



Contents lists available at ScienceDirect

## Immunology Letters

journal homepage: [www.elsevier.com/locate/immllet](http://www.elsevier.com/locate/immllet)

## IgG-effector functions: “The Good, The Bad and The Ugly”

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## ARTICLE INFO

Article history:  
Available online xxx

Keywords:  
IgG glycosylation  
IgG allotypes  
FcγR polymorphism

## ABSTRACT

IgG-antibodies are potent and versatile mediators of host protection. They elicit their biological effects through specific interaction of the Fc-part with complement, specific cellular receptors, or both. Several factors should be taken into consideration when analyzing the nature and intensity of the immunological response elicited via IgG-effector functions, especially for the family of IgG-Fc receptors (FcγRs) exclusively expressed on immune cells. These include the various classes of leukocyte FcγR, expressed variably on different immune cells, each with distinct affinity for every IgG subclass, as well as genetic FcγR-polymorphisms affecting expression and affinity for IgG. Furthermore, various aspects of the IgG itself are also crucial for the outcome of the biological response. These include endogenously encoded IgG-polymorphisms, such as IgG3 polymorphisms, and post-transcriptional IgG-modifications, in particular IgG-Fc-glycosylation, affecting IgG effector functions through modified binding affinity to FcγR. These latter aspects concerning the variability in IgG3 on its half-life and placental transport and the clinical consequences of altered IgG-quality through glycosylation, will be the focus of this review.

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## 1. Introduction

Immunoglobulins are crucial mediators of immunological protection against invading pathogens. They exert their biological effects through several effector systems. For IgG-antibodies the most important effector functions are mediated through complement and/or the Fcγ-receptors (FcγRs), a family of cell surface receptors on leukocytes that specifically bind to the Fc portion of IgG-antibodies, bridging the adaptive and innate immune systems [1]. In humans these receptors are termed FcγRIa (CD64a), FcγRIb (CD64b), FcγRIIa (CD32a), FcγRIIb (CD32b), FcγRIIc (CD32c), FcγRIIIa (CD16a), and FcγRIIIb (CD16b). With the exception of FcγRIIb, all the FcγR mediate activating functions (e.g. phagocytosis, antibody-dependent cell-mediated cytotoxicity (ADCC), release of inflammatory mediators and superoxide radicals) after FcγR-crosslinking by IgG-opsonized targets, while FcγRIIb mainly exhibits an inhibitory function, inhibiting the function of the activating FcγR. Exceptions include induction of anti-tumor responses of agonistic CD40 antibodies through FcγRIIb [2,3]. These receptors also have a varying distribution on cells, with FcγRI mostly restricted to macrophages, monocytes and activated granulocytes,

FcγRIIa having a widest range of expression on myeloid cells, FcγRIIb only present on granulocytes (neutrophils, basophils and possibly on eosinophils) [4] and FcγRIIIa on NK cells, macrophages and a subpopulation of monocytes, particularly in the spleen. Although it is clear that the inhibitory FcγRIIb is expressed on B cells and macrophages, the expression on other cells is less certain and may vary between individuals [1].

Two other receptors for IgG are also expressed ubiquitously in almost all cells; the neonatal Fc-receptor (FcRn), a homologue of the major histocompatibility complex (MHC) class I molecules, and the tripartite motif-containing protein 21 (TRIM21), an E3 ubiquitin-protein ligase. Both receptors are expressed inside cells, particularly of myeloid origin. FcRn is found within vacuoles and tubules transporting FcRn along with its cargo, binding both endocytosed IgG and albumin in a pH-dependent manner, recycling both ligands and thereby extending their half-life [5]. FcRn-mediated transport across cellular (e.g. epithelial, endothelial, syncytiotrophoblast) barriers is responsible for the IgG-transmission across mucosal barriers and from mother to child. In addition, FcRn participates in the process of IgG-mediated phagocytosis in myeloid cells in a pH-dependent manner independent of the IgG recycling [6]. Downstream of this pathway FcRn can also deliver immune complex-bound antigens into the antigen presenting pathway, boosting secondary responses [7,8].

TRIM21 on the other hand, is expressed in the cytosol, binding IgG with an even higher affinity than the other human IgG-receptors. It recognizes opsonized non-enveloped viruses,

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intracellular bacteria and targets them for ubiquitination and proteasome degradation [9,10]. Subsequently, TRIM21 activation has also been found to stimulate immune signaling via transcription factor pathways (NF- $\kappa$ B, AP-1, IRF3, IRF5, and IRF7), resulting in downstream secretion of pro-inflammatory cytokines, modulation of natural killer stress ligands and inducing an antiviral state [11]. Antibody-engagement through the surface-exposed Fc $\gamma$ Rs can also trigger intracellular signaling cascades (induced proximally and sequentially through Src- and Syk-kinases) [12]. This can result in immediate degranulation of the cells, with concomitant release of inflammatory mediators and initiation of cellular responses, such as phagocytosis (by phagocytes such as monocytes, macrophages, neutrophils) or ADCC (for example by NK-cells or all myeloid cells). Under normal conditions these processes are utilized beneficially by the host to eliminate invading pathogens. However, these processes can also cause adverse reactions for the host in numerous auto-or alloimmune diseases [13,14], for instance by antibody-mediated platelet destruction (immune thrombocytopenia; ITP, or fetal or neonatal alloimmune thrombocytopenia; FNAIT) [15] or antibody-mediated red blood cell destruction in hemolytic disease of the fetus or the newborn (HDFN) [16].

Besides different cellular distribution of Fc $\gamma$ Rs, their affinity and specificity for the different IgG subclasses (IgG1, IgG2, IgG3, IgG4) also varies considerably, reflecting the distinct biological effects of each subclass in triggering different cell types (reviewed by Hogarth et al. [1]). For instance, IgG2 only binds Fc $\gamma$ R11a, with slightly lower affinity for Fc $\gamma$ R11a, while IgG1 and IgG3 bind all of the Fc $\gamma$ Rs. This enables IgG1 and IgG3 to co-cross link all of the Fc $\gamma$ R (for instance Fc $\gamma$ R11a and Fc $\gamma$ R11b), while IgG2 targets only the Fc $\gamma$ R11a on neutrophils and possibly Fc $\gamma$ R11a on NK cells, macrophages and some macrophages [17]. The affinity for the receptor types differ greatly between Fc $\gamma$ R1 and the rest, but is also depending on the IgG subclass, as IgG1, IgG3 and IgG4 bind Fc $\gamma$ R1 in the nanomolar range, while IgG1 and IgG3 (and IgG4, but with slightly less affinity) bind Fc $\gamma$ R2 in the micromolar range [1,17].

In last two decades we have become increasingly aware of the importance of how these binding affinities are affected by genetic polymorphisms within the Fc $\gamma$ R family. A good example is Fc $\gamma$ R11a, which can have either arginine (R) or histidine (H) at position 131. The former binds human IgG2 with lower affinity than the latter, while the opposite is true for human IgG4 and mouse IgG1 [1,17].

Another important polymorphism in the Fc $\gamma$ R-family can be found within Fc $\gamma$ R11a, which contains either a valine (V) or phenylalanine (F) at position 158, with the V-variant showing stronger binding affinity for all the IgG subclasses [1,17–19]. Consequently, the V-variant is associated with a higher incidence of ITP [20,21], as well as with faster clearance of Rhesus D (RhD) expressing erythrocytes in the presence of anti-RhD IgG [22]. Conversely, the lower affinity Fc $\gamma$ R variants are associated with increased susceptibility to infectious diseases [23].

Within Fc $\gamma$ R11b, the inhibitory Fc $\gamma$ R, additional polymorphism exist within the trans-membrane region, with either a isoleucine (I) or threonine (T) at position 232 that determines their efficacy to co-aggregate with the activating Fc $\gamma$ R into lipid rafts (T232 being less efficient) and thereby their capacity to down regulate the activating responses [24,25].

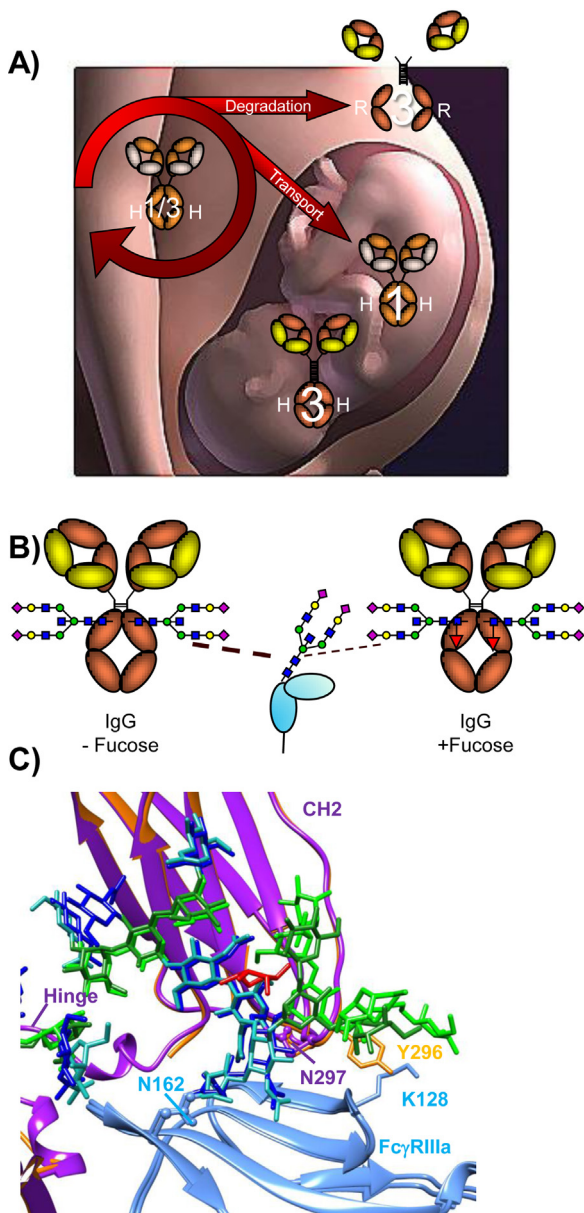
An added layer of variability exist within the Fc $\gamma$ R locus on the long arm of chromosome one, which entails copy number polymorphisms of the Fc $\gamma$ R11c genes as well as the Fc $\gamma$ R11c gene, which is a pseudogene in approximately 80% of healthy individuals. Those individuals expressing a functional copy of 11c have been found to be at increased risk for acquiring ITP (present in 34.4% of ITP patients), indicating that this polymorphism may also be important negative predictor for other autoimmune diseases [20]. These

polymorphisms and their importance for infectious diseases and auto- and allo- immunity have been extensively investigated and reviewed before [23,26–31]. However, polymorphisms within the IgG, both endogenously encoded as well as through posttranscriptional modification, can also greatly affect immune responses, as will be described further below.

## 2. Functional polymorphism within IgG3

Of the four IgG subclasses, human IgG3 stands out compared to the other IgG subclasses – also to other species – with up to four exons encoding for the hinge, extending its reach to up to 62 amino acids (compared with 15 for IgG1, 12 for IgG2 and IgG4) (Fig. 1). IgG3 has higher affinity for complement component C1q and Fc $\gamma$ Rs, providing it with its relatively stronger effector functions [1,17,32,33]. However, it has a relatively short half-life (7 days vs. 21 days for the other subclasses), is generally known to have poor placental transport and to have impaired transport to mucosal surfaces [34], suggesting IgG3 not to be compatible for FcRn-mediated transport [35–37]. However, we recently identified that IgG3 has a short half-life because of a single amino acid change at position 435; a position bearing a histidine in IgG in all known mammalian species. This histidine is normally neutral at physiological pH of 7.4, but becomes protonated in acidic lysosomes (pH < 6.5) after uptake by a pinocytotic or endocytotic event, acquiring a positive charge. This protonation is required for binding to FcRn, triggering transport of IgG away from the developing lysosome back to the cell surface, where it is released again at neutral pH. Unlike the other IgG subclasses, IgG3 generally bears an arginine at position 435 and is thus always positively charged at all physiological pH. Despite this difference, IgG3 can be transported normally by FcRn – but only when IgG3 is present alone. This has been observed both *in vitro* using transwell systems [33] and *in vivo* as IgG3 has a normal half-life in SCID mice [38] as opposed to wild type mice [39]. Using *in vitro* transwell assays, IgG3 was not transported effectively together with other IgG subclasses but was degraded instead. However, the transport was rescued after replacing arginine at position 435 with a histidine [33]. Conversely, IgG1 bearing R435 was rescued and transported normally by FcRn *in vitro*, but only when present alone, as after mixing with IgG3 H435 – or other IgG WT subclasses – both transport and recovery of both IgG1 was dramatically decreased. *In vivo* experiments in mice confirmed these findings, indicating the decreased transport and enhanced loss of IgG3 to be solely due to the arginine at position 435 [33].

In contrast to the other IgG subclasses, IgG3 is highly polymorphic in humans, consisting of at least 17 distinct variants, many of which are known to give rise to allo-specific antibodies (allotypes) [33,40]. Three distinct genetic IgG3 variants, previously identified by two different allo-epitopes (G3m15 and G3m16), do actually naturally contain histidine at position 435. They are uncommon in Europe (~1%) but much more prevalent in Asia (10–50%) [40,41]. We recently found that these H435-IgG3 allotypes do have an extended half-life in humans that is comparable to the other subclasses (Fig. 1A) [33]. In agreement with this, and with FcRn being the only receptor involved in transplacental transport, G3m16 IgG3-antibodies found in pregnant women were readily transported across the placenta by FcRn [41] as well as H435-containing but not R435-containing IgG3 in *ex vivo* perfused human placenta (Fig. 1A) [42]. As IgG3-antibodies are frequently found in pregnancy related cellular allo-immune pathologies, and generally mediate stronger effector functions than IgG1, fetuses and newborns of G3m16 (and the less common G4m15) positive mothers might therefore be more susceptible for adverse HDFN or FNAIT, in which the red blood cells or platelets, respectively, of the fetus or newborn are destroyed [43,44].



**Q4 Fig. 1.** IgG pharmacology and modulation of effector functions. (A) Due to FcRn-mediated recycling, all human IgG subclasses, except some allotypes of IgG3, have an extended half-life of three weeks whereas similar size proteins and IgG3 containing arginine (R) at position 435, have a half-life of only one week and are degraded. This is because the amino acid at position 435 resides at a key position for FcRn-binding, causing IgG3 to lose binding to FcRn in competition with the other subclasses – all bearing a histidine (H) at position 435. The same holds true for FcRn-mediated transport of IgG across the placenta, which is ineffective for the classical form of IgG3 with R435. However, H435-containing allotypes of IgG3 do exist at high frequency in some populations (allotypes G3m15 and G3m16, also termed G3m(s,t)), and these have normal half-life of three weeks and placental transport. As IgG3 has the highest affinity for FcγR and C1q, this may be beneficial for the young, providing it with enhanced immunity for the first weeks after birth. However, they are also of potential higher risk for allo-immune mediated diseases that occur frequently in pregnancy such as anemia and thrombocytopenia. 1: IgG1, 3: IgG3. (B) The approximate locations of the glycan attached to N297 in the IgG-Fc, and N162 for FcγRIIIa and IIIb affecting binding between IgG and FcγR. Although normal variations in the Fc-glycan have been shown to slightly affect binding to all FcγR, the IgG-Fc glycan is absolutely required for binding. Only the presence or absence of the core-Fc-fucose (red triangle, right) strongly affects binding to FcγR, but only to the FcγRIII family, bearing N162 that interacts directly with the IgG-Fc glycan. These allotypic variations and posttranslational modifications, and how they add an altered layer of complexity and control over the biology of human IgG, is discussed in more details in the main text. The thicker dashed line indicates a stronger binding affinity of nonfucosylated IgG with the human FcγRIII family members, compared to the thinner dashed line representing the weaker binding affinity of fucosylated IgG.

### 3. Regulation of IgG effector functions on the B-cell level through Fc-glycosylation

IgG antibodies are glycoproteins containing a highly-conserved branched sugar moiety attached to the asparagine (ASN)297 part of the antibody-Fc domain. This glycan is essential for the maintenance of a functional structure and is required for binding of IgG with FcγR [45–47]. Normally, this glycan consists of a core structure of N-acetylglucosamine and mannoses but with variable levels of galactose, sialic acid, bisecting N-acetylglucosamine (GlcNAc) and core fucose. Variation in this composition influences antibody affinity to FcγR and thus antibody effector activity. Increased sialic acid content of IgG-Fc has received a great amount of attention over the past years due their protective effect in IVIG, as the presence of sialic acid in IVIG has been described to enable IgG-binding to the mouse lectin SIGN-R1 (also known as DC-SIGN – dendritic cell-specific ICAM3-grabbing non-integrin – in humans), upregulating a cytokine cascade initiated by IL-33 and eventually leading to enhanced myeloid expression of FcγRIIIb via IL-4 [48–50]. The enrichment of sialic acid has been demonstrated to have an approximate 7-fold reduced binding affinity of murine IgG to FcγRIII in mice [48]. However, these findings in mice have recently been challenged by a study of Rheumatoid Arthritis, a disease well known for frequent remission during pregnancy. Although this remission seemed to go hand in hand with both increased galactosylation and sialylation, a further independent analysis of di-galactosylated (G2) IgG indicated that the association with sialylation to be an epiphenomenon due to its requirement for previous galactosylation. In fact, while G2- IgG was associated with remission, di-sialylated G2-IgG had an opposing effect apparent by the minor but positive association with disease activity [51].

Of the variable amount of glycans present in the IgG-Fc, the removal of the IgG-core fucose has by far the greatest effect on binding to FcγRs. A lack of core fucose has been demonstrated to result in an up to 50-fold stronger binding affinity to FcγRIIIa [45,52] and FcγRIIIb [52] but not to the other FcγRs. This restriction is caused by a conserved N-glycan in human FcγRIIIa and FcγRIIIb at position 162 (N162), which interacts with the Fc but also the Fc-glycan. This configuration is greatly affected by the presence or absence of the core-fucose within the IgG-Fc (Fig. 1B) [47,53]. The enhanced binding to the GPI-linked FcγRIIIb has been shown to result in enhanced neutrophil phagocytosis of rituximab-opsonized CD20<sup>+</sup> lymphoma cells [52] and of platelets [54]. In addition, the enhanced binding to FcγRIIIa resulted in enhanced ADCC on mononuclear cells [45,55–59], but remarkably not through neutrophil FcγRIIIb [60].

Until recently, the importance of the core fucosylation of the IgG-Fc has only received attention because of the possibilities to produce more efficacious therapeutic antibodies, like rituximab (reviewed by Yamane-Ohnuki et al. [61]). This is because core fucosylation was not known to be variable in humans until recently [54,62,63]. Indeed, ~94% of all naturally occurring IgG-derived Fc-glycopeptides in humans have the core-fucose attached [51,64]. Theoretically, this means that ~99.7% of all IgG

(C) Three-dimensional alignment of FcγRIIIa-Fc crystal structures, crystallized with- (accession number 3SGJ, Fc-heavy chains purple, darker glycan colors) and without- (accession number 3SGK, Fc-heavy chains orange, lighter glycan colors) core Fc-fucose, based on structures published by Ferrara et al. [47]. FcγRIIIa is depicted in light blue for both structures. The glycans are colored according to standard schemes with N-acetylglucosamine in blue, mannoses in green, and fucose in red. Without fucose, the FcγRIIIa glycan, in particular the mannoses of FcγRIII (right), structures shifts with increased hydrogen bond formation, but also clamping of the Y296 in the Fc onto K128 on FcγRIIIa [47], which may however also be influenced by the extended number of mannose residues found in that structure. (For interpretation of the references to color in figure legend, the reader is referred to the web version of the article.)



**Table 1**  
Overview of IgG-glycosylation patterns and their effects in disease-settings, observed in literature to date.

IgG-glycan	Disease setting	Affected-IgG	Effect of IgG-glycan
Galactosylation	Rheumatoid arthritis (RA)	Total IgG	Increased [66–68]; increased in remission of RA in pregnancy [51,66,67,69], decreased during relapse of RA in pregnancy [69], inversely related with N-acetylglucosamine [70,71]
	Juvenile onset chronic arthritis	Total IgG	Inversely related with N-acetylglucosamine [70,71]
	Crohn's disease	Total IgG	Inversely related with N-acetylglucosamine [71]
	Primary osteoarthritis	Total IgG	Decreased [72]
	Osteoarthritis	Total IgG	Parallel increase with N-acetylglucosamine [71]
	Sjögren's Syndrome	Total IgG	Decreased [70]. Parallel increase with N-acetylglucosamine [71]
	Tuberculosis	Total IgG	Decreased [73]
	Ovarian cancer	Total IgG	Decreased [74]
	Fetal or neonatal alloimmune thrombocytopenia (FNAIT)	Anti-platelet IgG	Increased [54,62]
	Refractory thrombocytopenia (RT)	Anti-HLA IgG	Increased [54]
	HIV	Anti-HIV in elite controllers	Decreased [63]
	Gastric cancer	Total IgG	Decreased [75]
Lambert–Eaton myasthenic syndrome	IgG1-anti presynaptic voltage gated Ca <sup>2+</sup> -channels	Decreased [76]	
Sialylation	RA	Total IgG	Increased in remission of RA in pregnancy [51,67]
	Gastric cancer	Total IgG	Decreased [75]
	FNAIT	Anti-platelet IgG	Increased [54,62]
	HIV	Anti-HIV in elite controllers	Decreased [63]
Fucose	FNAIT	Anti-platelet IgG	Decreased [54,62]
	HIV	Anti-HIV in elite controllers	Decreased [63]
	Gastric cancer (stage II–III)	Total IgG	Increased [75]
	Infertile leukospermic patients	Seminal IgG	Decreased compared to normal, fertile normozoospermic patients [77]
Bisecting N-acetylglucosamine	RT	Anti-HLA IgG	Decreased [54]
	Gastric cancer (stage II–III)	Total IgG	Decreased [75]
	Lambert–Eaton myasthenic syndrome (<50 years)	IgG1-anti presynaptic voltage gated Ca <sup>2+</sup> -channels	Increased [76]

contain either one (combination of a heavy chain without and with fucose on either side or  $2 \times 0.06 \times 0.94 \times 100\% = 11.3\%$ ) or two ( $0.94 \times 0.94 \times 100\% = 88.4\%$ ) core-Fc fucoses, with only 0.3% of circulating IgG completely devoid of core-fucose. However, individual differences do exist. This was recently exemplified in a genome-wide association study, identifying the loci containing fucosyltransferase 8 (FUT8) and the transcription regulator Ikaros to influence these levels – loci that in turn were previously reported to be associated with other diseases such as systemic lupus erythematosus, Crohn's disease, and multiple sclerosis [65]. In addition, antigen-specific IgG-fucosylation can be skewed in certain immune responses. In a previous pilot-study we observed that the anti-platelet specific antibodies, which mediated alloimmune reactions against platelets in pregnancies, displayed a decreased fucosylation [62]. In a follow-up study, we evaluated the glycosylation patterns of a large cohort of FNAIT-serum samples containing anti-platelet specific antibodies (anti-human platelet antigen (HPA)-1a antibodies) in pregnancy and found a clear skewing toward decreased Fc-fucosylation in the majority of anti-platelet-, but not total-IgG [54]. Most patients were identified because of their adverse clinical symptoms, but those identified without clinical symptoms had normal fucosylation of their anti-platelet IgG, while those most severely affected had fucosylation down to 10%. This indicated the immune setting during the pregnancy, the nature of the antigen, or both, to play a role in steering the quality of the antibodies. In this case with an adverse effect for the patient, as the lack of core-fucose in the anti-platelet IgG resulted in increased platelet destruction due to enhanced binding to either FcγRIIIa and/or FcγRIIIb. Furthermore, a significant relationship was observed between the level of anti-platelet IgG-core fucosylation and neonatal platelet numbers in FNAIT, as well as bleeding tendency, with decreased core-fucosylation of the pathogenic anti-HPA1a-antibodies being associated with decreased number of platelets and increased

clinical severity [54]. Conversely, a lack of Fc-fucose in IgG can theoretically be highly beneficial for responses against infectious diseases, as has also recently been demonstrated for HIV-specific antibodies in elite controllers – apparently a signature for improved HIV-neutralization and clearance [63]. The remarkable variation in IgG-Fc glycosylation patterns in various disease settings and their subsequent effects reported in the literature are summarized in Table 1.

In conclusion, more variables besides FcγR polymorphisms, IgG titer, and subclass responses affect IgG-effector functions and clinical outcomes. Strong effector functions and high binding affinities (FcγR profiles, FcγRIIc-ORF, a high number of FcγRIII and IIc gene copies, IgG3-G3m15/16, non-fucosylated IgG-variants) can be associated with a “good” outcome in terms of protection against infectious diseases or antibody-mediated therapies. However, these can also turn out “bad” or even “ugly” in allo- and auto-immune mediated diseases, for instance resulting in intracranial hemorrhages in FNAIT. All these factors should be taken into consideration when looking into the biological response, both from a diagnostic as well as a therapeutic perspective.

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