteins that belong to the IgG superfamily and are comprised of a ligand binding a-subunit consisting of two or three C2-type extracellular domains (Fig. 1). In mice, monkeys, humans and other mammalian species the family of FcγRs is comprised of several activating (FcγRIA, IIA, IIC, IIIA in humans; FcγRI, III, IV in mice) and one inhibitory (FcγRIIB) member (Hogarth 2002; Nimmerjahn and Ravetch 2008b; Takai 2002; Willcocks et al. 2009). Whereas the inhibitory FcγR has an immunoreceptor tyrosine based inhibitory motif (ITIM) in its cytosolic domain, the majority of activating FcγRs have to

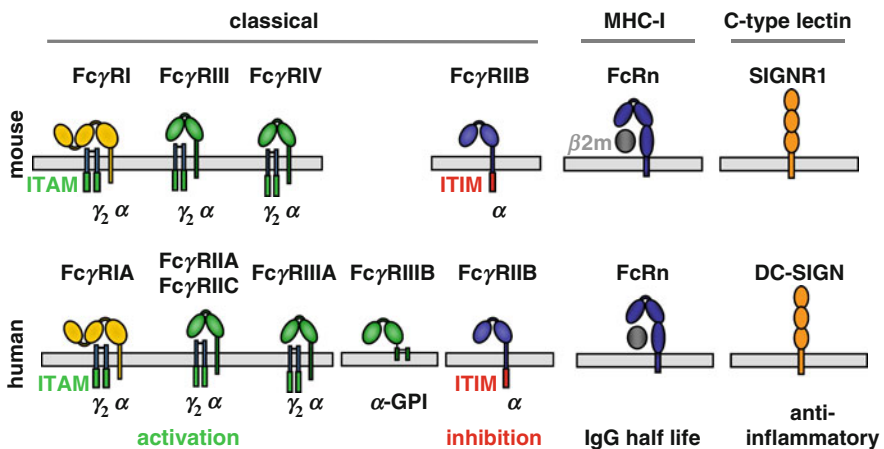


Fig. 1 The extended family of mouse and human Fcγ-receptors. In mice and humans the family of classical FcγRs consists of several activating and one inhibitory member. In addition, humans have a GPI-linked FcγR (FcγRIIB) exclusively expressed on neutrophils. The neonatal FcRn is responsible for IgG half life in mice and humans and belongs to the family of major histocompatibility class I (MHC I) molecules. More recently, mouse SIGNR1 and its human orthologue DC-SIGN joined the family of IgG binding proteins with a selective specificity for IgG glycoforms rich in terminal sialic acid residues (see text for further details)

associate with signaling adaptor proteins containing immunoreceptor tyrosine based activation motifs (ITAM) such as the FcR common γ -chain (γ -chain). In humans and monkeys, there are some exceptions to this rule as Fc γ RIIA and Fc γ RIIC have an ITAM in their cytosolic domain and do not require signaling adaptor molecules for cell surface expression and functionality (Fig. 1) (Willcocks et al. 2009). Besides these differences in signal transduction, the other distinguishing feature among the family members is the affinity and specificity for the different IgG subclasses. In analogy to the high affinity Fc-receptor for IgE (Fc ϵ R), there is one high affinity receptor for IgG (Fc γ RI or CD64), which has nanomolar affinity for select IgG subclasses (IgG2a/c in mice; IgG1/3 in humans) and is saturated in the presence of serum IgG on cells such as monocytes in the blood. All the other receptors have a low to medium affinity in the micromolar range and can only bind to IgG if present in the form of immune complexes (ICs) (Nimmerjahn and Ravetch 2008b). Structural analysis of human IgG together with Fc γ RIIIA showed that IgG–Fc γ R binding occurs in a one to one ratio and that the sugar side chains of IgG and Fc γ Rs are critically involved in this binding (Ferrara et al. 2006; Mimura et al. 2001; Radaev et al. 2001; Sondermann et al. 2000). Fc γ Rs are expressed on the majority of innate immune effector cells such as basophils, eosinophils, mast cells, monocytes, macrophages, NK cells and neutrophils. Among these cell lineages, monocytes and macrophages express the broadest repertoire of activating Fc γ Rs (I, III, and IV), whereas neutrophils express Fc γ RIII and IV, and NK cells selectively express Fc γ RIII. In addition, dendritic cells (DCs) essential for the initiation of adaptive immune responses, and B cells do express Fc γ Rs. Early studies have also identified Fc γ R expression on some T cell populations although the role of these receptors for T cell activity or development is unclear and requires further analysis (Anderson and Grey 1974; Leclerc et al. 1977; Stout and Herzenberg 1975). A hallmark of this receptor family is the coexpression of activating and inhibitory receptors on the majority of innate immune effector cells and DCs. Thus, the simultaneous triggering of activating and inhibitory signaling pathways sets a threshold for cell activation and regulates cellular effector functions. Indeed, deletion of the inhibitory Fc γ RIIB resulted in heightened IgG dependent proinflammatory reactions, DC maturation and antigen presentation *in vivo* (Boruchov et al. 2005; Dhodapkar et al. 2005; Kalergis and Ravetch 2002; Nimmerjahn and Ravetch 2008b; Takai et al. 1996). An exception to this rule is NK cells which solely express Fc γ RIIIA (CD16) in humans and Fc γ RIII in mice. Recently, a small subpopulation of NK cells has been shown to express Fc γ RIIB, although the functional role of this NK cell subset remains to be established (Dutertre et al. 2008). B cells do not express activating Fc γ Rs, but express the inhibitory Fc-receptor, which regulates positive signals initiated via the B cell receptor. The importance of Fc γ RIIB on B cells was demonstrated by the development of autoantibodies and a severe autoimmune disease similar to human systemic lupus erythematosus (SLE) in mice deficient for this receptor (Baerenwaldt and Nimmerjahn 2008; Bolland and Ravetch 1999, 2000; Daeron and Lesourne 2006; Ravetch and Lanier 2000; Takai 2002; Takai et al. 1996).

Based on genomic localization and sequence similarity in the extracellular portion, orthologous receptors can be identified between mice and humans (Hirano et al. 2007; Nimmerjahn and Ravetch 2006). Thus, the high affinity receptors Fc γ RIA/Fc γ RI and the low affinity receptors Fc γ RIIB cluster in the same group (Fig. 1). Similarly, human Fc γ RIIIA/mouse Fc γ RIV and human Fc γ RIIIA/mouse Fc γ RIII share a high level of sequence homology in their extracellular domains (Nimmerjahn and Ravetch 2006). Despite this similarity caution should be taken in a one to one transfer of data obtained in mouse models to the human system as the ligands (the IgG subclasses) and the cellular expression pattern of some of the receptors differ between mice and humans. Thus, human Fc γ RI binds two IgG subclasses (IgG1 and IgG3) with high affinity whereas mouse Fc γ RI only binds IgG2a/c with nanomolar affinity. Similarly, mouse Fc γ RIV (not expressed on NK cells) has the capacity to recognize IgE whereas human Fc γ RIIIA (expressed on NK cells) does not (Hirano et al. 2007; Mancardi et al. 2008). Moreover, humans express several allelic variants of the low affinity receptors Fc γ RIIA and Fc γ RIIIA which greatly differ in their affinity for the different IgG subclasses (Bruhns et al. 2009; Ravetch and Nimmerjahn 2008). Thus, human IgG2 binds only to an Fc γ RIIA variant carrying a histidine at position 131 (Fc γ RIIA-131H) whereas the allele carrying an arginine allele (Fc γ RIIA-131R) has a very low affinity for this IgG subclass. Similarly, Fc γ RIIIA with a valine residue at position 158 (Fc γ RIIIA-158V) has a much higher affinity for IgG1 and IgG3 than its allelic counterpart with a phenylalanine residue (Fc γ RIIIA-158F) at this position. Studies with human patient cohorts suggest that these differences in affinity impact the outcome of therapeutic success with antitumor antibodies, for example (Cartron et al. 2002; Weng et al. 2004; Weng and Levy 2003). To mimic these allelic differences in the future, novel mouse models carrying these allelic variants of the human Fc γ Rs will be essential. Nonetheless, classical mouse models have been and will continue to be detrimental for deciphering the role of the family of Fc γ Rs for antibody activity in infection and autoimmunity which will be discussed in the following paragraphs.

3 Regulation of IgG Activity *In Vivo*

Given the crucial role of Fc γ Rs for IgG mediated effector functions, several studies have addressed the issue about which activating Fc γ Rs were involved in mediating the activity of the individual IgG subclasses. *In vitro* studies indicated that IgG1 can only bind to Fc γ RIII, IgG2a/c can bind to all activating Fc γ Rs and IgG2b binds to Fc γ RIII and Fc γ RIV. IgG3, in contrast, did not bind with significant affinity to any of the known Fc γ Rs in C57BL/6 mice, although binding to an Fc γ RI allele in NOD mice was described (Gavin et al. 1998). Consistent with these *in vitro* data, IgG1 activity was abrogated in mouse strains deficient in Fc γ RIII (Hazenbos et al. 1996; Meyer et al. 1998; Nimmerjahn and Ravetch 2005, 2006). In contrast, the situation for IgG2a/c and IgG2b is more complicated: in some model systems the activity of

these subclasses was abrogated in Fc γ RIII knockout animals whereas in others it was not. In models of IgG2b dependent platelet depletion, B cell depletion, and nephrotoxic nephritis, for example, blockade of Fc γ RIV function prevented platelet and B cell depletion and kidney inflammation (Hamaguchi et al. 2006; Kaneko et al. 2006a; Nimmerjahn et al. 2005; Nimmerjahn and Ravetch 2005). In the case of IgG2b dependent autoimmune hemolytic anemia (AIHA), acute glomerular inflammation and IC induced lung inflammation, both Fc γ RIII and Fc γ RIV were essential for the activity of this IgG subclass (Baudino et al. 2008; Giorgini et al. 2008; Syed et al. 2009). For IgG2a/c a similar picture emerges as for IgG2b with additional contributions of the high affinity Fc-receptor depending on the system model used (Baudino et al. 2008; Bevaart et al. 2006; Ioan-Facsinay et al. 2002; Otten et al. 2008). Together with the aforementioned correlation of allelic variants of Fc γ RIIA and Fc γ RIIAA with the activity of therapeutic antibodies in human cancer patients this indicates that the low affinity Fc γ Rs are critical for IgG dependent effector functions in mice and humans.

While these studies confirmed the crucial role of Fc γ Rs for IgG activity they did not explain another observation that was made in several *in vivo* model systems of autoimmunity and infection, suggesting that the different IgG subclasses have a different activity *in vivo*. Using IgG subclass switch variants of platelet or red blood cell (RBC) specific antibodies it was demonstrated that IgG2a/c and IgG2b were superior to the other IgG subclasses in mediating phagocytosis of opsonized platelets or RBCs compared to IgG1 and IgG3, respectively (Fossati-Jimack et al. 2000; Nimmerjahn et al. 2005; Nimmerjahn and Ravetch 2005). Similarly, IgG2a/c mediated depletion of B cells, syngeneic melanoma cells, and T cell lymphomas was far more efficient compared to antibodies with an IgG1 Fc-fragment, for example, consistent with earlier results obtained *in vitro* (Kaminski et al. 1986; Kipps et al. 1985; Lambert et al. 2004; Nimmerjahn and Ravetch 2005; Uchida et al. 2004). Further confirming this observation glomerular inflammation induced by IgG subclass switch variants was most severe for the IgG2a/c subclass followed by IgG2b and a much weaker activity of IgG1 (Giorgini et al. 2008). Similarly, antimicrobial antibodies of the IgG2a/c subclass yielded enhanced protection from the development of poliomyelitis following infection with lactate dehydrogenase elevating virus or enhanced phagocytosis of opsonized *Cryptococcus neoformans* (Markine-Goriaynoff and Coutelier 2002; Schlageter and Kozel 1990). A possible explanation for this hierarchy of activities was afforded by the affinities of the different IgG subclasses toward their triggering activating and inhibitory Fc γ R pairs. Thus, IgG1 has a higher affinity for the inhibitory Fc γ RIIB than toward the activating Fc γ RIII, resulting in a high threshold for activation. In contrast, IgG2a/c and IgG2b have a much higher affinity for the activating Fc γ RIV than for the inhibitory Fc γ R, thus being less influenced by cotriggering. Consistent with this *in vitro* data, deletion of the inhibitory Fc γ RIIB most strongly enhances the activity of IgG1 in models of platelet depletion and tumor cell destruction (Nimmerjahn and Ravetch 2005). Of note, this affinity based model of IgG subclass activity can be influenced by several factors, including the varying Fc γ R repertoire of individual innate immune effector cells and DCs and cytokines that can alter the ratio of

activating to inhibitory Fc γ R expression. Thus, TH1-type cytokines, LPS, and the anaphylatoxin C5a have been shown to increase activating Fc γ R expression (Nimmerjahn and Ravetch 2008b; Schmidt and Gessner 2005). In contrast, TH2-signature cytokines such as IL4 had the opposite effect, with the exception of B cells where IL4 was suggested to downmodulate expression of Fc γ RIIB (Nimmerjahn and Ravetch 2006). Apart from the expression level of the individual Fc γ Rs, recent studies have highlighted the role of the sugar side-chain of IgG which is attached to the asparagine 297 (N297) residue in the IgG heavy chain in modulating the affinity to activating Fc γ Rs which will be discussed in the next chapter.

4 Influence of Antibody Glycosylation and Novel Fc γ -Receptors

All immunoglobulin isotypes are glycoproteins with a varying amount of sugar side chains attached to the protein backbone. In contrast to IgM, IgA, and IgE which contain multiple exposed sugar side chains, the IgG associated sugar domain is constrained by the groove formed by the two individual IgG heavy chains (Nimmerjahn and Ravetch 2008b). Deletion of this sugar domain results in an altered conformation and severely impaired binding to cellular Fc γ Rs and diminished activation of the complement pathway (Shields et al. 2001). Compared to the homogeneous composition of the sugar domain of the other Ig isotypes the IgG associated sugar moiety is heterogeneous. Thus, in a healthy individual more than 30 different IgG glycosylation variants can be detected in the serum of mice and humans (Arnold et al. 2007). This heterogeneity stems from variable additions of terminal and branching sugar residues such as sialic acid, galactose, *N*-acetylglucosamine and fucose. Interestingly, this glycosylation pattern of serum IgG changes during active autoimmune disease in mice and humans where glycoforms rich in terminal sialic acid and galactose residues were diminished (Bond et al. 1990; Kaneko et al. 2006b; Mizuochi et al. 1990; Nimmerjahn and Ravetch 2008a). A similar change in serum IgG glycosylation pattern was observed with older age, whereas during pregnancy IgG glycoforms rich in terminal sialic acid and galactose residues were increased and correlated with remission of disease (Arnold et al. 2007; Rook et al. 1991; van de Geijn et al. 2009). Although the function of this altered glycosylation pattern is not fully understood, recent evidence points toward an important role of differential IgG glycosylation in modulation of IgG activity (Jefferis 2009). The absence of the branching fucose residue, for example, results in a selective increase of affinity of IgG subclasses to human Fc γ RIIA and its mouse orthologue Fc γ RIV (Nimmerjahn and Ravetch 2005; Shields et al. 2002; Shinkawa et al. 2003). This increased affinity results in enhanced *in vivo* activity as demonstrated by the ability to prevent tumor growth in various model systems (Nimmerjahn and Ravetch 2007a). In contrast, the presence of high levels of terminal sialic acid residues diminished the affinity of human and mouse IgG for the family of classical Fc γ Rs, consistent with a lower proinflammatory activity (Anthony et al. 2008a; Kaneko et al. 2006b; Scallon et al. 2007). Importantly,

however, sialic acid rich IgG glycovariants not only display reduced proinflammatory activity, as a result of the diminished binding to classical Fc γ Rs, but they actually gained an active anti-inflammatory activity of IgG, which was able to suppress the proinflammatory activity of other autoantibodies (Anthony et al. 2008a, b; Kaneko et al. 2006b; Nimmerjahn and Ravetch 2007b). This finding might explain the long known anti-inflammatory activity of infusion of high doses of pooled serum IgG from several thousands of donors (IVIg therapy), which has been in use for nearly three decades as an efficient symptomatic treatment of different human autoimmune diseases, including thrombocytopenia, rheumatoid arthritis and chronic inflammatory demyelinating polyneuropathy (Nimmerjahn and Ravetch 2008a). A recent study identified SIGNR-1 (specific ICAM3 grabbing nonintegrin related 1) and its human orthologue DC-SIGN (dendritic cell specific ICAM3 grabbing nonintegrin) as cellular receptors that can specifically bind to IgG glycovariants containing high levels of terminal sialic acid residues. Consistent with this *in vitro* binding, IVIg lost its anti-inflammatory activity in SIGNR-1 knockout mice in a model of rheumatoid arthritis (Anthony et al. 2008b). During the steady state SIGNR-1 expression is most dominant on splenic marginal zone macrophages characterized by expression of another cell surface receptor called MARCO (macrophage receptor with collagenous structure) (Fig. 2). Consistent with an important function of this SIGNR-1 positive splenic macrophage population, splenectomized mice, mice with a disturbed splenic structure or osteopetrotic op/op mice lacking this macrophage subpopulation were no longer protected by IVIg (Anthony et al. 2008b; Bruhns et al. 2003). Thus, in analogy to the family of Toll-like receptors which can recognize microbial as well as self ligands, these studies highlight the dual function of receptors such as SIGNR1 and DC-SIGN in recognition of microbial and self ligands. Further studies showed that IVIg infusion changes the threshold for innate immune effector cell activation through ICs through an upregulation of the inhibitory Fc γ RIIB and a downregulation of activating Fc γ Rs in different mouse model systems and in patients with chronic inflammatory demyelinating polyneuropathy (Fig. 2) (Bruhns et al. 2003; Kaneko et al. 2006a, b; Samuelsson et al. 2001; Tackenberg et al. 2009). It is tempting to speculate that pathogens, such as HIV and *Mycobacterium tuberculosis*, which bind to DC-SIGN use this anti-inflammatory pathway to escape an initial immune response. Besides the important function of sialic acid residues, it has been proposed that the additional lack of galactose residues, which exposes the mannose rich core sugar structure, would result in the capacity to activate the lectin pathway of complement activation via mannan binding lectin (MBL) and thereby enhance the proinflammatory activity of this so called IgG-G0 glycovariant (lacking terminal sialic acid and galactose residues) (Malhotra et al. 1995). However, recent *in vivo* studies using MBL1/2 knockout animals could not confirm these previous *in vitro* observations and rather suggest that IgG glycoforms with or without galactose are still fully dependent on cellular Fc γ Rs and do not gain proinflammatory activity through the MBL pathway of complement activation (Nimmerjahn et al. 2007).

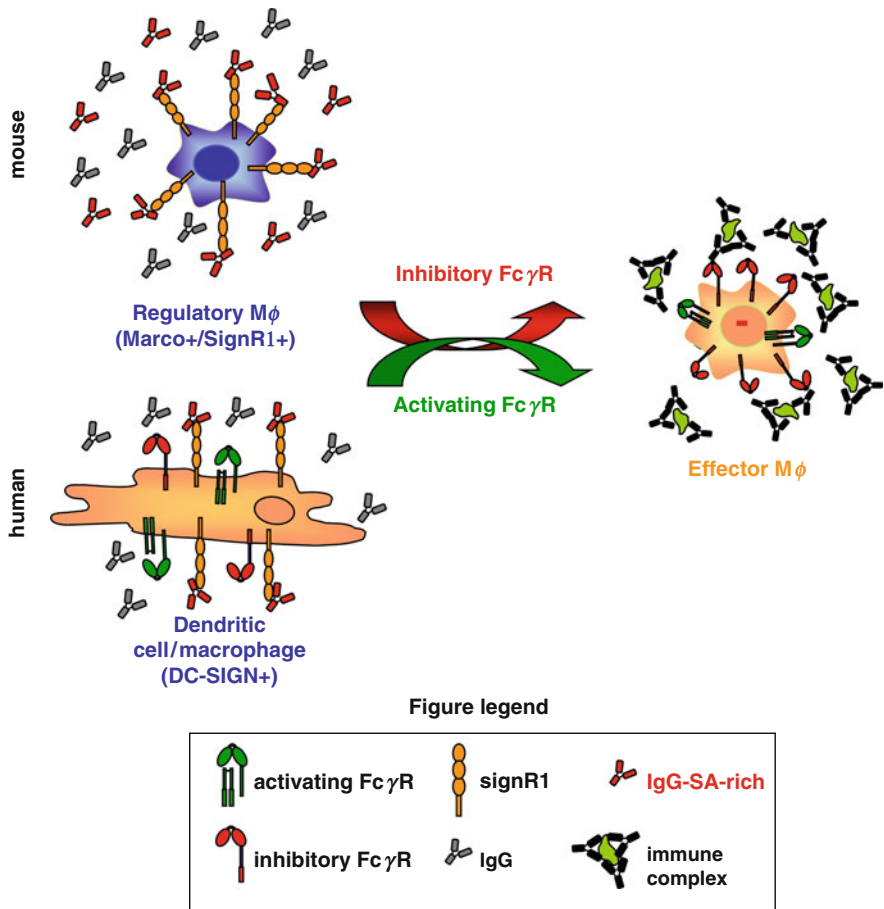


Fig. 2 Model for the anti-inflammatory activity of IgG. Immunoglobulin G glycovariants rich in terminal sialic acid residues (SA-rich IgG) loose affinity for classical FcγRs but gain the capacity to bind to C-type lectin receptors such as mouse SIGNR1 and human DC-SIGN. Binding of SA-rich IgG to splenic resident MARCO positive macrophages heightens the threshold for innate immune effector cell activation by upregulation of inhibitory FcγRIIB expression and lowering expression of activating FcγRs. In humans, DC-SIGN positive dendritic cells or macrophages might be involved in the IgG dependent anti-inflammatory pathway

5 Role of FcγRs for Infection

A role for IgG antibodies in the prevention of infection is demonstrated by the heightened susceptibility of patients with hypogammaglobulinemia or hyper-IgM syndrome to recurrent infections with encapsulated bacteria, viruses and with some protozoan infections (Ballow 2002; Wood 2009). Major efforts have been undertaken to identify broadly neutralizing antibodies capable of protecting the host from

infection with a wide range of microorganisms (especially highly pathogenic viruses such as influenza and HIV) from the same or different species (Karlsson Hedestam et al. 2008; Walker and Burton 2008). One general issue with respect to many human pathogens is that they do not infect mice. Therefore, one has to rely on in vitro model systems and readouts to evaluate the capacity of pathogen specific antibodies to prevent infection of host cells. Such an approach may be severely biased by the choice of target cells used in such an assay. For example, HIV infects both T cells and myeloid cells, of which only the latter cell lineage expresses Fc γ Rs. In screening for neutralizing antibodies by using T cells as a readout one selectively screens for antibodies preventing the interaction of viral ligands with cellular receptors such as CD4 expressed on T cells, which would be solely dependent on the specificity (the F(ab)2 fragment) of the antibody. By doing so one might miss a potential role for the antibody Fc-fragment and Fc γ Rs in antibody mediated protection from a productive infection or viral replication (Fig. 3). Along these lines, it was recently demonstrated that different cell lines used for in vitro neutralization assays with antibodies specific for the anthrax toxin express different

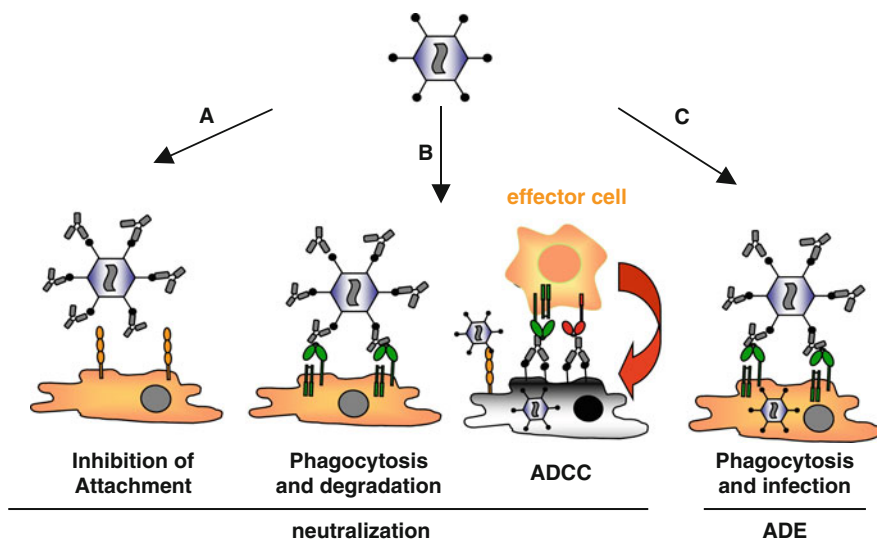


Fig. 3 Pathways of IgG dependent pathogen neutralization or enhancement of infection. Pathogen specific IgG can either block infection (neutralization) of host cells (A, B) or lead to antibody dependent enhancement (ADE) of pathogen infectivity (C). (A) Binding of IgG to the surface of bacterial or viral receptors essential for the attachment to host cells blocks pathogen entry and prevents an infection. This mechanism of neutralization is solely dependent on the specificity of the antibody and independent of the Fc-fragment. (B) Opsonized pathogens or pathogen specific IgG binding to infected cells results in pathogen clearance via phagocytosis and destruction of the microorganism in acidic endosomal/lysosomal vesicles or to killing of infected host cells by effector cells via antibody dependent cell-mediated cytotoxicity (ADCC). (C) For some opsonized microorganisms Fc γ R dependent uptake results in enhanced infection of target cells instead of degradation in lysosomal vesicles (see text for further details)

levels of Fc γ Rs and that toxin neutralization was more efficient in the cell line expressing higher levels of Fc γ Rs (Verma et al. 2009). Moreover, blocking Fc γ Rs impaired IgG dependent anthrax toxin neutralization in this *in vitro* assay. Thus, *in vitro* neutralization assays should screen for both, Fc γ R dependent and independent mechanisms of neutralization to ensure the highest level of predictability for *in vivo* functionality. The importance of ADCC or other Fc γ R dependent pathways for inhibition of viral replication and spread (also referred to as antibody dependent cell-mediated viral inhibition; ADCVI) *in vivo* have only recently become appreciated. Thus, γ -chain deficient mice lacking the activity of all activating Fc γ Rs were more susceptible to influenza virus infection due to reduced phagocytosis and ADCC dependent killing of infected cells (Fig. 3) (Huber et al. 2001). Along the same lines, the capacity of immune serum to trigger ADCC *in vitro* has been associated with protection from HIV infection in some (but not all) studies and nonneutralizing antibodies (as defined by classical *in vitro* assays) were able to inhibit HIV replication in human macrophages *in vitro* (Florese et al. 2006; Gomez-Roman et al. 2005; Holl et al. 2006a). More recently it was demonstrated that the protective activity of the broadly neutralizing HIV specific antibody b12 directed against the CD4 binding site of gp120 mediates its activity at least in part via engaging activating Fc γ Rs but not the complement pathway *in vivo* (Hessell et al. 2007). Several studies have addressed the role of individual activating Fc γ Rs for this antiviral activity and have suggested that especially Fc γ RIA and Fc γ RIIA were involved in conferring protection (David et al. 2006; Forthal and Moog 2009; Holl et al. 2004, 2006b; Perez-Bercoff et al. 2003). Apart from a simple ADCC and phagocytosis followed by destruction of antibody bound virus in endosomal/lysosomal vesicles, other mechanisms such as Fc γ R dependent induction of transcription factors are discussed to be involved in inhibition of virus infection and replication (Bergamaschi et al. 2009). Although more studies are necessary to elucidate the molecular pathways involved in Fc γ R dependent protection from virus infection, the available data suggest a critical involvement of IgG-Fc dependent pathways in parallel to the IgG-F(ab)₂ dependent interference with virus binding to cellular receptors (Fig. 3).

Consistent with the results obtained for HIV and influenza, antibody dependent phagocytosis of *Bordetella pertussis* was enhanced via Fc γ Rs but not via complement receptor 3 (CR3) in mouse models *in vivo* and with human effector cells *in vitro* (Hellwig et al. 2001; Rodriguez et al. 2001). With respect to parasitic infections, mice deficient in activating Fc γ Rs were less efficient in clearing microfilariae of *Brugia malayi* and showed a decreased antibody mediated phagocytosis of *Plasmodium bergi* and enhanced susceptibility to infection in this murine malaria model (Gray and Lawrence 2002; Yoneto et al. 2001). Confirming the role of the inhibitory Fc γ RIIB in setting a threshold for cell activation, mice deficient in the inhibitory Fc γ R were more efficient in the phagocytosis of bacteria and showed enhanced resistance to infection with *Plasmodium chabaudi chabaudi*, *Staphylococcus aureus* and *Streptococcus pneumoniae* (Clatworthy and Smith 2004; Clatworthy et al. 2007; Gjertsson et al. 2002). Another line of evidence for an involvement of Fc γ Rs in antibacterial responses in humans comes from IgG

subclass deficiencies. An IgG2 deficiency, for example, predisposes to infections with microorganisms such as *Haemophilus influenzae* (causing upper respiratory tract infections and pneumonia), *S. pneumoniae* (causing pneumonia, peritonitis and meningitis) and *Nisei meningitides* (causing meningitis and septicemia) (Ballou 2002; Pathan et al. 2003). IgG2 is a poor activator of the complement pathway and selectively binds the Fc γ R1A-131H allele (Ravetch and Nimmerjahn 2008). Supporting a role for this activating Fc γ R in phagocytosis of opsonized bacteria of these species, it was demonstrated that humans with the low affinity Fc γ R1A-131R allele had a higher susceptibility to invasive pneumococcal disease and higher risk for fulminant meningococcal septic shock (Bredius et al. 1994; Fijen et al. 2000; Rodriguez et al. 1999; Willcocks et al. 2009; Yee et al. 2000; Yuan et al. 2003). Moreover, neutrophils of Fc γ R1A-131H donors were more efficient in phagocytosing opsonized bacteria in vitro (Fijen et al. 2000; Pathan et al. 2003; Rodriguez et al. 1999). Consistent with this finding murine IgG1 antibodies against cell wall components of *S. pneumoniae*, which cannot activate the complement pathway, could protect mice from lethal infection (Briles et al. 1984a, b). Taken together, there is evidence that Fc γ Rs are involved in antibody dependent control at least of certain bacterial and viral infections in mice and humans. For genetic association studies in humans, larger patient cohorts will be essential to provide convincing evidence as some of the current studies show contradicting results (Smith et al. 2003). Of note, Fc γ Rs are not only involved in protection from microbial infections but can also be responsible for promoting susceptibility of the host, a phenomenon that has been termed antibody mediated enhancement (ADE) of infection (Fig. 3). Thus, *Leishmania major* infection of susceptible mouse strains is severely impaired in γ -chain knockout animals (Kima et al. 2000; Padigel and Farrell 2005). Similar results have been obtained for many viruses including HIV and members of the dengue virus family (Brouwer et al. 2004; Littaua et al. 1990; Loke et al. 2002; Takeda et al. 1988). Despite this Fc γ R dependent effect of ADE, this does not preclude the use of neutralizing antibodies to block virus infection. Thus, dengue virus specific IgG was efficient in protecting animals from infection if used in an aglycosyl form which can no longer interact with cellular Fc γ Rs (Balsitis et al. 2010).

6 Microbial Immune Escape Mechanisms Targeting the IgG–Fc γ R Interaction

Further evidence that the interaction of antimicrobial antibodies with Fc γ Rs is of importance is provided by the fact that several viruses and bacteria have developed strategies to interfere with this interaction. Prime examples are protein A (*S. aureus*) and protein G (*Streptococcus spec.*) which immobilize IgG to inactivate its effector functions (Langone 1982). Herpes simplex virus (HSV) as well as cytomegalovirus express viral Fc γ Rs which compete with cellular Fc γ Rs for IgG

binding and thereby prevent direct virus recognition and detection of infected cells through innate immune effector cells (Atalay et al. 2002; Dubin et al. 1991; Frank and Friedman 1989; Sprague et al. 2008). As demonstrated for gp68 of human cytomegalovirus (HCMV), viral Fc γ Rs bind to IgG independent of the N297 attached sugar moiety, which is crucial for binding to cellular Fc γ Rs. In contrast to classical Fc γ Rs which bind to IgG in the CH2/hinge domain in a one to one ratio, HCMV gp68 binds IgG more closely to the CH3 domain with nanomolar affinity and in a two to one stoichiometry (Sprague et al. 2008). More recently, several secreted glycosidases and proteases derived from *Streptococcus pyogenes* with a high specificity for the IgG attached sugar moiety or the IgG Fc-fragment have been identified (Collin and Olsen 2001; Johansson et al. 2008). Thus, Endoglycosidase S (EndoS) efficiently cleaves the N297-attached sugar moiety after the first *N*-acetylglucosamine residue, which results in a decreased binding to cellular Fc γ Rs. In a variety of models of IgG dependent autoimmune disease, injection of purified EndoS resulted in decreased autoantibody activity and reduced tissue damage, suggesting that EndoS might help *S. pyogenes* to inactivate the antimicrobial activity of IgG (Albert et al. 2008; Allhorn et al. 2008; Nandakumar et al. 2007a). Interestingly, EndoS treatment showed an IgG subclass specific activity and was not able to impair the activity of the most potent subclass IgG2a/c (Albert et al. 2008). In contrast, the protease Ide S efficiently cleaves the IgG Fc-fragment of all human IgG subclasses and of mouse IgG2a/c, resulting in inactivation of (auto) antibody activity in vitro and *in vivo* (Johansson et al. 2008; Nandakumar et al. 2007b). Taken together, pathogenic microorganisms have evolved several mechanisms to escape the potent effector pathways initiated through the IgG Fc-fragment. These studies may provide the basis to develop not only novel antimicrobial therapies, but also be helpful to limit the destructive potential of autoantibodies during autoimmune disease (Allhorn and Collin 2009; Nandakumar and Holmdahl 2008).

7 Other Ligands for Fc γ -Receptors

Apart from IgG, there is evidence that other proteins unrelated to IgG can bind to Fc γ Rs and use the potent effector functions initiated via these receptors. The most prominent examples are members of the pentraxin superfamily which are evolutionary conserved proteins with a multimeric cyclic structure (Agrawal et al. 2009). Two members of this family, C-reactive protein (CRP) and serum amyloid P (SAP), have been shown to bind to human and mouse Fc γ Rs (Bharadwaj et al. 1999, 2001; Lu et al. 2008; Marjon et al. 2009; Thomas-Rudolph et al. 2007). Whereas these proteins are present only in minute amounts in the serum in the steady state they become greatly upregulated during inflammatory responses such as microbial infections. Similar to antimicrobial antibodies, CRP and SAP can directly bind to a variety of pathogens including bacteria, fungi and viruses marking them for phagocytosis by neutrophils and macrophages of the host (Agrawal et al. 2009; Marnell et al. 2005). Besides the activation of the classical complement pathway

through these pentraxins a role of Fc γ Rs in the CRP dependent phagocytosis of microorganism was suggested by *in vitro* studies with Fc γ R expressing cell lines and more recently by a cocrystal structure of SAP together with Fc γ RIIA, demonstrating that CRP and SAP can bind to the low affinity Fc γ RIIA and Fc γ RIIB and to the high affinity Fc γ RI (Bharadwaj et al. 1999, 2001; Lu et al. 2008). Although the relevance of this binding for the phagocytosis of CRP opsonised microorganisms *in vivo* remains to be established it was recently demonstrated that Fc γ R dependent uptake of CRP opsonised *S. pneumoniae* enhances the immune response against this microorganism (Thomas-Rudolph et al. 2007). In addition to this antimicrobial function CRP has also been shown to have an anti-inflammatory activity which seems to be dependent on cellular Fc γ Rs. Thus, mice deficient in Fc γ Rs are not protected from lethal LPS challenge, nephrotoxic nephritis and ITP by injection of human CRP. For the latter two autoimmune models it has been shown that Fc γ RI was crucial for this CRP dependent suppression of autoimmune disease although the exact mechanism of this activity requires further studies (Marjon et al. 2009; Rodriguez et al. 2007).

8 Conclusions

Work over the last years has highlighted the central importance of Fc γ Rs in mediating the proinflammatory activity of IgG. By setting a threshold for innate immune effector cell activation activating and inhibitory Fc γ Rs modulate the strength of the immune response and prevent an unwanted activation of the immune system which might result in destruction of healthy tissues. The identification of novel IgG glycosylation variants involved in the long known but poorly understood anti-inflammatory activity of IgG was an important step toward a more complete picture of the underlying mechanism of this activity. It is tempting to speculate that molecules such as SIGNR-1 which have the capacity to recognize pathogens directly during an infection might have another function during the steady state and help to maintain the immune system in a resting state. The immune escape mechanisms which have been developed by different microorganisms are as complex as these novel pathways responsible for IgG effector functions. It is a safe assumption that many more microbial molecules that target the IgG–Fc γ R interaction will be identified in future studies, which might not only be useful for fighting microbial infections but also for the development of novel strategies to interfere with the deleterious activities of IgG during autoimmune disease.

Acknowledgments We apologize to all our colleagues whose important work could not be cited directly due to limited amount of space. These references can be found in the different review articles cited in the manuscript. This work was supported by grants from the NIH (to J.V.R.), by the German Research Foundation (FOR 832, SFB 643 to F.N.) and the Bavarian Genome Research Network (to F.N.).

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