Rituximab-Dependent Cytotoxicity by Natural Killer Cells: Influence of FCGR3A Polymorphism on the Concentration-Effect Relationship

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ABSTRACT

The FCGR3A gene dimorphism generates two allotypes: FcγRIIa-158V and FcγRIIa-158F. The genotype homozygous for FcγRIIa-158V (VV) is associated with higher clinical response to rituximab, a chimeric anti-CD20 IgG1 used in the treatment of B lymphoproliferative malignancies. Our objective was to determine whether this genetic association relates to rituximab-dependent cytotoxicity mediated by FcγRIIa/CD16a+ cells. The number of CD16+ circulating monocytes, T cells, and natural killer (NK) cells in 54 donors was first shown to be unrelated to FCGR3A polymorphism. We then demonstrated that FcγRIIa-158V displays higher affinity for rituximab than FcγRIIa-158F by comparing rituximab concentrations inhibiting the binding of 3G8 mAb (anti-CD16) with VV NK cells and NK cells homozygous for FcγRIIa-158F (FF). VV and FF NK cells killed Daudi cells similarly after FcγRIIa engagement by saturating concentrations of rituximab or 3G8. However, the rituximab concentration resulting in 50% lysis (EC50) observed with NK cells from VV donors was 4.2 times lower than that observed with NK cells from FF donors (on average 0.00096 and 0.00402 µg/ml, respectively, P = 0.0043).

Finally, the functional difference between VV and FF NK cells was restricted to rituximab concentrations weakly sensitizing CD20. This study supports the conclusion that FCGR3A genotype is associated with response to rituximab because it affects the relationship between rituximab concentration and NK cell-mediated lysis of CD20+ cells. Rituximab administration could therefore be adjusted according to FCGR3A genotype.

INTRODUCTION

FcγRIIa/CD16a, one of the low-affinity receptors for IgG Fc, is involved in antibody-dependent cell-mediated cytotoxicity (ADCC). It links IgG-sensitized target cells to FcγRIIa/CD16a-bearing cytotoxic cells, i.e., CD56dim natural killer (NK) cells, a fraction of monocyte/macrophages, and a fraction of T cells, and activates these effector cells. The FCGR3A gene, which encodes FcγRIIa, displays a functional allelic dimorphism generating allotypes with either a phenylalanine (F) or a valine (V) residue at amino acid position 158 (1, 2). This residue directly interacts with the lower hinge region of IgG1, as recently shown by IgG1-FcγRII co-crystallization (3, 4). Accordingly, flow cytometry studies have shown that NK cells from donors homozygous for FcγRIIa-158V (VV) bound more human IgG1 and IgG3 than did NK cells from donors homozygous for FcγRIIa-158F (FF; Refs. 1 and 2). This difference might result from higher affinity of the FcγRIIa-158V allotype (2) or alternatively from higher FcγRIIa membrane expression on NK cells expressing this allotype (5).

Rituximab (Mabthera, Rituxan) is a chimeric anti-CD20 IgG1 monoclonal antibody (mAb) consisting of human y1 and k constant regions linked to murine variable domains (6). Over the past few years, rituximab has considerably modified the therapeutic strategy for B lymphoproliferative malignancies, particularly non-Hodgkin’s lymphomas (NHLs). Rituximab, alone or in combination with chemotherapy, has been shown to be effective in the treatment of both low-intermediate and high-grade NHLs (7–12), although the response rate varies with the histological type, with low-grade/follicular lymphomas displaying the best response rate (8, 10, 11). Nevertheless, 30–50% of patients with low-grade NHLs exhibit no clinical response, and the actual causes of treatment failure remain largely unknown.

In vitro studies suggest that rituximab induces lymphoma cell lysis through ADCC (6, 13), complement-dependent cytotoxicity (6, 13–16), FcγRI/CD32-dependent phagocytosis (13), or direct signaling leading to apoptosis (17–19). The implication of both FcγR and complement activation in the in vivo antitumor effect of rituximab against CD20+ lymphoma cell lines has been clearly demonstrated in murine models (20, 21). We have recently shown an association between FCGR3A genotype and response to rituximab in previously untreated follicular NHL patients with low tumor burden (22). Indeed, VV patients had a higher probability of experiencing a clinical response compared with F carriers. The association between FCGR3A genotype and clinical response to rituximab has also been observed in relapsed follicular NHL patients (23) and in Waldenström’s macroglobulinemia patients (24).

In addition, systemic lupus erythematosus patients with the VV or VF genotype had better B-cell depletion after rituximab treatment than FF patients (25). Although the genetic association does not demonstrate that the mode of action of rituximab involves FcγRIIa, we postulated that VV patients show a better response because they have a more efficient rituximab-dependent ADCC against CD20+ cells. The ADCC efficiency may depend on variability of target cells and/or effector cells. However, lymphoma cells from patients with distinct histological types expressing different levels of CD20 are equally sensitive to ADCC in the presence of rituximab (13). The aim of this study was therefore to investigate the influence of the FCGR3A polymorphism on rituximab-dependent ADCC mediated by CD16+ effector cells.

We first investigated the number of circulating CD16+ mononuclear cells in relation to FCGR3A-158V/F polymorphism in 54 blood donors. We then compared the affinity of the two allotypic forms of FcγRIIa for rituximab. Finally, we studied the influence of FCGR3A-158V/F polymorphism on the relationship between rituximab concentration and rituximab-dependent NK cell-mediated cytotoxicity.

MATERIALS AND METHODS

mAbs. 679.1 Mc7 control irrelevant mAb, unconjugated and FITC-conjugated 3G8 mAb specific for CD16, unconjugated T199 and phycoerythrin-conjugated NKH-1 mAbs specific for CD56, and phycoerythrin-cyanin 5.1-conjugated UCHT1 mAb specific for CD3 were purchased from Beckman Coulter (Villepinte, France). FITC-conjugated DJ130c mAb specific for CD16 was obtained from Dako (Trappes, France). All of these mAbs are mouse

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CD16/H11001 FCGR3A by flow cytometry analysis. Gates were set on PBMC, monocytes, and lymphocytes with forward and side scatters. The concentration-effect relationship of rituximab-dependant cytotoxicity by NK cells was analyzed for each individual with an Emax (maximum cpm) comparison of Peripheral Blood Lymphocytes, Monocytes, T Cells, and NK Cells. PBMCs and peripheral blood lymphocytes were prepared from the peripheral venous blood of blood donors by Lymphoprep (AbCys S.A., Paris, France) centrifugation as described previously (26). Monocytes and T cells were positively selected using MACS CD14 and MACS CD3 MicroBeads (Miltenyi Biotec, Paris, France), respectively, and NK cells were negatively selected using MACS NK Cell Isolation Kit (Miltenyi Biotec) according to the manufacturer’s recommendations. The labeled cells were retained on a MACS column in the magnetic field of a VarioMACS separator (Miltenyi Biotec).

Preparation of Target Cells. Daudi cells were washed and resuspended in RPMI 1640. Cells (10 × 10^6) were labeled for 90 min with 100 µCi of Na^25CrO_4 (DuPont-NEC, Les Ulis, France) at 37 °C in 5% CO_2, washed three times in RPMI 1640, and incubated for 1 h with culture medium to allow spontaneous release. Finally, Cr-labeled cells were washed twice and resuspended in culture medium, and 2 × 10^6 cells/well were added to 96-well round-bottomed plates.

Cytotoxicity Assay. Cytotoxicity assay was performed as described previously (26). Rituximab or 3G8 mAb at the indicated final concentration was incubated with varying concentrations of rituximab leading to 50% of Emax. Pharmacodynamic parameters were compared by Kruskal-Wallis nonparametric ANOVA test followed by Mann-Whitney nonparametric test. Statistica 5.5 A (StatSoft) was used, and results were considered significant if P < 0.05.

RESULTS

Circulating CD16+ Mononuclear Cells in FCGR3A-158VF Genotyped Donors. The number of peripheral blood CD16+ mononuclear cells, CD16+ monocytes, CD3+CD16+ T cells, and CD3-CD16+ NK cells were analyzed by flow cytometry in 54 blood donors simultaneously tested for the FCGR3A-158VF polymorphism. Of the 54 donors, 7 and 21 were homozygous for FCGR3A-158V and FCGR3A-158F, respectively, and 26 were heterozygous (Table 1). The three groups were not different in terms of sex or age.

### Table 1. Enumeration of circulating CD16+ mononuclear cells according to FCGR3A genotype

<table>
<thead>
<tr>
<th></th>
<th>All samples</th>
<th>F/F samples</th>
<th>V/F samples</th>
<th>V/V samples</th>
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<td>(n = 54)</td>
<td>(n = 21)</td>
<td>(n = 26)</td>
<td>(n = 7)</td>
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<tr>
<td>Total PBMCs</td>
<td>2630 ± 530</td>
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<tr>
<td>CD16+ PBMCs</td>
<td>362 ± 190</td>
<td>361 ± 185</td>
<td>364 ± 211</td>
<td>357 ± 138</td>
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<tr>
<td>Total Monocytes</td>
<td>457 ± 136</td>
<td>446 ± 112</td>
<td>476 ± 157</td>
<td>420 ± 121</td>
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<tr>
<td>CD16+ Monocytes</td>
<td>43 ± 20</td>
<td>40 ± 18</td>
<td>45 ± 21</td>
<td>44 ± 23</td>
</tr>
<tr>
<td>(28.1 ± 5.0)^a</td>
<td>(25.0 ± 3.8)^d</td>
<td>(29.7 ± 5.1)^e</td>
<td>(31.5 ± 1.8)^f</td>
<td></td>
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<tr>
<td>Total Lymphocytes</td>
<td>2130 ± 450</td>
<td>2060 ± 310</td>
<td>2160 ± 520</td>
<td>2210 ± 560</td>
</tr>
<tr>
<td>CD3-CD16+ Lymphocytes</td>
<td>35 ± 31</td>
<td>26 ± 20</td>
<td>39 ± 36</td>
<td>44 ± 34</td>
</tr>
<tr>
<td>(4.5 ± 2.5)</td>
<td>(4.7 ± 2.8)</td>
<td>(4.3 ± 2.6)</td>
<td>(4.0 ± 0.9)</td>
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<tr>
<td>CD3-CD16+ Lymphocytes</td>
<td>279 ± 166</td>
<td>292 ± 176</td>
<td>271 ± 174</td>
<td>267 ± 117</td>
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<td>(20.3 ± 4.3)</td>
<td>(16.8 ± 2.3)</td>
<td>(22.5 ± 3.3)^g</td>
<td>(23.2 ± 2.9)^g</td>
<td></td>
</tr>
</tbody>
</table>

^a Phenotypic analysis of PBMC was performed according to a standard no-wash whole-blood procedure using a PrepPlus workstation (Beckman Coulter). Blood samples (100 µl) were incubated with 20 µl of FITC-conjugated anti-CD16, 5 µl of phycoerythrin-conjugated anti-CD56, and 20 µl of phycocyanin-CD5 1-conjugated anti-CD3 mAbs for 15 min at 18–20°C. RBC lysis and cell fixation were performed using a TQ-Prep workstation and ImmunoPrep reagent system (Beckman Coulter) following the manufacturer’s recommendations. Cells were analyzed using an EPICS-XL-MCL flow cytometer (Beckman Coulter) as described previously (27).

^b Results are expressed as the mean ± SD of cells/µl.

^c Results are expressed as the mean ± SD of cells/µl.

^d Differences between the three genotypes were compared by Kruskal-Wallis nonparametric ANOVA test. Statistica 5.5 A (StatSoft) was used, and results were considered significant if P < 0.05.

^e P < 0.001 versus MFI of CD3-CD16+ lymphocytes with the same genotype.

^f P < 0.001 versus MFI of CD3-CD16+ lymphocytes.

^g P < 0.001 versus MFI of CD3-CD16+ lymphocytes.

^h P < 0.001 versus MFI of CD3-CD16+ lymphocytes.

^i P < 0.001 versus MFI of CD3-CD16+ lymphocytes.

^j P < 0.001 versus MFI of CD3-CD16+ lymphocytes.
When all samples were analyzed together, we found that 13.8% of PBMCs, 9.4% of monocytes, and 14.7% of lymphocytes were CD16+. The vast majority of CD16+ PBMCs were NK cells (77.1%), whereas CD16+ monocytes and CD3+CD16+ lymphocytes represented 11.9% and 9.7% of these cells, respectively. No difference was found among the three genotype groups in terms of number of circulating CD16+ mononuclear cells, CD16+ monocytes, CD3+CD16+ T cells, and CD3-CD16+ NK cells (Table 1). The level of CD16 expression on monocytes was slightly higher than that observed on NK cells whatever the genotype, whereas it was very low on CD3+CD16+ T cells. Finally, higher binding of anti-CD16 3G8 mAb to NK cells and monocytes was observed in FCGR3A-158V homozygous and heterozygous donors compared with homozygous FCGR3A-158F donors (Table 1). Given that the binding of several other anti-CD16 mAbs is similar on NK cells from VV and FF donors (2), it is likely that the difference in binding of 3G8 reflects a greater affinity of this mAb for the V allotype.

Influence of FCGR3A-158V/F Polymorphism on RituXimab-Binding Properties of NK Cell FcγRIIIa. It has been assumed that the FCGR3A-158V/F polymorphism affects FcγRIIIa affinity for IgG1 (2). To address this question, we compared the ability of rituximab (IgG1) to inhibit the binding of FITC-conjugated 3G8 mAb (29) with NK cells from VV and FF donors. A 50% inhibition of 3G8 mAb binding to VV and FF NK cells was achieved with less than 0.15 μg/ml rituximab (2). To address this question, we compared the ability of rituximab, Daudi cells were incubated with varying concentrations of rituximab followed by FITC-conjugated goat antihuman IgG F(ab')₂ and then analyzed by flow cytometry. Fluorescence intensity is displayed on the X axis (in log scale) and cell number on the Y axis (results are from one representative experiment among three).

Binding of Rituximab to Daudi Cells. To study the in vitro susceptibility of B cells to ADCC in the presence of rituximab, Daudi cells (HLA class I negative and CD20 positive) were used as target cells. To study the binding of rituximab, Daudi cells were incubated with rituximab concentrations ranging from 0.0002 to 2 μg/ml followed by FITC-conjugated antihuman IgG F(ab')₂ that did not recognize the membrane IgM on Daudi cells (Fig. 2). Weak binding of rituximab was detected with 0.0006 μg/ml rituximab. Binding then increased dramatically with increasing concentrations reaching a maximum at 0.2 μg/ml.

Cytolytic Potential of NK Cells from VV and FF Donors in Response to Optimal FcγRIIIa Stimulation. As expected, Daudi cells were resistant to lysis in the absence of rituximab but were killed efficiently by PBMCs and peripheral blood lymphocytes in the presence of 0.2 μg/ml rituximab (not shown). In addition, lysis did not increase in the presence of 20 μg/ml rituximab, and Daudi cells were not killed by purified monocytes or by purified T cells, but they were killed very efficiently by purified NK cells in the presence of rituximab (not shown). We next addressed the question of the influence of FCGR3A polymorphism on the cytotoxic response of NK cells to optimal FcγRIIIa engagement. Daudi cells express CD32/FcγRII, which binds mouse IgG1 (30). They may therefore be used as targets in a redirected killing assay in the presence of anti-CD16 3G8 mAb. Daudi cells were resistant to lysis in the presence of anti-CD56 T199 mAb (data not shown), whereas they were killed very efficiently in the presence of 3G8 mAb (Fig. 3). Although 3G8 mAb bound slightly more efficiently to NK cells from VV donors (Table 1), the lysis observed with VV and FF NK cells in the presence of 3G8 mAb was similar and was also equivalent to that observed in the presence of saturating amounts of rituximab (Fig. 3).

Influence of FCGR3A-158V/F Polymorphism on the Concentration-Effect Relationship of Rituximab-Dependent NK Cell-Mediated Cytotoxicity. The influence of the FCGR3A-158V/F genotype on the lysis of Daudi cells was then analyzed in the presence of decreasing concentrations of rituximab (0.2 to 0.0002 μg/ml), with NK cells from six VV and six FF donors (E:T ratio = 2.5:1). As expected, for each donor, the observed lysis of Daudi cells increased with increasing concentrations of rituximab and reached a plateau at high concentrations (Fig. 4). The relationship between Daudi cell lysis and rituximab concentrations was analyzed for each individual using an Emax model. Basal lysis and maximal lysis induced by rituximab with NK cells from VV and FF donors were not different. E0 values obtained with VV and FF NK cells were 11.3 ± 9.9% and 8.3 ± 3.5% specific lysis, respectively, P = 1; whereas Emax values were 47.4 ± 6.2% and 41.9 ± 9.5% specific lysis, respectively.

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Fig. 1. Binding of rituximab to NK cells from FCGR3A-158V VV and FF donors. Purified NK cells from homozygous VV and FF blood donors were incubated with varying concentrations of rituximab for 30 min at 4°C followed by FITC-conjugated anti-CD16 3G8 mAb and then analyzed by flow cytometry. Percentages of inhibition of 3G8 binding were calculated as described in “Materials and Methods,” and the results are expressed as the mean ± SD (n = 3 VV and 3 FF).

Fig. 2. Binding of rituximab to Daudi cells. Daudi cells were incubated with varying concentrations of rituximab followed by FITC-conjugated goat antihuman IgG F(ab')₂ and then analyzed by flow cytometry. Fluorescence intensity is displayed on the X axis (in log scale) and cell number on the Y axis (results are from one representative experiment among three).

Fig. 3. Binding of rituximab to Daudi cells. Daudi cells were incubated with varying concentrations of rituximab for 30 min at 4°C followed by FITC-conjugated antihuman IgG F(ab')₂ and then analyzed by flow cytometry. Fluorescence intensity is displayed on the X axis (in log scale) and cell number on the Y axis (results are from one representative experiment among three).

Fig. 4. Influence of FCGR3A-158V/F Polymorphism on the Concentration-Effect Relationship of Rituximab-Dependent NK Cell-Mediated Cytotoxicity. The influence of the FCGR3A-158V/F genotype on the lysis of Daudi cells was then analyzed in the presence of decreasing concentrations of rituximab (0.2 to 0.0002 μg/ml), with NK cells from six VV and six FF donors (E:T ratio = 2.5:1). As expected, for each donor, the observed lysis of Daudi cells increased with increasing concentrations of rituximab and reached a plateau at high concentrations (Fig. 4). The relationship between Daudi cell lysis and rituximab concentrations was analyzed for each individual using an Emax model. Basal lysis and maximal lysis induced by rituximab with NK cells from VV and FF donors were not different. E0 values obtained with VV and FF NK cells were 11.3 ± 9.9% and 8.3 ± 3.5% specific lysis, respectively, P = 1; whereas Emax values were 47.4 ± 6.2% and 41.9 ± 9.5% specific lysis, respectively.
obtained with NK cells from FF donors, whereas Enmax and E0 were not different. These results are in accordance with the previous observation that human low-IgG-binding NK cells were able to lyse chicken erythrocytes better than NK cells from high-IgG-binding NK cells in the presence of low concentrations of rabbit antichicken erythrocyte IgG (5). Shields et al. (33) have shown that some substitutions in the Fc sequence improved both the binding of monomeric human anti-IgE to FcyRIIIA-transfected Chinese hamster ovary cells and Herceptin-mediated ADCC of SKBR-3 cells by NK cells. These effects were more pronounced on the FcyRIIIA-158F than on the FcyRIIIA-158V allotype. In addition, it was shown that the more the substitutions improved binding to FcyRIIIA, the more they increased ADCC, whatever the genotype. Finally, the differences in ADCC were observed in the presence of a concentration of Herceptin variant (2 ng/ml) that is very close to the EC50 observed in our study. Thus, our results are consistent with these findings. Interestingly, it can be calculated from the results shown in Fig. 2 and Fig. 4 that less than 5% and 15% of CD20 molecules on Daudi cells are bound by rituximab at the EC50 obtained with VV and FF NK cells, respectively. In addition, rituximab concentrations yielding more than 40% occupancy of CD20 (i.e., above 0.02 µg/ml) were sufficient to obtain more than 80% of maximum lysis, whatever the genotype. Thus, the increased ADCC associated with expression of the FcyRIIIA-158V allotype on NK cells was restricted to a rituximab concentration range weakly sensitizing CD20 on Daudi cells. We therefore conclude that both the level of opsonization and the 158VF/FcγRIIIA polymorphism influence the killing of Daudi cells.

The fact that VV and FF NK cells killed Daudi cells similarly after optimal FcγRIIIA engagement by saturating concentrations of rituximab or by 3G8 anti-CD16 mAb and respond by an indistinguishable rise in Ca²⁺ to 3G8 (2) shows that the two FcyRIIIA allotypes are not different in terms of intracellular signaling and cytolytic potential. Thus, the functional difference between the two allotypes that we demonstrated at low concentrations results primarily from their difference in IgG1 binding. Flow cytometry studies have shown that human IgG1 binds more strongly to NK cells from low- and high-IgG-binding individuals, Vance et al. (5) concluded that the absolute number of FcγRIIIA receptors rather than FcγRIIIA affinity accounts for the difference in IgG binding. Conversely, the fact that
similar fluorescence intensities were observed with several anti-CD16 mAbs on NK cells from VV and FF donors led Wu et al. (2) to propose that these cells express similar levels of FcyRIIIa and that 158-V/F polymorphism affects FcyRIIIa affinity. However, we observed a significantly higher binding of 3G8 anti-CD16 mAb on NK cells and monocytes from VV and VF donors compared with FF donors in accordance with previous reports (1, 5). Conversely, the binding of the DJ130 anti-CD16 mAb is higher on NK cells from FF donors in accordance with previous reports (1, 5). Conversely, the binding of the DJ130 anti-CD16 mAb is higher on NK cells from FF donors in accordance with previous reports (1, 5). Conversely, the binding of the DJ130 anti-CD16 mAb is higher on NK cells from FF donors in accordance with previous reports (1, 5). Conversely, the binding of the DJ130 anti-CD16 mAb is higher on NK cells from FF donors in accordance with previous reports (1, 5). Conversely, the binding of the DJ130 anti-CD16 mAb is higher on NK cells from FF donors in accordance with previous reports (1, 5). Conversely, the binding of the DJ130 anti-CD16 mAb is higher on NK cells from FF donors in accordance with previous reports (1, 5).

The rituximab-depleting effect observed in vivo is the result of different complementary mechanisms including complement-dependent cytotoxicity (6, 13-16), apoptosis (17-19), phagocytosis, and ADCC (6, 13). The implication of both FcyR and C1q in the in vivo antitumor effect of rituximab against CD20+ lymphoma cell lines has been clearly demonstrated in murine models (20, 21), suggesting that ADCC and complement activation are essential for rituximab therapeutical effect. In addition, the fact that opsonization of target cells with complement components results in increased lysis by NK cells that express the CD11b/CD18 receptor (34, 35) strongly suggests that ADCC and complement activation may have a cooperative activity in vivo (32, 36). Complement-dependent cytotoxicity is mainly dependent on lymphoma cell variability, especially on both their CD20 and complement regulatory protein membrane expression (13, 14, 16), although response to rituximab therapy has been shown to be independent of the level of expression of these proteins on the tumor tissue (37). These parameters have no detectable influence on apoptosis, phagocytosis, or ADCC (13). By contrast, the present study is the first to show that rituximab-mediated ADCC is dependent on the allotypic form of FcyRIIIa expressed by NK cells. Therefore, variability at both the tumor cell level and the patient’s immune system level may influence the response to rituximab, in addition to the tumor burden at the time of treatment (10) and rituximab concentrations obtained in patients (8, 38).

In agreement with results obtained with Raji and WIL-2-S B-cell lines (39, 40), lysis of Duadi cells was detected with concentration around 0.0001 μg/ml rituximab and reached a maximum at around 0.1 μg/ml, whatever the genotype. The difference in the cytotoxic response between VV and FF NK cells was observed over the 0–0.02 μg/ml range. On the other hand, serum rituximab concentrations observed in vivo range from around 1000 μg/ml for peak concentrations to around 20 μg/ml several weeks after ending the infusions (38, 41), raising the question of the clinical relevance of our in vitro result. However, rituximab concentrations at the site of action (mainly in lymphadenopathies) may be different from those measured in the blood. In addition, for antitumor agents, the duration of drug exposure above a defined threshold concentration is sometimes more important than the extent of the exposure (42, 43). Using the data presented by Bernstein et al. (38), it can be calculated that responders have a longer half-life than nonresponders (12 versus 8 days) and that the former group has been exposed to concentrations above 0.0001 μg/ml (i.e., the concentration at which ADCC was detected in vitro) during 20 months versus 13 months for nonresponders. It has also been reported that some NHL patients have delayed clinical response (between day 78 and month 12 after rituximab infusion; Ref. 10). This observation shows that long-lasting effector mechanisms are involved in the therapeutical effect of rituximab and suggests that the difference between VV and FF NK cells observed in our in vitro model may be clinically relevant. Thus, the present study supports the conclusion that the FCGRA3A genotype is associated with the therapeutical action of rituximab because it affects the relationship between rituximab concentration and B-cell lysis by NK cells. The consequence of the present findings is that rituximab dose or administration schedule may be adjusted in FF patients to ensure a longer exposure to effective concentrations to obtain a better clinical response. More generally, such a pharmacogenetic approach has to be taken into account to improve therapeutic efficacy of cytolytic mAbs in addition to methods that have been shown to enhance NK cell response to tumor cells, such as engineering the Fc portion to increase mAb binding to FcγRIIa (32, 44) or stimulating NK cells by cytokines (35, 45, 46).

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