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Published in: Annals of the Rheumatic Diseases

DOI: 10.1136/annrheumdis-2017-212568

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Document Version
Publisher's PDF, also known as Version of record

Publication date: 2018

Link to publication in University of Groningen/UMCG research database

Citation for published version (APA):

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Acquiring new N-glycosylation sites in variable regions of immunoglobulin genes by somatic hypermutation is a common feature of autoimmune diseases

With great interest, we read the contribution of Vergroesen et al1 that was published recently in Annals of the Rheumatic Diseases. In this manuscript, the authors describe the observation that immunoglobulin variable (V) region heavy and light chain transcripts from anti-citrullinated protein antibody (ACPA) IgG-expressing B cells in patients with rheumatoid arthritis (RA) contain N-glycosylation sites (Nglycs) acquired by somatic hypermutation, whereas these acquired Nglycs (ac-Nglycs) were absent in IgG encoding transcripts from a number of publicly available data sets from patients with primary Sjögren’s syndrome (pSS; n=576), RA (n=1331), systemic lupus erythematosus (SLE; n=361), multiple sclerosis (n=200), chronic Chagas’ heart disease (cChD; n=70), ankylosing spondylitis (n=29) and granulomatosis with polyangiitis (GPA; n=242). As controls, we collected published data sets of IGHV sequences derived from various healthy, non-autoimmune individuals (n=2131) and from vaccination or infection studies on antigen-specific B cells (n=817) (see online supplementary table 1). Sequences identical to germline IGHV sequences (±2 nucleotide mutations in the V and J genes), naturally occurring germline Nglycs and sequences lacking fully designated VDJ rearrangements were excluded from analysis. In each study, the number of ac-Nglycs was predicted by the NetNglyc V1.0 program (http://www.cbs.dtu.dk/services/NetNglyc/) based on the consensus sequence in the protein motif N-X-S/T (asparagine-X-serine/threonine). As shown in figure 1A, the combined frequency of ac-Nglycs in IGHV sequences is significantly higher (P<0.0001; Pearson’s χ² test) in autoimmune disease data sets (9.0%; 95% CI 8.0 to 10.1) than that in control data sets (2.3%; 95% CI 1.7 to 3.0) as well as in antigen-specific data sets (2.7%; 95% CI 1.7 to 4.0).

Interestingly, the number of ac-Nglycs is elevated in nearly all autoimmune diseases with well-established B cell involvement except for GPA (figure 1B); we observed a higher amount of ac-Nglycs in the IGHV sequences from pSS (15%), RA (10%), SLE (6%), multiple sclerosis (9%) and for cChD (19%) compared with the normal control data set (3%). Although GPA is an auto-immune disease, well known for its B cell involvement, ac-Nglycs were completely absent in the IGHV sequences. Possible explanations could be the over-representation of IgM encoding sequences in these data sets (online supplementary table 1). In patients with ankylosing spondylitis, the number of ac-Nglycs (3%) is similar to normal controls.

To test if ac-Nglycs created by somatic hypermutation could be a common phenomenon for B cells in rheumatic and non-rheumatic autoimmune diseases, we performed a meta-analysis of the presence of ac-Nglycs in IGHV sequences from a number of publicly available data sets from patients with pSS (n=576), RA (n=1331), systemic lupus erythematosus (SLE; n=361), multiple sclerosis (n=200), chronic Chagas’ heart disease (cChD; n=70), ankylosing spondylitis (n=29) and granulomatosis with polyangiitis (GPA; n=242). As controls, we collected published data sets of IGHV sequences derived from various healthy, non-autoimmune individuals (n=2131) and from vaccination or infection studies on antigen-specific B cells (n=817) (see online supplementary table 1). Sequences identical to germline IGHV sequences (±2 nucleotide mutations in the V and J genes), naturally occurring germline Nglycs and sequences lacking fully designated VDJ rearrangements were excluded from analysis. In each study, the number of ac-Nglycs was predicted by the NetNglyc V1.0 program (http://www.cbs.dtu.dk/services/NetNglyc/) based on the consensus sequence in the protein motif N-X-S/T (asparagine-X-serine/threonine). As shown in figure 1A, the combined frequency of ac-Nglycs in IGHV sequences is significantly higher (P<0.0001; Pearson’s χ² test) in autoimmune disease data sets (9.0%; 95% CI 8.0 to 10.1) than that in control data sets (2.3%; 95% CI 1.7 to 3.0) as well as in antigen-specific data sets (2.7%; 95% CI 1.7 to 4.0).

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Figure 1 Prevalence of acquired N-glycosylation sites in IGHV sequences. (A) This figure depicts a simplified version of the meta-analysis shown in online supplementary figure 1. The percentages of ac-Nglycs were compared between autoimmune diseases and non-autoimmune or normal controls (N) and vaccination and infection controls (AgS) regardless of isotype. All the studies combined revealed 275 ac-Nglycs out of 2809 IGHV sequences from patients with autoimmune disease (9.0%; 95% CI 8.0 to 10.1) which was significantly higher than the 64 ac-Nglycs out of 2131 IGHV sequences in these data sets (2.3%; 95% CI 1.7 to 3.0) and from vaccination or infection studies on antigen-specific B cells (n=817) (see online supplementary table 1). Sequences identical to germline IGHV sequences (±2 nucleotide mutations in the V and J genes), naturally occurring germline Nglycs and sequences lacking fully designated VDJ rearrangements were excluded from analysis. In each study, the number of ac-Nglycs was predicted by the NetNglyc V1.0 program (http://www.cbs.dtu.dk/services/NetNglyc/) based on the consensus sequence in the protein motif N-X-S/T (asparagine-X-serine/threonine). As shown in figure 1A, the combined frequency of ac-Nglycs in IGHV sequences is significantly higher (P<0.0001; Pearson’s χ² test) in autoimmune disease data sets (9.0%; 95% CI 8.0 to 10.1) than that in control data sets (2.3%; 95% CI 1.7 to 3.0) as well as in antigen-specific data sets (2.7%; 95% CI 1.7 to 4.0).

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In conclusion, in addition to Vergroesen et al in RA, and our previous work in pSS, the meta-analysis described here clearly indicates that there is an increase in ac-Nglycs by somatic hypermutation of immunoglobulin genes during humoral immune responses in various autoimmune diseases. This phenomenon is thus clearly not restricted to ACPA-expressing B cells in RA as shown by Vergroesen et al. It is not known yet whether the absence of ac-Nglycs in TT-specific cells is a property of TT specificity or due to the fact that these cells are from healthy, vaccinated individuals. It would therefore be of great interest to see whether also in patients with RA ac-Nglycs are absent in TT-specific B cells and other non-ACPA-expressing B cells. The explicit tendency for ac-Nglycs to occur also within the FRs strongly suggests that the increased frequency of ac-Nglycs in autoimmune diseases may offer Ig-producing cells alternative forms of selection to classical antigen selection. This could point to a very fundamental basis to understand the origin of autoreactive B cells in autoimmune diseases and possible targets for early intervention.

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Contributors AV wrote the concept of manuscript and performed the analysis of the data sets. NH performed the initial analysis of the data set. NAB and FGMK were involved in writing and discussion of the data.

Competing interests None declared.

Provenance and peer review Not commissioned; externally peer reviewed.

Data sharing statement Data are already publicly available.

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To cite Visser A, Hamza N, Kroese FGM, et al. Ann Rheum Dis Published Online First: [please include Day Month Year]. doi:10.1136/annrheumdis-2017-212568

Received 19 October 2017
Accepted 22 October 2017


REFERENCES
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Ann Rheum Dis published online November 4, 2017