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Research Paper

Galactosylation and Sialylation Levels of IgG Predict Relapse in Patients With PR3-ANCA Associated Vasculitis

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ABSTRACT

Objective: The objective of our study is to investigate the Fc glycosylation profiles of both antigen-specific IgG targeted against proteinase 3 (PR3-ANCA) and total IgG as prognostic markers of relapse in patients with Granulomatosis with Polyangiitis (GPA).
Methods: Seventy-five patients with GPA and a PR3-ANCA rise during follow-up were included, of whom 43 patients relapsed within a median period of 8 (2–16) months. The N-glycan at Asn297 of affinity-purified and denatured total IgG and PR3-ANCA was determined by mass spectrometry of glycopeptides in samples obtained at the time of the PR3-ANCA rise and at the time of the relapse or time-matched during remission.
Results: Patients with total IgG1 exhibiting low galactosylation or low sialylation were highly prone to relapse after an ANCA rise (HR 3.46 [95%-CI 1.73–6.96], $p < 0.0001$ and HR 3.22 [95%-CI 1.52–6.83], $p = 0.002$, respectively). In relapsing patients, total IgG1 galactosylation, sialylation and bisection significantly decreased and fucosylation significantly increased from the time of the PR3-ANCA rise to the relapse ($p < 0.0001$, $p = 0.0087$, $p < 0.0001$ and $p = 0.0025$), while the glycosylation profile remained similar in non-relapsing patients. PR3-ANCA IgG1 galactosylation, sialylation and fucosylation of PR3-ANCA IgG1 decreased in relapsing patients ($p = 0.0073$, $p = 0.0049$ and $p = 0.0205$), but also in non-relapsing patients ($p = 0.0007$, $p = 0.0114$ and $p = 0.0002$), while bisection increased only in non-relapsing patients ($p < 0.0001$).
Conclusion: While Fc glycosylation profiles have been associated with clinically manifest autoimmune diseases, in the present study we show that low galactosylation and sialyation in total IgG1 but not PR3-ANCA IgG1 predicts disease reactivation in patients with GPA who experience an ANCA rise during follow-up. We postulate that glycosylation profiles may be useful in pre-emptive therapy studies using ANCA rises as guideline.

1. Introduction

Granulomatosis with Polyangiitis (GPA; Wegener's), Microscopic Polyangiitis (MPA) and Eosinophilic Granulomatosis with Polyangiitis (EGPA; Churg Strauss Syndrome) are inflammatory disease entities affecting small to medium vessels. They are characterized by the presence of anti-neutrophil cytoplasmic antibodies (ANCA) against proteinase-3 (PR3) or myeloperoxidase (MPO) and are frequently grouped together under the term ANCA-associated vasculitis (AAV) (Wilde et al., 2011).

The pathogenic potential of ANCA to cause necrotizing glomerulonephritis (NCGN) is well established in mouse models (Xiao et al., 2002; Little et al., 2012; Huugen et al., 2005). Patients with severe NCGN are almost always positive for either PR3- or MPO-ANCA, (Tervaert et al., 1990) while ANCA are less often detected in patients with localized forms of vasculitis (Nolle et al., 1989; Cohen Tervaert and Damoiseaux, 2012). After remission induction, a rise in the ANCA titer is detected in some patients and disease reactivation may occur shortly thereafter (Cohen Tervaert et al., 1989). However, the relation between longitudinal ANCA measurements and disease reactivation is far from absolute since many ANCA rises are not followed by a relapse and relapses may occur without a preceding ANCA rise (Boomsma et al., 2000; Birck et al., 2006). Recently, it has been shown that ANCA rises are highly predictive for disease activity in patients with severe vasculitic disease, e.g. NCGN or alveolar hemorrhage, but not in patients with limited granulomatous disease

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(Kemna et al., 2015; Fussner et al., 2016; Koh et al., 2016; Yamaguchi et al., 2015). Our current hypothesis is that the pathogenicity of an ANCA rise is modulated by the quality of the auto-antibody, for which the glycosylation profile is an important factor.

The glycosylation profile of the crystallizable fragment (Fc) of the immunoglobulin G (IgG) is characterized by a single N-linked glycan attached to each heavy chain at the asparagine-297 (Anthony et al., 2012). The Fc N-glycan composition affects Fcγ receptor (FcγR) affinity (Anthony et al., 2012; Brady et al., 2015; Subedi and Barb, 2016; Thomann et al., 2015) and can influence complement activation (Malhotra et al., 1995). The lack of a core fucose, *N*-acetylneuraminic (sialic) acids and galactose residues on the Fc N-glycan have been found to increase the inflammatory capacity of IgG, at least in mice (Anthony and Nimmerjahn, 2011; Karsten et al., 2012; Kaneko et al., 2006). The Fc N-glycan is essential for the pathogenicity of the antibody, since deglycosylation of MPO-ANCA significantly attenuates ANCA-mediated neutrophil activation and reduces glomerular crescent formation in a mouse model (van Timmeren et al., 2010).

Already in the early eighties, it was recognized that total IgG in patients with rheumatoid arthritis (RA) contained less galactose and sialic acid at the non-reducing termini compared to healthy controls (Parekh et al., 1985). A difference in the glycosylation profile of total IgG has since been demonstrated in patients with various other auto-immune diseases when compared to healthy controls, including systemic lupus erythematosus, inflammatory bowel disease, myasthenic gravis, ankylosing spondylitis, primary Sjögren's syndrome, psoriatic arthritis and multiple sclerosis (Watson et al., 1999; Wuhrer et al., 2015a; Vuckovic et al., 2015; Trbojevic Akmacic et al., 2015; Selman et al., 2011). Furthermore, significant differences have been observed in the glycosylation profile of total IgG and specific auto-antibodies, such as anti-citrullinated protein antibodies (ACPA), anti-β2GP1 and anti-histone IgG (Scherer et al., 2010; Rombouts et al., 2015; Magorivska et al., 2016; Fickentscher et al., 2015). Finally, Fc glycosylation of auto-antibodies may change during disease development. For example, the glycosylation profile of ACPA changes prior to the onset of RA towards a more inflammation-associated phenotype (Rombouts et al., 2015; Ercan et al., 2010).

In patients with PR3-ANCA, it was previously shown with lectin assays that total IgG exhibits a lower degree of galactosylation when compared to healthy controls (Holland et al., 1760, 2002). In addition, the degree of sialylation of PR3-ANCA is lower during active disease compared to inactive disease (Espy et al., 2011). Recently, it has been shown with mass spectrometric IgG Fc glycosylation analysis that total IgG Fc of patients with severe AAV exhibits lower levels of galactosylation, sialylation and bisecting *N*-acetylglucosamine (GlcNAc) compared to healthy controls (Wuhrer et al., 2015b). This finding was more pronounced for PR3-ANCA compared to total IgG (Wuhrer et al., 2015b). Correlations were observed between the glycosylation profile of PR3-ANCA and several cytokine concentrations, suggesting that the glycosylation of ANCA may be driven by T-cell activation in an antigen-specific manner (Wuhrer et al., 2015b). Potential differences and similarities in the glycosylation profile of total IgG and antigen-specific IgG between patients with PR3-ANCA and patients with MPO-ANCA associated vasculitis have not yet been investigated.

The objective of our study is to investigate differences in the glycosylation profile of both PR3-ANCA and total IgG and the prognostic value at the time of a rise in PR3-ANCA in patients with GPA. The primary question is whether patients with a particular glycosylation profile are more prone to relapse. Furthermore, upon an ANCA rise, changes in glycosylation profiles associated with a relapse are examined. To increase the homogeneity of our cohort, we included only GPA patients that are PR3-ANCA positive, the disease subgroup that is most prevalent in our area.

2. Materials and Methods

2.1. Inclusion Criteria

All patients who visited the clinic at the Maastricht University Medical Center (MUMC) between January 1, 2000 and November 1, 2011 were evaluated. Inclusion criteria were a diagnosis of GPA according to the EMA classification system and a rise in PR3-ANCA during remission (Kemna et al., 2015; Hellmich et al., 2007; Watts et al., 2007).

Clinical characteristics were recorded in all subjects according to the Dutch law on Medical Treatment Act (WGBO), the Personal Data Protection Act (Wbp) and the Code of Conduct for Health Research (Federa) (Central Committee on Research Involving Human Subjects, 2013). Ethics approval was waived by our local ethics committee.

2.2. Classification of Patients

Renal involvement was preferably determined by a kidney biopsy showing pauci-immune necrotizing glomerulonephritis (Berden et al., 2010; Hilhorst et al., 2013). However, surrogate markers such as haematuria in combination with red cell casts, dysmorphic erythrocytes (>10) and/or proteinuria sufficed (Watts et al., 2007). All patients have been treated according to the European League against Rheumatism (EULAR) guidelines (Hilhorst et al., 2013; Mukhtyar et al., 2009).

The definitions recommended by the EULAR of 2007 were applied to define disease activity states (Hellmich et al., 2007). Remission was defined as absence of disease activity attributable to active disease during maintenance immunosuppressive therapy of a prednisone dosage of 7.5 mg or lower. A relapse was defined as re-occurrence or new onset of disease attributable to active disease combined with an increase or addition of immunosuppressive treatment. Relapses were further subdivided in “major” or “minor” depending on whether the relapse was potentially organ- or life-threatening or not (Hellmich et al., 2007).

2.3. ANCA Measurements

Patients were routinely evaluated during follow-up, generally every three months during the first two years after diagnosis and/or a relapse and 2–3 per year later on. At every visit, patients were screened for potential symptoms of a relapse (Hellmich et al., 2007) and blood was drawn.

Antigen-specific solid-phase ANCA tests were performed for the detection and quantification of PR3-ANCA. Initially, commercially available direct PR3-ANCA enzyme linked immunosorbent assays (ELISA) were used (Euro Diagnostica, Malmö, Sweden) (Boomsma et al., 2003). On October 1, 2005, this assay was replaced by a fluorescent-enzyme immune-assay (FEIA) for PR3-ANCA (EliA, Thermo Fisher, Freiburg, Germany) (Damoiseaux et al., 2005). During the transition, ANCA measurements were performed using both methods.

2.4. Definition of an ANCA Rise

For the detection of an ANCA rise, the ANCA titer was compared to all measurements made with the same assay in the past 6 months. We defined a rise using the slope of an increase as previously described (Kemna et al., 2015), thereby taking into account the relative increase (in %) and the time between measurements (in days). A receiver operating characteristics (ROC) curve was calculated to determine the optimal cut-off value of the slope. The chosen cut-off values as determined by the ELISA and FEIA method were 2.56 and 2.25%/day, respectively. This is equivalent to a relative increase of 78% and 68% over one month or 233% and 205% over three months.

To ensure that small elevations were above the intra-assay coefficient of variation, a rise had to constitute to a relative increase of at least 25% and an absolute increase equivalent to a doubling of the lowest value of a borderline result (at least 10 AU for the ELISA and 5 U/ml for

the FEIA). Because our analysis is focused on patients in remission, only serum samples drawn at least 3 months after the previous disease activity were eligible for detection of an ANCA rise (Kemna et al., 2015).

2.5. Serum Selection

In all 75 patients, a serum sample was selected at the time of an ANCA rise ('T1') (Kemna et al., 2015). In relapsing patients, either renal or non-renal, a second serum sample was selected prior to the start of the immunosuppressive induction therapy at the time of the relapse ('T2rel'). In non-relapsing patients, a second serum sample was selected after the ANCA rise during remission ('T2rem'), of which the time between the first and second sample was matched with the time between the first and second sample in the renal relapsing patients. For 4 relapsing patients no serum sample was available at the time of the relapse, and therefore only 71 T2 serum samples were analyzed.

2.6. Total IgG Purification

For total IgG purification, the wells of two filter plates (Multiscreen filter plates with Durapore membrane, pore size 0.65 μm; Merck Millipore, Darmstadt, Germany) were filled with 15 μl of Protein G Sepharose 4 Fast Flow beads (GE Healthcare, Uppsala, Sweden) in 200 μl PBS, followed by the addition of 2 μl of the serum samples. Furthermore, 10 of the serum samples were purified in duplicate. Fifteen wells were filled with 2 μl Milli-Q-purified water to serve as negative control and 20 wells were filled with 2 μl of the serum of a healthy donor to serve as positive control. The plates were incubated on a shaker at room temperature for 1 h. The samples were then washed on a vacuum manifold with 4 × 200 μl PBS and 3 × 200 μl Milli-Q-purified water, followed by the addition of 100 μl 100 mM formic acid (Fluka, Steinheim, Germany) for elution into a V-bottom 96-well plate (Greiner Bio-One, Frickenhausen, Germany), which has been shown to result in near-complete denaturation of IgG (Falck et al., 2015). Eluates were dried in a centrifugal vacuum concentrator (Eppendorf, Hamburg, Germany) at 60 °C for approximately 2 h.

2.7. PR3-ANCA Purification

An ELISA kit (Wieslab PR3-ANCA; Euro Diagnostica) was used for purification of PR3-ANCA. 80 μl diluent containing PBS (Wieslab kit) and 20 μl of the serum samples were added to two PR3-coated 96-well plates. Ten of the serum samples were purified in duplicate in separate wells. Fifteen wells were filled with 20 μl Milli-Q-purified water to serve as negative control and 20 wells were filled with 20 μl of the serum of a healthy donor to serve as a further negative control. The samples were incubated on a shaker at room temperature for 1 h, followed by washing 4× with 250 μl wash buffer (Wieslab kit) and 1× with 150 μl 50 mM ammonium bicarbonate buffer (Sigma-Aldrich, St. Louis, MO). The PR3-ANCA was eluted by adding 100 μl 100 mM formic acid to the wells and collected into a V-bottom 96-well plate. The samples were then dried in a centrifugal vacuum concentrator at 60 °C for approximately 2 h.

2.8. Trypsin Digestion

The dried total IgG and PR3-ANCA samples were resuspended in 20 μl 50 mM ammonium bicarbonate and incubated on a shaker at room temperature for 15 min. 20 μl of 0.01 μg/μl trypsin (sequencing grade modified trypsin, Promega, Madison, WI) was then added to each well. The samples were again incubated on a shaker at room temperature for 15 min, followed by overnight incubation at 37 °C. Samples were stored at −20 °C.

2.9. LC-MS/MS Analysis

The digested samples were analyzed by nanoLC-reversed phase (RP)-electrospray ionization (ESI) – quadrupole time-of-flight (qTOF)-MS on an Ultimate 3000 HPLC system (Dionex/Thermo Scientific, Sunnyvale, CA) coupled to a MaXis Impact (Bruker Daltonics, Bremen, Germany). The samples were concentrated on a Dionex Acclaim PepMap100 C18 trap column (particle size 5 μm, internal diameter 300 μm, length 5 mm) and separated on an Ascentis Express C18 nano column (2.7 μm HALO fused core particles, internal diameter 75 μm, length 50 mm; Supelco, Bellefonte, PA). The following linear gradient was applied, with solvent A consisting of 0.1% trifluoroacetic acid (TFA; Fluka) and solvent B of 95% acetonitrile (Biosolve, Valkenswaard, The Netherlands): t = 0 min, 3% solvent B; t = 2, 6%; t = 4.5, 18%; t = 5, 30%; t = 7, 30%; t = 8, 1%; t = 10.9, 1%. The sample was ionized in positive ion mode with a CaptiveSprayer (Bruker Daltonics) at 1100 V. A nanoBooster (Bruker Daltonics) was used to enrich the nitrogen gas with acetonitrile to enhance the ionization efficacy. A mass spectrum was acquired every second (frequency of 1 Hz), with the ion detection window set at *m/z* 550–1800. In between every 12 measurements an external IgG standard was run. A mass spectrum of both total IgG and PR3-ANCA can be seen in Fig. 1.

2.10. Data Processing

Mass spectrometric identification and processing of tryptic IgG glycopeptide data was done as described previously (Selman et al., 2012), with a few differences as stated below, and was performed blindly in order to prevent bias. The LC-MS data files were examined in Compass DataAnalysis 4.2 software (Bruker Daltonics). Negative controls were inspected and found to contain no significant intensity of IgG signals.

First, the *m/z* axis of the mass spectra was calibrated internally using several known IgG glycopeptides masses. Next, the files were converted to the .mzXML data format using the MSconvert program from the ProteoWizard 3.0 suite (Chambers et al., 2012). The *m/z* and retention times of all the tryptic IgG glycopeptides were manually determined using MZmine version 2.10 (Pluskal et al., 2010) and can be found in Supplemental Table 1. The time axes were aligned based on a list of the most prominent IgG glycopeptide peaks and their retention times, using an alignment tool designed in-house (Plomp et al., 2015). The intensity of the first three isotopes of every analyte was extracted using a window of ± 0.04 Thomson and ± 10 s around the manually determined retention time. This was achieved using the in-house developed 3D Total Extractor (3DTE) program (software code can be found in the Supplemental data). A list of analytes is provided to 3DTE, which then uses a binary search to find the retention time and mass region around each analyte. Afterwards, the maximum intensity of each analyte is determined per mass spectrum that falls within the retention time window. The value that is reported for each analyte by 3DTE is the sum of the highest intensity values from the individual mass spectra. Lastly, the program generates a tab-separated output file that lists all the compositions and their respective total intensities. Background correction was optimized to minimize intensity biases in the determination of glycopeptide ratios. In Excel 14.0, the background-corrected signal intensities of the three isotopic peaks in both 2+ and 3+ charge state were summed to obtain a single value for each glycopeptide. IgG1 G2 and G2S2 were excluded because of overlap with contaminant peaks. Isotopic peaks for several other IgG1 glycopeptides were also excluded due to peak overlap, and these values were replaced by an estimate based on the remaining isotopic peaks and the theoretical isotopic pattern (these isotopic peaks account for <3% of the total glycopeptide signal intensity). Afucosylated IgG4 glycopeptides were excluded due to peak overlap with IgG1 glycopeptides. In order to obtain a percentage value for each glycopeptide, this value was then divided by the sum of all signal intensities of glycopeptides, and this was done separately for IgG1, IgG2/3 and IgG4. In Caucasian populations the tryptic glycopeptide of IgG3 generally has the same peptide sequence as IgG2 (Zauner et al., 2013). Therefore it was not possible to distinguish between IgG2 and IgG3 glycopeptides with the methods we used, and these glycopeptides will be referred to as IgG2/3. The IgG percentage data can be seen in

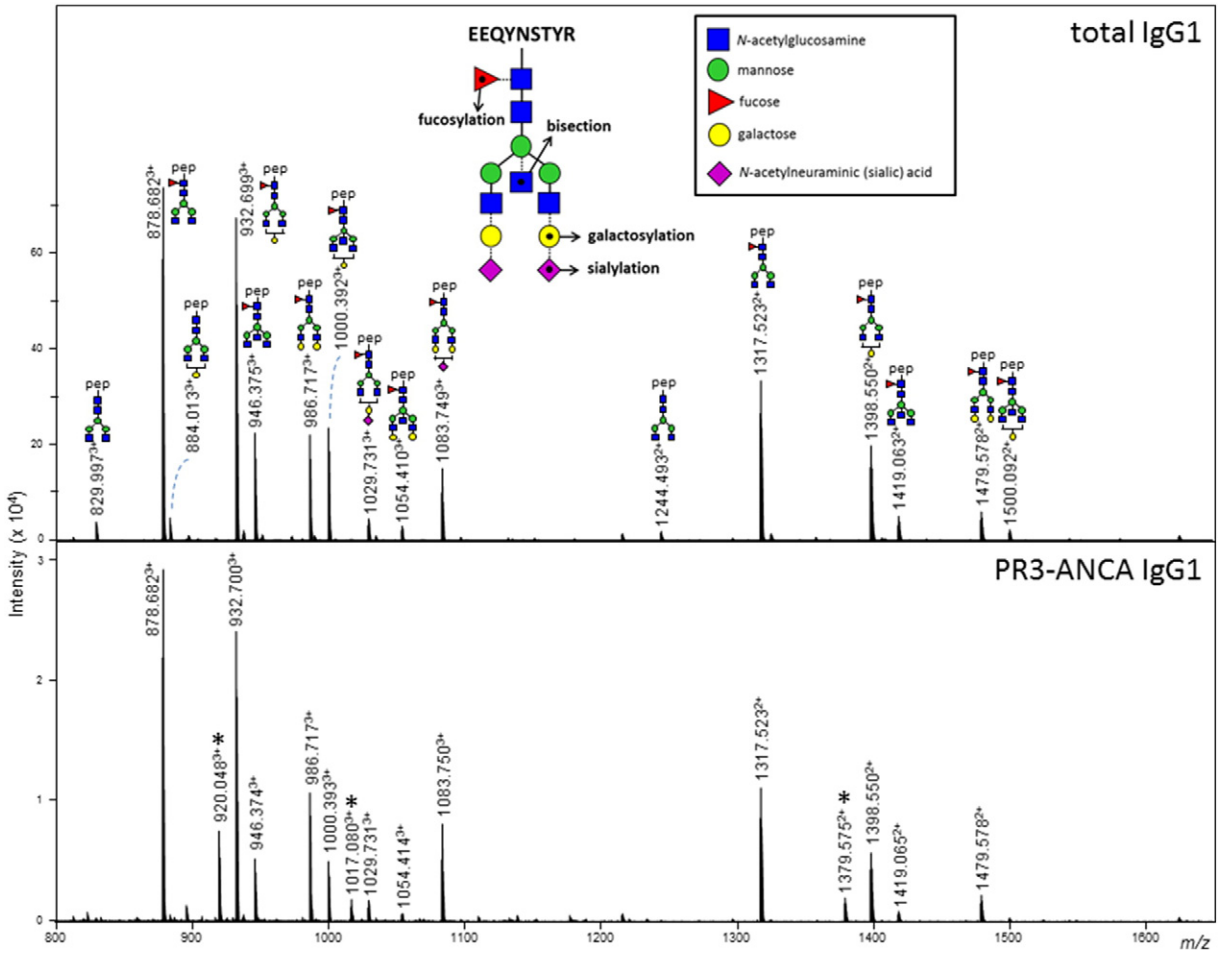

Fig. 1. LC-MS spectra showing tryptic IgG1 glycopeptides for total IgG and PR3-ANCA belonging to an AAV patient (#9; details in Supplemental Table 1) at the time of relapse. The peaks denoted with an asterisk belong to a co-enriched contaminant (an apolipoprotein *O*-glycopeptide). Pep = peptide.

Supplemental Table 2. Several glycosylation features were calculated from this data: fucosylation (% of glycans bearing a core fucose), bisection (% of glycans with a bisecting GlcNAc), galactosylation (% of antennae carrying a galactose) and sialylation (% of antennae carrying a sialic acid, see Supplemental data for the exact definitions).

In order to guard the quality of the acquired data, an intensity threshold was set. If the sum of the signal intensities of G0F, G1F and G2F in triple charge state for an IgG subclass did not exceed this threshold, all data for that subclass was excluded. Additionally, data was excluded if the signal/background of the highest peak per subclass did not exceed 20. Finally, because of the chance of overlap between IgG4 glycopeptide peaks and later eluting IgG2/3 peaks, IgG2/3 data was excluded if more IgG4 was present than IgG2/3 (as determined by G0F + G1F + G2F (3+) signals). Lastly, we determined the average relative standard deviation (RSD) of eight prominent glycans (G0F, G1F, G2F, G0FN, G1FN, G2FN, G1FS and G2FS) to further examine the quality of the data.

2.11. Statistical Analysis

Numerical variables were expressed as median (interquartile range [IQR]) and categorical variables as relative abundances (percentages). Two unpaired variables were compared with the Mann Whitney *U* test. Two paired variables were compared with the Wilcoxon signed rank test.

Receiver operating characteristic (ROC) curves were constructed for galactosylation, sialylation, fucosylation and bisection at the time of an ANCA rise to discriminate relapsing patients from patients who remained in remission. If a trend towards significance was observed in an ROC curve, an optimal cut-off value was derived that was closest to the upper left corner (the cut-off value with the highest sum of sensitivity and specificity). Patients were subsequently categorized as high (above or equal to the cut-off) or low (below cut-off) level for the concerning glycosylation trait. Differences in the time to relapse between high and low were assessed using the log-rank test. The time to relapse was estimated using the Kaplan-Meier method. An event was defined as a relapse at the time of the start or increase of immunosuppressive treatment. Subjects were censored at the time of last follow-up. Hazard ratios (HR) with the 95% confidence interval were derived using the Cox regression analysis, adjusted for age and sex. The proportional hazards assumption was assessed by visually inspecting log-log plots.

All statistical analyses were performed using GraphPad Prism version 6.04 for Windows (GraphPad Software, La Jolla, California, USA) and SPSS statistics for Windows, version 23.0 (IBM, Armonk, NY, USA). Bonferroni corrections were applied to the statistical testing, in which a p-value of <0.0125 was considered significant and <0.05 was considered as a trend.

3. Results

3.1. Patient Characteristics

Seventy-five patients with Granulomatosis with Polyangiitis positive for PR3-ANCA were included in this study, of whom 51 patients had

renal involvement in the past and 24 patients did not (see Table 1). Forty-three (57.3%) patients relapsed within a median time of 8 (2–16) months since the ANCA rise.

Out of 156 samples total (75 at the time of ANCA rise, 71 at a second time point, and 10 duplicates), PR3-ANCA IgG1 data was excluded in 16 samples, total IgG1 data in 0 samples, total IgG2/3 data in 14 samples and total IgG4 in 20 samples. Because the signal intensity of PR3-ANCA IgG2/3 and IgG4 in the majority of samples did not surpass the threshold, we excluded this data group altogether. For 8 prominent glycoforms, the external IgG standard run in between every 12 measurements showed an average RSD of 4.2% for IgG1, 4.0% for IgG2/3 and 7.1% for IgG4. The on-plate healthy donor serum-derived total IgG samples exhibited an average RSD of 4.0% for IgG1, 3.0% for IgG2/3 and 3.5% for IgG4. Finally, for the aforementioned 8 glycoforms, the 10 ANCA serum samples which were processed in duplicate showed an average RSD of 2.3%, 1.5% and 1.3% for total IgG1, IgG2/3 and IgG4, and 3.1% for PR3-ANCA IgG1. Two LC-MS spectra of total IgG and PR3-ANCA IgG, belonging to an AAV patient at the time of relapse, can be seen in Fig. 1.

For better readability, the results of total IgG1 and PR3-ANCA IgG1 are presented in the manuscript, while the results of total IgG2/3 and total IgG4, which exhibit the same general trend as total IgG1, can be found in the Supplemental data.

Table 1
Patient characteristics. The organ involvement refers the organ involvement during any previous periods of disease activity in the past (at the diagnosis or any previous relapse). The induction treatment refers to the treatment regimen that was used to induce remission during the most recent period of disease activity only.

	Renal		Non-renal	
	Relapse (n = 31)	Remission (n = 20)	Relapse (n = 12)	Remission (n = 12)
Demographics				
Age (in years + SD)	58.2 (14.5)	54.7 (14.2)	58.1 (9.0)	66.2 (11.3)
Male	23 (74.2%)	13 (65%)	6 (50%)	4 (33.3%)
Organ involvement at previous disease activities				
Arthralgia	19 (61.3%)	10 (50%)	7 (58.3%)	5 (41.7%)
Cutaneous	13 (41.9%)	3 (15%)	2 (16.7%)	0 (0%)
Eyes	8 (25.8%)	5 (25%)	3 (25%)	3 (25%)
Ear, nose, throat	26 (83.4%)	17 (85%)	10 (83.3%)	11 (91.7%)
Lung	23 (74.2%)	14 (70%)	10 (83.3%)	10 (83.3%)
Cardiovascular	1 (3.2%)	2 (10%)	0 (0%)	0 (0%)
Renal	31 (100%)	20 (100%)	0 (0%)	0 (0%)
Central nervous system	1 (3.2%)	0 (0%)	0 (0%)	1 (8.3%)
Peripheral nervous system	7 (22.6%)	4 (20%)	1 (8.3%)	2 (16.7%)
Induction treatment at previous disease activity resulting in remission				
Cyclophosphamide + GC	19 (61.3%)	14 (70%)	6 (50%)	10 (83.3%)
Rituximab + GC	1 (3.2%)	3 (15%)	0 (0%)	0 (0%)
Methothrexate + GC	5 (16.1%)	0 (0%)	4 (33.3%)	1 (8.3%)
Mofetil mycophenolate + GC	3 (9.7%)	3 (15%)	0 (0%)	0 (0%)
Gusperimus + GC	2 (6.4%)	0 (0%)	1 (8.3%)	0 (0%)
GC monotherapy	1 (3.2%)[a]	0 (0%)	1 (8.3%)	1 (8.3%)
Immunosuppressive therapy at the time of the ANCA rise				
Immunosuppressive therapy	27 (87.1%)	16 (80%)	8 (66.7%)	8 (66.7%)
None	4 (12.9%)	4 (20%)	4 (33.3%)	4 (33.3%)
Follow-up				
Follow-up time (in months + SD)[b]	12.9 (20.4)	42.0 (20.8)	13.9 (16.1)	45.6 (35.3)
Persistently ANCA positive	10 (32.3%)	6 (30%)	2 (16.7%)	3 (25%)
Relapse				
Major	18 (58.1%)	–	4 (33.3%)	–
Minor	13 (41.9%)	–	8 (66.7%)	–

Abbreviations: SD, standard deviation. GC, glucocorticosteroid therapy.
[a] This patient was included after a minor relapse which was treated with GC monotherapy, while remission was induced after diagnosis using cyclophosphamide + GC.
[b] The follow-up time refers to the time from the most recent disease activity to the endpoint of the study (at the time of relapse or at the last time of follow-up).

3.2. IgG1 Fc Glycosylation of Total IgG and PR3-ANCA at the Time of the ANCA Rise

At the time of the ANCA rise, we analyzed whether there were differences in the glycosylation profile of total IgG1 and PR3-ANCA IgG1. The degree of galactosylation, sialylation and fucosylation of total IgG1 was lower compared to PR3-ANCA IgG1 (46.0% [39.1–49.7%] versus 47.4% [40.4–57.5%], $p = 0.0175$; 6.2% [5.2–7.1%] versus 6.9 [5.1–9.0%]; $p = 0.0289$ and 93.3% [89.9–95.5%] versus 98.4% [97.3–99.0%], $p < 0.0001$, respectively). In contrast, the level of bisection of total IgG1 was higher compared to PR3-ANCA IgG1 (19.0 [15.9–21.7%] versus 11.4% [10.1–13.9%], $p < 0.0001$, see Fig. S1 in the Supplemental data).

3.3. IgG1 Fc Glycosylation as a Predictor of a Relapse at the Time of an ANCA Rise

Thereafter, we investigated whether patients with a particular IgG1 Fc glycosylation profile at the time of an ANCA rise are more prone to relapse after an ANCA rise. The ROC curve of total IgG1 galactosylation and sialylation were found to differentiate relapsing patients from non-relapsing patients (Supplemental Fig. S2; AUC 0.6533, $p = 0.02385$ and AUC 0.6563, $p = 0.02131$, respectively). Total IgG1 bisection and fucosylation did not yield significant discrimination between relapsing and non-relapsing patients ($p = 0.9488$ and $p = 0.9402$, respectively; data not shown). The ROC curve of PR3-ANCA IgG1 was not significant for any of the glycosylation traits (data not shown). An optimal cut-off value was derived from the significant ROC curves, and patients were classified as 'low galactosylation' if the galactosylation rate of total IgG1 was lower than 46.1% and as 'low sialylation' if the sialylation rate of total IgG1 was lower than 6.9% (see Fig. S2 in the Supplemental data).

Forty-one of 75 (54.7%) patients were classified as low galactosylation, of whom 30 (73.2%) patients relapsed within a median of 6 (1–15) months after the ANCA rise. In comparison, only 13 of 34 (38.2%) patients who were classified as high galactosylation relapsed in a median of 10 (2.5–17.5) months. Thus, patients with low galactosylation total IgG1 were highly prone to relapse after an ANCA rise (HR 3.46 [95%-CI 1.73–6.96], $p < 0.0001$, adjusted for age and sex, see Fig. 2a).

Similar results were found for the degree of sialylation. Forty-seven of 75 (62.7%) patients were classified as low sialylation, of whom 34 (72.3%) patients relapsed within a median of 8 (1–17) months after the ANCA rise. In comparison, only 9 of 28 (32.1%) patients with a high sialylation relapsed in a median of 7 (2−12) months. Low sialylation patients were highly prone to relapse after an ANCA rise (HR 3.22 [95%-CI 1.52–6.83], $p = 0.002$, adjusted for age and sex; see Fig. 2b).

Because the degree of sialylation and galactosylation are highly correlated (terminal *N*-acetylneuraminic acid is attached to galactose), we in addition calculated the sialic acid per galactose. No association was observed between the sialic acid per galactose and the time to relapse (see Figs. S3 and S4 in the Supplemental data).

3.4. Changes in IgG1 Fc Glycosylation During Follow-up

Next, we looked at potential changes of the glycosylation profile during follow-up. With regards to the total IgG1, the degree of

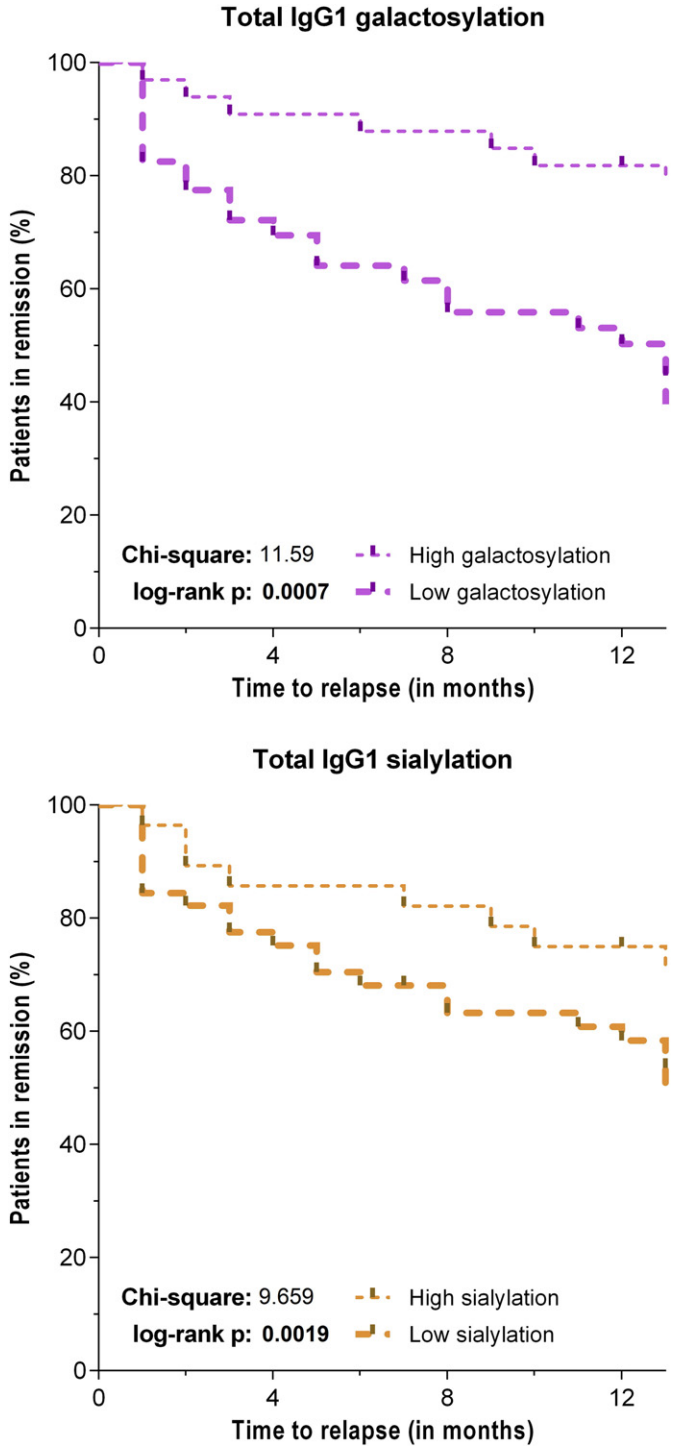

Fig. 2. Time to relapse after an ANCA rise, (a) according to the degree of galactosylation of total IgG 1 Fc and (b) according to the degree of sialylation of total IgG 1 Fc.

galactosylation, sialylation and bisection significantly decreased and fucosylation significantly increased in relapsing patients ($p < 0.0001$, $p = 0.0087$, $p < 0.0001$ and $p = 0.0025$, respectively), while the glycosylation profile remained similar in patients who remained in remission (see Figs. 3, S5 and S6 in the Supplemental data).

With regard to PR3-ANCA IgG1, in relapsing patients, a significant reduction in the degree of galactosylation and sialylation and a trend towards a reduction in fucosylation were observed from the ANCA rise to the time of the relapse ($p = 0.0073$, $p = 0.0049$ and $p = 0.0205$, respectively, see Fig. 4). Similarly, in patients who remained in remission, a significant reduction in the degree of galactosylation, sialylation and fucosylation was observed from the ANCA rise to the time of the second sample ($p = 0.0007$, $p = 0.0114$ and $p = 0.0002$, respectively). Moreover, the proportion of bisection of PR3-ANCA IgG1 significantly increased from the ANCA rise to the time-matched sample during remission ($p < 0.0001$).

3.5. IgG1 Fc Glycosylation at the Time of the Relapse or Time-matched During Remission

The changes in the glycosylation profile over time lead to significant differences between patients in relapse or in remission at the second time point. With regard to total IgG1, a significantly lower degree of galactosylation and sialylation and a trend towards a lower degree of bisection was observed in relapsing patients compared to patients who remain in remission ($p = 0.0015$, $p = 0.0120$ and $p = 0.0443$, respectively, see Figs. 5 and S7 in the Supplemental data). Conversely, the glycosylation profile of PR3-ANCA was only significantly different with regard to bisection, which was lower in relapsing patients compared to patients who remained in remission ($p = 0.0009$).

4. Discussion

In this study we investigate with mass spectrometry the changes in Fc glycosylation over time in both total IgG and PR3-ANCA of patients with AAV. In patients who were in clinical remission, a first serum sample was taken at the time of an ANCA rise, whereas a second sample was acquired either after relapse but before therapy was started, or for patients who remained in remission, after a similar length of time. Analysis of the two longitudinal samples revealed a significant reduction in galactosylation, sialylation and bisection and an increase in fucosylation in total IgG Fc of relapsing patients, while these glycosylation traits did not change significantly in patients who remain in remission. Most importantly, the Fc glycosylation profile of total IgG at the time of an ANCA rise predicts a relapse. Namely, patients with low galactosylation or low sialylation in total IgG are more prone to relapse compared to patients with high galactosylation or sialylation in total IgG. In addition, we observed that the level of sialylation and galactosylation of PR3-ANCA is decreased over time, both in relapsing and non-relapsing patients. Therefore, it appears that PR3-ANCA gains a more inflammation-associated phenotype during follow-up in both groups of patients, independent of disease course.

While IgG with a low degree of galactosylation has repeatedly been found to be associated with pro-inflammatory autoimmune responses, the underlying mechanisms are still largely elusive (Bondt et al., 2013; Matsumoto et al., 2000; Albrecht et al., 2014; Rademacher et al., 1994). In addition, highly galactosylated IgG may confer anti-inflammatory activities through the association with the inhibiting receptor FcγRIIb and the C-type lectin-like receptor Dectin-1 in mice (Karsten et al., 2012). This latter pathway has been shown to block C5a effector functions in vitro and C5a-dependent inflammatory responses in animal mouse models (Karsten et al., 2012). This is highly relevant in AAV, since C5a plays a pivotal role in the pathophysiology (Wilde et al., 2011; Hilhorst et al., 2015). Mouse models have shown that the blocking of C5a or C5a receptor (C5aR) ameliorates anti-MPO induced necrotizing glomerulonephritis (Xiao et al., 2014; Huugen et al., 2007). The safety and efficacy in the treatment of non-life-threatening AAV with CCX168, a C5aR inhibitor, is currently being tested in a phase 2 study (EudraCT Number: 2011-001222-15). The addition of galactose to the glycan structure also no longer enables the interaction of MBL with IgG, and may thereby block the lectin pathway (Malhotra et al., 1995). The clinical relevance of the lectin pathway in AAV is questionable however, since mannose-binding lectin (MBL) deposition in the kidney was found in only a minority of patients and complement activation in AAV occurs predominantly via the alternative pathway (Hilhorst et al., 2015).

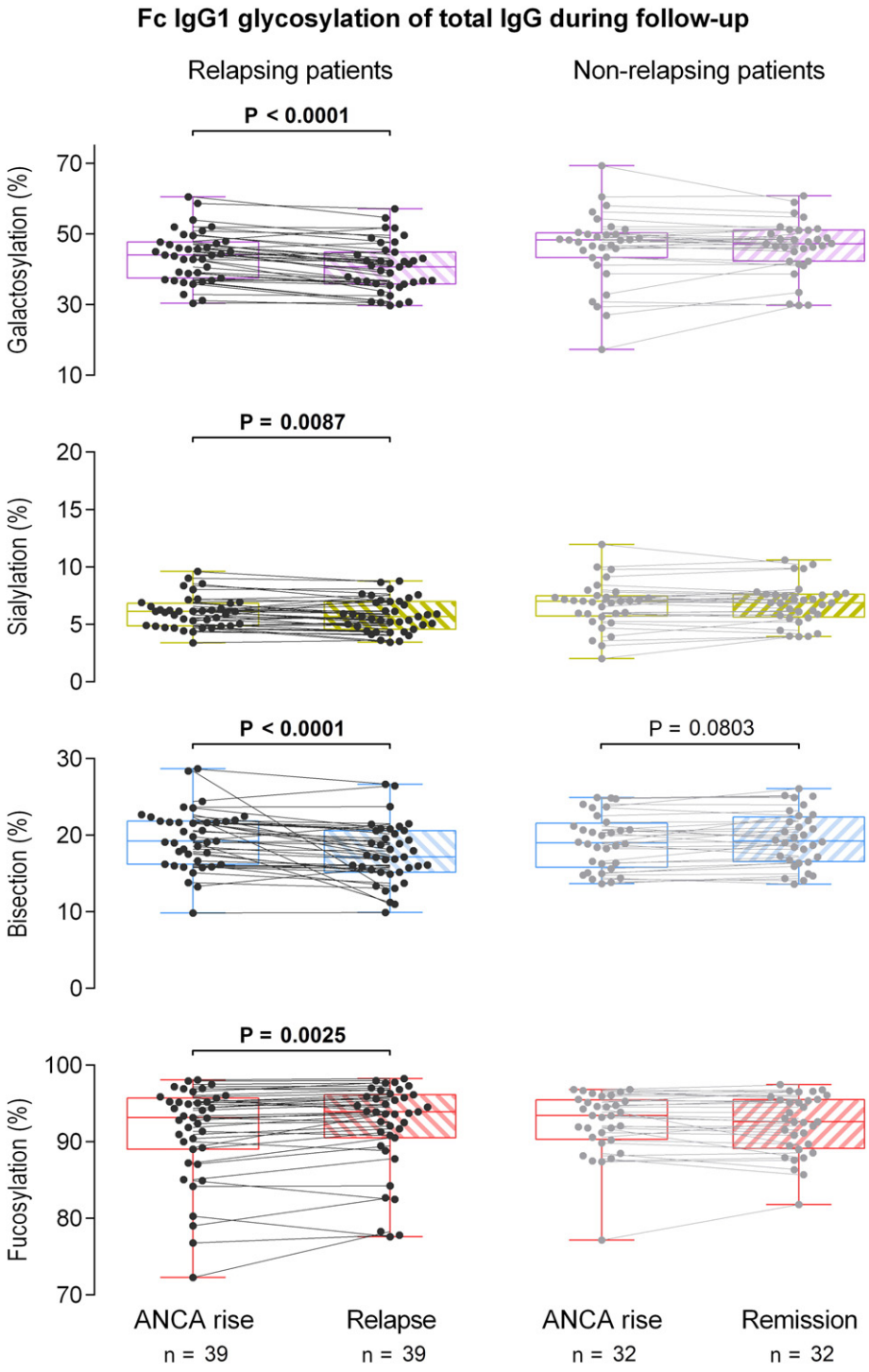

Fig. 3. The glycosylation profile of total IgG1 Fc at the time of an ANCA rise (T1) and at the time of a relapse (T2rel) in relapsing patients (black dots) and time-matched during remission (T2rem) in patients who remain in remission (gray dots). Dots represent individual patients, lines indicate corresponding pairs. The box represents the median with interquartile range, the whiskers delineate the min-max range. Significant differences were evaluated using the Wilcoxon signed rank test, p-values are shown if <0.10 and in bold if <0.0125.

Sialylated IgG has been reported to have anti-inflammatory properties likely mediated through interaction with the murine C-type lectin receptor SIGN-R1 (a homologue of the human DC-SIGN) and FcγRIIb (Kaneko et al., 2006; Collin and Ehlers, 2013). In our study, we found that total IgG preserved an anti-inflammatory glycosylation profile in patients who remained in remission, but changed to an inflammation-associated phenotype in relapsing patients. It remains unclear whether this change merely represent a bystander acute-phase reaction or whether the loss of anti-inflammatory effector function of total IgG enabled PR3-ANCA to induce disease reactivation. Notably, low galactosylation and sialylation at the ANCA rise predicts disease reactivation, suggesting that the change of total IgG towards an inflammation-associated phenotype precedes the onset of disease reactivation. We hypothesize that these anti-inflammatory mechanisms of total IgG are involved in the suppression of active disease in our AAV patients who remain in remission.

One may wonder what causes the change of the glycosylation profile of total IgG from an anti-inflammatory towards a pro-inflammatory phenotype. One study observed an average reduction of total IgG sialylation by 40% upon antigenic challenge in a mouse model

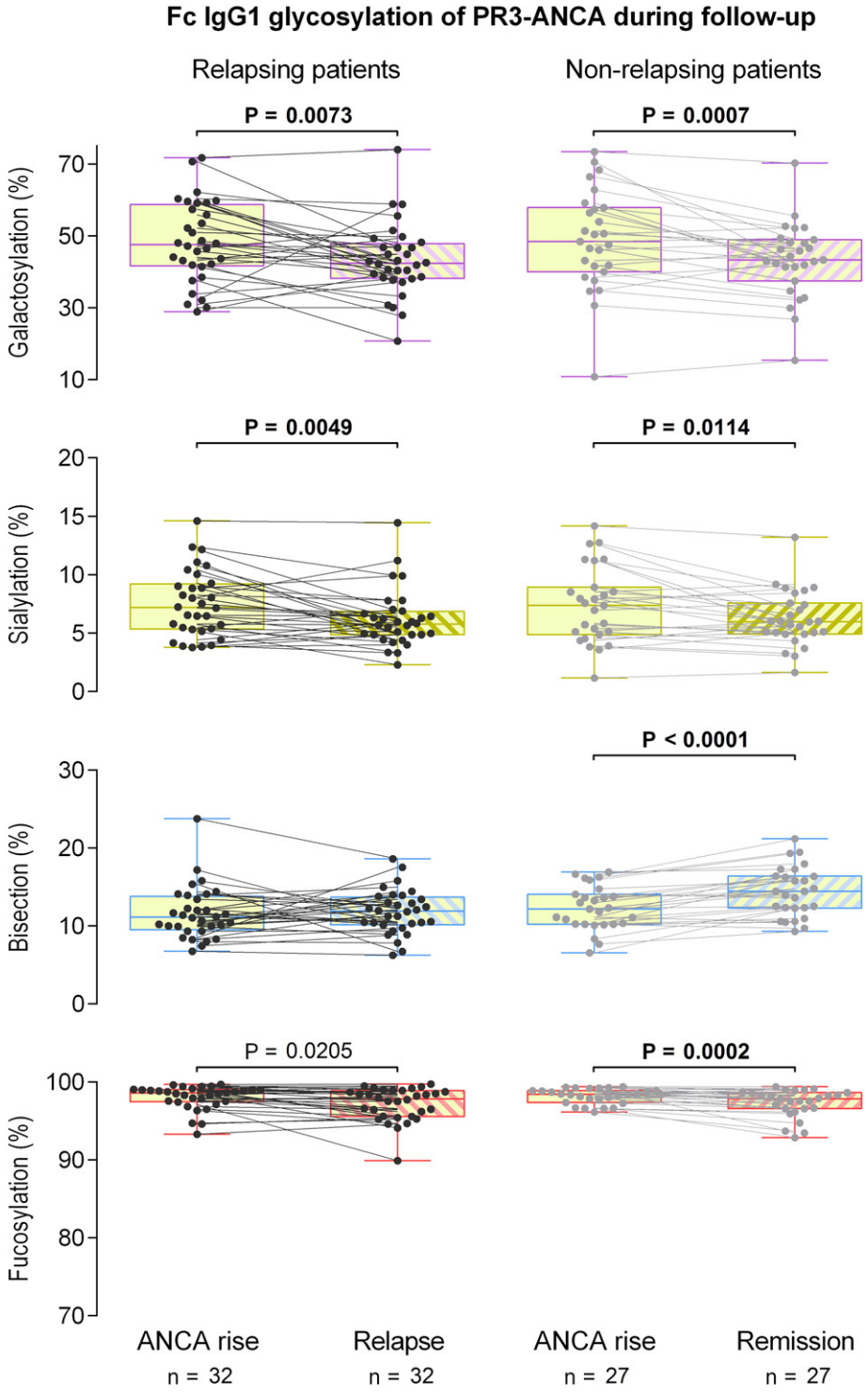

Fig. 4. The glycosylation profile of antigen specific PR3-ANCA IgG1 Fc at the time of an ANCA rise (T1) and at the time of a relapse (T2rel) in relapsing patients (black dots) and time-matched during remission (T2rem) in patients who remain in remission (gray dots). Dots represent individual patients, lines indicate corresponding pairs. The box represents the median with interquartile range, the whiskers delineate the min-max range. Significant differences were evaluated using the Wilcoxon signed rank test, p-values are shown if <0.10 and in bold if <0.0125.

(Kaneko et al., 2006). Based on our findings, we speculate that a second hit that is not related to the presence of PR3-ANCA nor the glycosylation profile of PR3-ANCA is required for a relapse after an ANCA rise (the "first hit"). Several candidates for such a second hit have been postulated, such as microorganisms (Popa et al., 2002), environmental factors (Gatenby et al., 2009; de Lind van Wijngaarden et al., 2008), and/or other auto-antibodies (Kain et al., 2012). No functional data are currently available regarding the role of the glycosylation profile of total IgG and/or antigen-specific IgG in the capacity of PR3-ANCA to induce inflammation and this should be further studied.

A recent study reported a novel correlation between bisection of PR3-ANCA and disease state (Wuhrer et al., 2015b). In our study we find a correlation between bisection and relapse/remission. The level of bisection of total IgG decreases significantly in relapsing patients, while it stays stable in non-relapsing patients. In PR3-ANCA the level of bisection remains stable in relapsing patients, while it increases in

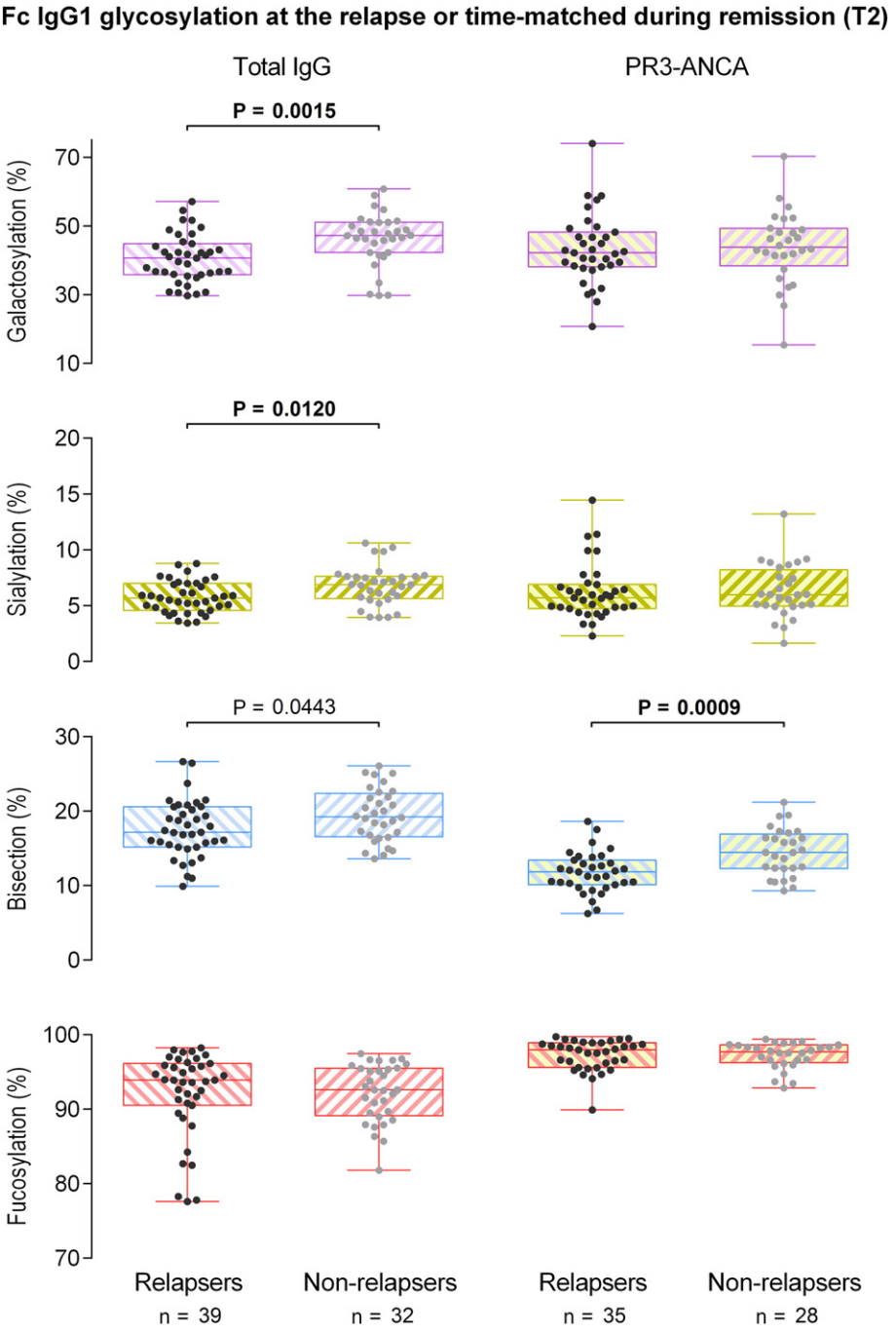

Fig. 5. The glycosylation profile at the time of a relapse in relapsing patients and time-matched during remission in patients who remain in remission (gray dots). IgG1 Fc glycosylation of total IgG (left side, white background) and antigen specific PR3-ANCA (right side, yellow background) is shown. Dots represent individual patients. The box represents the median with interquartile range, the whiskers delineate the min-max range. Significant differences were evaluated using the Mann Whitney *U* test, p-values are shown if <0.10 and in bold if <0.0125.

non-relapsing patients. While the effect of a bisecting GlcNAc on IgG effector functions is minor compared to that of the other glycosylation features, it has been reported that bisection can enhance antibody-dependent cellular cytotoxicity (ADCC) through increased FcγRIIIa affinity (Davies et al., 2001; Shinkawa et al., 2003). Since a reduction in bisection is seen during AAV relapse, it is likely that the minor anti-inflammatory effect of decreased bisection is overshadowed by effects of other changes in glycosylation and that ADCC may only play a minor role in the pathogenesis of AAV (Mayet et al., 1994). A decrease in IgG bisection has not been reported for any other autoimmune disorders, while an increase in bisection has been observed for Lambert-Eaton Myasthenic Syndrome (LEMS) (Selman et al., 2011). A slight increase in fucosylation over time was seen in total IgG of relapsing patients. In contrast, PR3-ANCA showed a minor decrease in fucosylation for both relapsing and non-relapsing patients. While the absence of a core fucose can greatly enhance the inflammatory properties of IgG through increased FcγRIIIa affinity, the differences in fucosylation in our study cohort are likely too small to be of much influence.

Our findings regarding the glycosylation profile of total IgG compared to antigen-specific PR3 markedly differ from those of a previous study, which reported a reduction of galactosylation, sialylation and bisection of PR3-ANCA as compared to total IgG, while we observe that bisection, but not galactosylation and sialylation is reduced in PR3-ANCA. These differences may be largely

caused by the pronounced differences in study design (Wuhrer et al., 2015b). First, we included patients with severe AAV as well as patients with more limited forms of AAV, while the previous report only included patients with severe AAV (Wuhrer et al., 2015b). Second, our patients were in remission at the time of sampling, while the patients of Wuhrer et al. were sampled at the time of active disease (Wuhrer et al., 2015b). Interestingly, both studies observe a lower degree of bisection in PR3-ANCA compared to total IgG.

Our study is limited by the amount of included patients, hence only the N-glycan analysis was included in the statistical evaluation. Future validation in other, larger study cohorts is warranted in which the predictive value of a multitude of factors, in particular the IgG N-glycan analysis, should be evaluated using multivariate techniques, including principle components analysis. A strong aspect of our study is that our patients are highly characterized and we only included patients with GPA positive for PR3-ANCA. Yet differences still remain in organ involvement and immunosuppressive therapy. Our findings, however, may not apply to patients with MPA or patients positive for MPO-ANCA and this should be further investigated.

Most importantly, we addressed the clinical value of the aberrant glycosylation which we observe in AAV patients. Changes in IgG glycosylation, especially galactosylation and sialylation, might be useful to screen patients for their risk of relapse. Our data indicates that analysis of total IgG would be sufficient for this purpose. Already in the first serum sample, acquired a median time of 8 months before the time of relapse, we could identify patients that are at risk for a future disease relapse. Differences in the glycosylation profile between relapsing and non-relapsing patients become more pronounced as the time of relapse approaches. Longitudinal acquisition of serum samples taken every few months would reveal changes in the personal glycosylation profile of each patient that could possibly help as a guide when to start treatment in these patients. It remains to be studied, however, whether treatment based on this information will be able to minimize tissue and organ damage.

Supplementary data to this article can be found online at http://dx.doi.org/10.1016/j.ebiom.2017.01.033.

Conflict of Interest

All authors report no conflict of interest-financial or otherwise-that may directly or indirectly influence the content of the manuscript submitted.

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Authors' Contribution

The study was designed by MW, JWCT, RP and MK.

Patient data was collected by PVP and JWCT.

Data management and sample selection was done by MK.

ANCA measurements were performed by JD.

Sample analysis of the glycosylation profile was executed by RP and CK, assisted by BJ.

Statistical data analysis was carried out by MK.

The first draft of the manuscript was written by RP and MK.

All authors contributed to data interpretation and writing of the manuscript.

References

Albrecht, S., Unwin, L., Muniyappa, M., Rudd, P.M., 2014. Glycosylation as a marker for inflammatory arthritis. Cancer Biomark. 14, 17–28.

Anthony, R.M., Nimmerjahn, F., 2011. The role of differential IgG glycosylation in the interaction of antibodies with FcγRs in vivo. Curr. Opin. Organ Transplant. 16, 7–14.

Anthony, R.M., Wermeling, F., Ravetch, J.V., 2012. Novel roles for the IgG Fc glycan. Ann. N. Y. Acad. Sci. 1253, 170–180.

Berden, A.E., Ferrario, F., Hagen, E.C., et al., 2010. Histopathologic classification of ANCA-associated glomerulonephritis. J. Am. Soc. Nephrol. 21, 1628–1636.

Birck, R., Schmitt, W.H., Kaelsch, I.A., van der Woude, F.J., 2006. Serial ANCA determinations for monitoring disease activity in patients with ANCA-associated Vasculitis: systematic review. Am. J. Kidney Dis. 47, 15–23.

Bondt, A., Selman, M.H., Deelder, A.M., et al., 2013. Association between galactosylation of immunoglobulin G and improvement of rheumatoid arthritis during pregnancy is independent of sialylation. J. Proteome Res. 12, 4522–4531.

Boomsma, M.M., Stegeman, C.A., Van Der Leij, M.J., et al., 2000. Prediction of relapses in Wegener's granulomatosis by measurement of antineutrophil cytoplasmic antibody levels: a prospective study. Arthritis Rheum. 43, 2025–2033.

Boomsma, M.M., Damoiseaux, J.G.M.C., Stegeman, C.A., et al., 2003. Image analysis: a novel approach for the quantification of antineutrophil cytoplasmic antibody levels in patients with Wegener's granulomatosis. J. Immunol. Methods 274, 27–35.

Brady, L.J., Velayudhan, J., Visone, D.B., et al., 2015. The criticality of high-resolution N-linked carbohydrate assays and detailed characterization of antibody effector function in the context of biosimilar development. MAbs 7, 562–570.

Central Committee on Research Involving Human Subjects, 2013. Non WMO Research. [Internet. Accessed June 22, 2016]. Available from: http://www.ccmo.nl/en/non-wmo-research.

Chambers, M.C., Maclean, B., Burke, R., et al., 2012. A cross-platform toolkit for mass spectrometry and proteomics. Nat. Biotechnol. 30, 918–920.

Cohen Tervaert, J.W., Damoiseaux, J.G.M.C., 2012. Antineutrophil cytoplasmic autoantibodies: how are they detected and what is their use for diagnosis, classification and follow-up? Clin. Rev. Allergy Immunol. 43, 211–219.

Cohen Tervaert, J., van der Woude, F., Fauci, A., et al., 1989. Association between active Wegener's granulomatosis and anticytoplasmic antibodies. Arch. Intern. Med. 159, 2461–2465.

Collin, M., Ehlers, M., 2013. The carbohydrate switch between pathogenic and immunosuppressive antigen-specific antibodies. Exp. Dermatol. 22, 511–514.

Damoiseaux, J.G.M.C., Slot, M.C., Vaessen, M., Stegeman, C.A., Van Paassen, P., Cohen Tervaert, J.W., 2005. Evaluation of a new fluorescent-enzyme immuno-assay for diagnosis and follow-up of ANCA-associated vasculitis. J. Clin. Immunol. 25, 202–208.

Davies, J., Jiang, L., Pan, L.Z., LaBarre, M.J., Anderson, D., Reff, M., 2001. Expression of GnTIII in a recombinant anti-CD20 CHO production cell line: expression of antibodies with altered glycoforms leads to an increase in ADCC through higher affinity for FC gamma RIII. Biotechnol. Bioeng. 74, 288–294.

Ercan, A., Cui, J., Chatterton, D.E., et al., 2010. Aberrant IgG galactosylation precedes disease onset, correlates with disease activity, and is prevalent in autoantibodies in rheumatoid arthritis. Arthritis Rheum. 62, 2239–2248.

Espy, C., Morelle, W., Kavian, N., et al., 2011. Sialylation levels of anti–proteinase 3 antibodies are associated with the activity of granulomatosis with polyangiitis (Wegener's). Arthritis Rheum. 63, 2105–2115.

Falck, D., Jansen, B.C., Plomp, R., Reusch, D., Haberger, M., Wuhrer, M., 2015. Glycoforms of immunoglobulin G based biopharmaceuticals are differentially cleaved by trypsin due to the glycoform influence on higher-order structure. J. Proteome Res. 14, 4019–4028.

Fickentscher, C., Magorivska, I., Janko, C., et al., 2015. The pathogenicity of anti-β2GP1-IgG autoantibodies depends on Fc glycosylation. J. Immunol. Res. 2015, 12.

Fussner, L.A., Hummel, A.M., Schroeder, D.R., et al., 2016. Factors determining the clinical utility of serial measurements of antineutrophil cytoplasmic antibodies targeting proteinase 3. Arthritis Rheum. 68, 1700–1710.

Gatenby, P.A., Lucas, R.M., Engelsen, O., Ponsonby, A.-L., Clements, M., 2009. Antineutrophil cytoplasmic antibody-associated vasculitides: could geographic patterns be explained by ambient ultraviolet radiation? Arthritis Care Res. 61, 1417–1424.

Hellmich, B., Flossmann, O., Gross, W.L., et al., 2007. EULAR recommendations for conducting clinical studies and/or clinical trials in systemic vasculitis: focus on anti-neutrophil cytoplasm antibody-associated vasculitis. Ann. Rheum. Dis. 66, 605–617.

Hilhorst, M., Wilde, B., van Breda, V.P., van Paassen, P., Cohen Tervaert, J.W., 2013. Estimating renal survival using the ANCA-associated GN classification. J. Am. Soc. Nephrol. 24, 1371–1375.

Hilhorst, M., van Paassen, P., van Rie, H., et al., 2015. Complement in ANCA-associated glomerulonephritis. Nephrol. Dial. Transplant. (Epub ahead of print).

Holland, M., Yagi, H., Takahashi, N., et al., 1760. Differential glycosylation of polyclonal IgG, IgG-Fc and IgG-Fab isolated from the sera of patients with ANCA-associated systemic vasculitis. Biochim. Biophys. Acta 2006, 669–677.

Holland, M., Takada, K., Okumoto, T., et al., 2002. Hypogalactosylation of serum IgG in patients with ANCA-associated systemic vasculitis. Clin. Exp. Immunol. 129, 183–190.

Huugen, D., Xiao, H., van Esch, A., et al., 2005. Aggravation of anti-myeloperoxidase antibody-induced glomerulonephritis by bacterial lipopolysaccharide: role of tumor necrosis factor-α. Am. J. Pathol. 167, 47–58.

Huugen, D., van Esch, A., Xiao, H., et al., 2007. Inhibition of complement factor C5 protects against anti-myeloperoxidase antibody-mediated glomerulonephritis in mice. Kidney Int. 71, 646–654.

Kain, R., Tadema, H., McKinney, E.F., et al., 2012. High prevalence of autoantibodies to hLAMP-2 in anti-neutrophil cytoplasmic antibody-associated vasculitis. J. Am. Soc. Nephrol. 23, 556–566.

Kaneko, Y., Nimmerjahn, F., Ravetch, J.V., 2006. Anti-inflammatory activity of immunoglobulin G resulting from fc sialylation. Science 313, 670–673.
Karsten, C.M., Pandey, M.K., Figge, J., et al., 2012. Anti-inflammatory activity of IgG1 mediated by Fc galactosylation and association of FcγRIIB and dectin-1. Nat. Med. 18, 1401–1406.
Kemna, M.J., Damoiseaux, J.G.M.C., Austen, J., et al., 2015. ANCA as a predictor of relapse: useful in patients with renal involvement but not in patients with nonrenal disease. J. Am. Soc. Nephrol. 26, 537–542.
Koh, J.H., Kemna, M.J., Cohen Tervaert, J.W., Kim, W.U., 2016. Can an increase in antineutrophil cytoplasmic autoantibody titer predict relapses in antineutrophil cytoplasmic antibody-associated vasculitis? Arthritis Rheum. 68, 1571–1573.
de Lind van Wijngaarden, R.A.F., van Rijn, L., Hagen, E.C., et al., 2008. Hypotheses on the etiology of antineutrophil cytoplasmic autoantibody-associated vasculitis: the cause is hidden, but the result is known. Clin. J. Am. Soc. Nephrol. 3, 237–252.
Little, M.A., Al-Ani, B., Ren, S., et al., 2012. Anti-proteinase 3 anti-neutrophil cytoplasm autoantibodies recapitulate systemic vasculitis in mice with a humanized immune system. PLoS One 7, e28626.
Magorivska, I., Muñoz, L.E., Janko, C., et al., 2016. Sialylation of anti-histone immunoglobulin G autoantibodies determines their capabilities to participate in the clearance of late apoptotic cells. Clin. Exp. Immunol. 184, 110–117.
Malhotra, R., Wormald, M.R., Rudd, P.M., Fischer, P.B., Dwek, R.A., Sim, R.B., 1995. Glycosylation changes of IgG associated with rheumatoid arthritis can activate complement via the mannose-binding protein. Nat. Med. 1, 237–243.
Matsumoto, A., Shikata, K., Takeuchi, F., Kojima, N., Mizuochi, T., 2000. Autoantibody activity of IgG rheumatoid factor increases with decreasing levels of galactosylation and sialylation. J. Biochem. 128, 621–628.
Mayet, W.J., Schwarting, A., Meyer Zum Buschenfelde, K.H., 1994. Cytotoxic effects of antibodies to proteinase 3 (C-ANCA) on human endothelial cells. Clin. Exp. Immunol. 97, 458–465.
Mukhtyar, C., Guillevin, L., Cid, M.C., et al., 2009. EULAR recommendations for the management of primary small and medium vessel vasculitis. Ann. Rheum. Dis. 68, 310–317.
Nolle, B., Specks, U., Ludemann, J., Rohrbach, M.S., DeRemee, R.A., Gross, W.L., 1989. Anticytoplasmic autoantibodies: their immunodiagnostic value in Wegener granulomatosis. Ann. Intern. Med. 111, 28–40.
Parekh, R.B., Dwek, R.A., Sutton, B.J., et al., 1985. Association of rheumatoid arthritis and primary osteoarthritis with changes in the glycosylation pattern of total serum IgG. Nature 316, 452–457.
Plomp, R., Dekkers, G., Rombouts, Y., et al., 2015. Hinge-region O-glycosylation of human immunoglobulin G3 (IgG3). Mol. Cell. Proteomics 14, 1373–1384.
Pluskal, T., Castillo, S., Villar-Briones, A., Oresic, M., 2010. MZmine 2: modular framework for processing, visualizing, and analyzing mass spectrometry-based molecular profile data. BMC Bioinforma. 11, 395.
Popa, E.R., Stegeman, C.A., Kallenberg, C.G., Cohen Tervaert, J.W., 2002. *Staphylococcus aureus* and Wegener's granulomatosis. Arthritis Res. 4, 77–79.
Rademacher, T.W., Williams, P., Dwek, R.A., 1994. Agalactosyl glycoforms of IgG autoantibodies are pathogenic. Proc. Natl. Acad. Sci. U. S. A. 91, 6123–6127.
Rombouts, Y., Ewing, E., van de Stadt, L.A., et al., 2015. Anti-citrullinated protein antibodies acquire a pro-inflammatory Fc glycosylation phenotype prior to the onset of rheumatoid arthritis. Ann. Rheum. Dis. 74, 234–241.
Scherer, H.U., van der Woude, D., Ioan-Facsinay, A., et al., 2010. Glycan profiling of anti-citrullinated protein antibodies isolated from human serum and synovial fluid. Arthritis Rheum. 62, 1620–1629.
Selman, M.H., Niks, E.H., Titulaer, M.J., Verschuuren, J.J., Wuhrer, M., Deelder, A.M., 2011. IgG fc N-glycosylation changes in Lambert-Eaton myasthenic syndrome and myasthenia gravis. J. Proteome Res. 10, 143–152.
Selman, M.H., Derks, R.J., Bondt, A., et al., 2012. Fc specific IgG glycosylation profiling by robust nano-reverse phase HPLC-MS using a sheath-flow ESI sprayer interface. J. Proteome 75, 1318–1329.
Shinkawa, T., Nakamura, K., Yamane, N., et al., 2003. The absence of fucose but not the presence of galactose or bisecting N-acetylglucosamine of human IgG1 complex-type oligosaccharides shows the critical role of enhancing antibody-dependent cellular cytotoxicity. J. Biol. Chem. 278, 3466–3473.
Subedi, G.P., Barb, A.W., 2016. The immunoglobulin G1 N-glycan composition affects binding to each low affinity Fc y receptor. MAbs 8, 1512–1524.
Tervaert, J.W., Goldschmeding, R., Elema, J.D., et al., 1990. Autoantibodies against myeloid lysosomal enzymes in crescentic glomerulonephritis. Kidney Int. 37, 799–806.
Thomann, M., Schlothauer, T., Dashivets, T., et al., 2015. In vitro glycoengineering of IgG1 and its effect on fc receptor binding and ADCC activity. PLoS One 10, e0134949.
van Timmeren, M.M., van der Veen, B.S., Stegeman, C.A., et al., 2010. IgG glycan hydrolysis attenuates ANCA-mediated glomerulonephritis. J. Am. Soc. Nephrol. 21, 1103–1114.
Trbojevic Akmacic, I., Ventham, N.T., Theodoratou, E., et al., 2015. Inflammatory bowel disease associates with proinflammatory potential of the immunoglobulin G glycome. Inflamm. Bowel Dis. 21, 1237–1247.
Vuckovic, F., Kristic, J., Gudelj, I., et al., 2015. Association of systemic lupus erythematosus with decreased immunosuppressive potential of the IgG glycome. Arthritis Rheum. 67, 2978–2989.
Watson, M., Rudd, P.M., Bland, M., Dwek, R.A., Axford, J.S., 1999. Sugar printing rheumatic diseases: a potential method for disease differentiation using immunoglobulin G oligosaccharides. Arthritis Rheum. 42, 1682–1690.
Watts, R., Lane, S., Hanslik, T., et al., 2007. Development and validation of a consensus methodology for the classification of the ANCA-associated vasculitides and polyarteritis nodosa for epidemiological studies. Ann. Rheum. Dis. 66, 222–227.
Wilde, B., van Paassen, P., Witzke, O., Cohen Tervaert, J.W., 2011. New pathophysiological insights and treatment of ANCA-associated vasculitis. Kidney Int. 79, 599–612.
Wuhrer, M., Selman, M.H., McDonnell, L.A., et al., 2015a. Pro-inflammatory pattern of IgG1 Fc glycosylation in multiple sclerosis cerebrospinal fluid. J. Neuroinflammation 12, 235.
Wuhrer, M., Stavenhagen, K., Koeleman, C.A., et al., 2015b. Skewed Fc glycosylation profiles of anti-proteinase 3 immunoglobulin G1 autoantibodies from granulomatosis with polyangiitis patients show low levels of bisection, galactosylation, and sialylation. J. Proteome Res. 14, 1657–1665.
Xiao, H., Heeringa, P., Hu, P., et al., 2002. Antineutrophil cytoplasmic autoantibodies specific for myeloperoxidase cause glomerulonephritis and vasculitis in mice. J. Clin. Invest. 110, 955–963.
Xiao, H., Dairaghi, D.J., Powers, J.P., et al., 2014. C5a receptor (CD88) blockade protects against MPO-ANCA GN. J. Am. Soc. Nephrol. 25, 225–231.
Yamaguchi, M., Ando, M., Kato, S., et al., 2015. Increase of antimyeloperoxidase antineutrophil cytoplasmic antibody (ANCA) in patients with renal ANCA-associated vasculitis: association with risk to relapse. J. Rheumatol. 42, 1853–1860.
Zauner, G., Selman, M.H., Bondt, A., et al., 2013. Glycoproteomic analysis of antibodies. Mol. Cell. Proteomics 12, 856–865.