ABSTRACT

Background The type 1 interferon (IFN) pathway has been identified to potentially affect the response to rituximab (RTX) for rheumatoid arthritis (RA), which suggests the contribution of type 1 IFN pathway genes such as IFN regulatory factor 5 and 7 (IRF5 and IRF7), tyrosine kinase 2 (TYK2), signal transducer and activator of transcription 4 (STAT4) and osteopontin (SPP1). Our objective was to study functional variants of these IFN pathway genes as predictors of the European League Against Rheumatism (EULAR) response to RTX for RA at week 24 (W24).

Methods Logistic regression analysis with a stepwise multivariate model adjusted for sex, age and DAS28-CRP (Disease Activity Score in 28 joints with C reactive protein) in 115 patients from the SMART randomised study was used to analyse the association between the candidate variants and W24 EULAR response. Because the variant TNFSF13B rs9514828 was previously found associated with RTX response in the same population, it was included in the analysis.

Results The combination of IRF5 rs2004640, SPP1 rs9138 and TNFSF13B rs9514828 was strongly associated with good/moderate EULAR response to RTX at W24: p=9.34×10⁻⁶, OR 11.37 (95% CI 4.03 to 35.28), positive predictive value 91% and negative predictive value 54%.

Conclusion Our results support the contribution of the IRF5, SPP1 and TNFSF13B genotypic combination in the response to RTX for RA at W24.

BACKGROUND

Rheumatoid arthritis (RA) is a complex systemic autoimmune disorder with environmental, genetic and stochastic factors implicated. The anti-CD20 chimeric monoclonal antibody that targets B cells, rituximab (RTX), is an effective treatment for RA refractory to tumour necrosis factor blockers. Currently, we cannot offer personalised medicine for patients with RA receiving biologics, including RTX, because we cannot identify those who will not respond to a given treatment, nor do we understand the pathogenesis underlying these interindividual variances. To improve this situation, the identification of prognostic factors of RTX response is needed.

The type 1 interferon (IFN) pathway was recently identified to potentially affect the RTX response in RA. Indeed, transcriptome studies found that the only distinction between RTX responders and non-responders at week 24 (W24) was pharmacodynamic changes in the expression of a selective group of genes all regulated by type 1 IFN. As well, the pharmacological effect of RTX on
IFN-response gene activity was found associated with IFN-response activity before the start of treatment.\(^5\)\(^6\)

Several genes encoding proteins that are key components of the type 1 IFN system include IFN regulatory factor 5 and 7 (\textit{IRF5/7}), tyrosine kinase 2 (\textit{TYK2}), and signal transducer and activator of transcription 4 (\textit{STAT4}) and osteopontin (\textit{SPP1}). These genes have recently been found to play a role in the risk of several autoimmune diseases including RA.\(^7\)--\(^9\) Here, we aimed to investigate whether putative or proven functional variants of \textit{IRF5/7}, \textit{TYK2}, \textit{STAT4} and \textit{SPP1} could modulate the European League Against Rheumatism (EULAR) response to RTX in RA.

**METHODS**

**Study population**

In this retrospective, multicentric study, all patients from the SMART study (\textit{A Study of Re-treatment With MabThera (Rituximab) in Patients With Rheumatoid Arthritis Who Have Failed on Anti-TNF Alfa Therapy}) who consented to genetic studies were included. Characteristics of the SMART study have been previously described.\(^10\) Briefly, 224 patients fulfilling the 1987 American College of Rheumatology criteria for RA with inadequate response, intolerance or contraindication to anti-TNF\(\alpha\) were included in the SMART study (NCT01126541), a 2-year national multicentric randomised open-label study evaluating the efficacy and safety of two doses of RTX for re-treatment after one course of RTX (1000 mg on days 1 and 15). Only corticosteroids and non-steroidal anti-inflammatory drugs were permitted if at stable doses. B-cell activating factor (BAFF) level was measured at RTX initiation using a Quantikine ELISA (R&D Systems). The main SMART study was approved by the local ethics committee (Groupe Hospitalier Pitié-Salpêtrière, Paris), and all patients gave their informed consent according to the Declaration of Helsinki.

**Selection of single-nucleotide polymorphisms (SNPs)**

All patients underwent genotyping for the SNPs for \textit{IRF5} (rs2004640), \textit{IRF7} (rs1131665), \textit{STAT4} (rs7574865), \textit{TYK2} (rs2304256, rs280519 and rs12720356) and \textit{SPP1} (rs11439060 and rs9138). Genotyping was performed at KBiosciences, Manchester, UK. We selected these eight variants by their previously reported putative or proven functional relevance in the type 1 IFN pathway.\(^2\)--\(^9\) Because of the recently reported association between \textit{TNFSF13B} (encoding BAFF) rs9514828 and RTX response in the SMART study,\(^11\) this variant was also integrated into the multivariate analysis.

**Statistical analysis**

The association between the variants and EULAR response to RTX was analysed by logistic regression.\(^12\) Responders were defined by a good/moderate EULAR response at W24. First, response rate was compared across risk genotypes by univariate analysis with the \(\chi^2\), with Yates’ continuity correction as appropriate. Both dominant and recessive models were tested, and results of the most significant one were reported. Note that the additive model was also tested but results were not reported, as it did not improve the results. Variables significant at \(p<0.20\) were selected, combined with \textit{TNFSF13B} rs9514828 and entered into a logistic regression adjusted on sex, age and Disease Activity Score in 28 joints with C reactive protein (DAS28-CRP), rheumatoid factor (RF) and anti-Cyclic Citrullinated Peptide (CCP) status. The best fitting model was determined using the backward procedure implemented in the step function of R. ORs and 95% CIs were calculated. Conformity with Hardy-Weinberg equilibrium was tested by a classical \(\chi^2\)
test with one degree of freedom in controls. All statistical analyses involved the use of R V.3.1.2. p-value <0.05 was considered statistically significant.

RESULTS
Among the 224 patients with RA included in the SMART study, 115 gave consent for genetic analysis and their data were analysed in this study; 92 were women (80%), mean age was 55.50±11.15 years, 93 had anti-CCP antibodies (80.9%) and 82 were positive for RF (71.3%). Mean DAS28-CRP was 5.68±0.90 at RTX initiation and 3.94±1.07 at W24, with a mean change of −1.74±1.14. At W24, 30 (26.3%) patients were considered good responders, 62 (54.4%) moderate responders and 22 (19.3%) non-responders (table 1). Genotype frequencies were in Hardy-Weinberg equilibrium for all SNPs investigated (data not shown). Genotyping results are in table 2.

Table 2 Univariate analysis of good/moderate EULAR response at W24 by genotype

<table>
<thead>
<tr>
<th>Candidate gene</th>
<th>Candidate variants</th>
<th>Genotype*</th>
<th>Good/moderate responders</th>
<th>Non-responders</th>
<th>p Value</th>
</tr>
</thead>
<tbody>
<tr>
<td>IRF5</td>
<td>rs2004640</td>
<td>0 (T/T)</td>
<td>17</td>
<td>10</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>1 (T/G)</td>
<td>56</td>
<td>8</td>
<td>0.030‡</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2 (G/G)</td>
<td>12</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>IRF7</td>
<td>rs1131665</td>
<td>0 (T/T)</td>
<td>45</td>
<td>15</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>1 (T/C)</td>
<td>35</td>
<td>6</td>
<td>0.180†</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2 (C/C)</td>
<td>11</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td>SPP1</td>
<td>rs11439060</td>
<td>0 (–/–)</td>
<td>48</td>
<td>13</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>1 (–/G)</td>
<td>30</td>
<td>7</td>
<td>0.410</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2 (G/G)</td>
<td>13</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>rs9138</td>
<td>0 (A/A)</td>
<td>45</td>
<td>6</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>1 (C/A)</td>
<td>33</td>
<td>12</td>
<td>0.085‡</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2 (C/C)</td>
<td>11</td>
<td>4</td>
<td></td>
</tr>
<tr>
<td>STAT4</td>
<td>rs7574865</td>
<td>0 (G/G)</td>
<td>41</td>
<td>12</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>1 (G/T)</td>
<td>42</td>
<td>6</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>2 (T/T)</td>
<td>7</td>
<td>4</td>
<td>0.284</td>
</tr>
<tr>
<td>TNFSF13B</td>
<td>rs9514828</td>
<td>0 (C/C)</td>
<td>36</td>
<td>3</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>1 (C/T)</td>
<td>43</td>
<td>11</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>2 (T/T)</td>
<td>13</td>
<td>8</td>
<td>0.035‡</td>
</tr>
<tr>
<td>TYK2</td>
<td>rs12720356</td>
<td>0 (T/T)</td>
<td>73</td>
<td>20</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>1 (T/G)</td>
<td>13</td>
<td>2</td>
<td>0.490</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2 (G/G)</td>
<td>3</td>
<td>0</td>
<td></td>
</tr>
<tr>
<td></td>
<td>rs2304256</td>
<td>0 (C/C)</td>
<td>45</td>
<td>8</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>1 (C/A)</td>
<td>35</td>
<td>11</td>
<td>0.515</td>
</tr>
<tr>
<td></td>
<td></td>
<td>2 (A/A)</td>
<td>8</td>
<td>1</td>
<td></td>
</tr>
<tr>
<td></td>
<td>rs280519</td>
<td>0 (A/A)</td>
<td>27</td>
<td>6</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>1 (A/G)</td>
<td>37</td>
<td>12</td>
<td></td>
</tr>
<tr>
<td></td>
<td></td>
<td>2 (G/G)</td>
<td>28</td>
<td>4</td>
<td>0.376</td>
</tr>
</tbody>
</table>

Grey indicates the selected model (dominant or recessive).
*0 denotes patients homozygous for the major allele; 1, heterozygous; 2, homozygous for the rare allele.

Univariate analysis revealed an increase in the minor allele frequency for IRF5 rs2004640, IRF7 rs1131665 and SPP1 rs9138 in good/moderate responders at W24 (ie, p<0.20, table 2). To further define the model best fitting a EULAR response to RTX at W24, we added the variant TNFSF13B rs9514828 in the multivariate analysis.

Multivariate analysis revealed an allelic combination of the three distinct variants IRF5 rs2004640, SPP1 rs9138 and TNFSF13B rs9514828 strongly associated with EULAR response to RTX at W24, independent of the anti-citrullinated protein antibodies (ACPA) status of the patients, defined by homozygosity for the common allele of SPP1 rs9138 (genotype A/A) and TNFSF13B rs9514828 (genotype C/C) and carrying at least one rare allele of IRF5 rs2004640 (genotype G/T or G/G). This predictive allelic combination was found in 69 of good/moderate responders (75.0%) compared with seven

Figure 1 (A) Number and percentage of patients with rheumatoid arthritis (RA) who were European League Against Rheumatism (EULAR) responders and non-responders to rituximab by carriage of the IRF5 rs2004640, SPP1 rs9138 and TNFSF13B rs9514828 genotypic combination; (B) EULAR responders and non-responders with and without the genotypic combination. R, responders; Non R, non-responders.

Discussion

RA is a clinical heterogeneous disease and the therapeutic strategy is challenging because of its interindividual variability. Since the last decade, medicine has begun to embrace genomic tools that allow for more precise prediction in treatment response. However, to date, predictive tools to identify patients with RA who will respond to a given biologic remains to be identified. Recently, a type 1 IFN signature was found associated with good response to RTX in RA. Consequently, we investigated functional genetic variants in genes encoding proteins involved in the type 1 IFN pathway and found a strong association of the allelic combination of IRF5 rs2004640, SPP1 rs9138 and TNFSF13B rs9514828 and response to RTX at W24.

Our results suggest an impact of genetic variations of IRF5 and SPP1, involved in the type 1 IFN pathway, and TNFSF13B, implicated in B-cell maturation, homoeostasis and survival, in RA on the response to RTX in RA. This impact might explain part of the interindividual variability in RTX response observed in RA. We recently identified SPP1 rs9138 as a new RA susceptibility variant, which was also identified as having a prognostic effect by contributing to the progression of joint damage in ACPA-negative RA.14 Our results reinforce the role of SPP1 as a modifier gene in RA by affecting the RTX response. Of interest, similar to SPP1, IRF5 has also been reported as a susceptibility and modifier gene in RA.15 To our knowledge, this is the first study providing evidence of a strong contribution of an allelic combination and RTX response in RA; the magnitude of the association between the IRF5–SPP1–TNFSF13B allelic combination is 2.8 times higher than that observed for TNFSF13B rs9514828 alone, which suggests a synergistic effect of the type 1 IFN variants.11

Our results were based on the analysis of a single population of RA cases, which is one limitation of our study; the study needs to be replicated in an independent larger population to further confirm a strong contribution of the IRF5–SPP1–TNFSF13B allelic combination in the RTX response. Given a power of detection >0.95, the OR of 11.37, the frequency of the IRF5–SPP1–TNFSF13B allelic combination and the rate of 20% of non-responders, a sample of 400 individuals would be required to replicate our findings.

The pooled functional consequences of the IRF5–SPP1–TNFSF13B allelic combination remains to be determined; however, IRF5 rs2004640 is in complete linkage disequilibrium with a 5 bp (CGGGG insertion/deletion) promoter polymorphism found correlated with mRNA levels of IFN-induced genes,16 and SPP1 rs9138 affects osteopontin level,17 an extracellular-matrix-glycosylated phosphoprotein implicated in type I IFN production. In addition, the TNFSF13B rs9514828 rare allele has been found associated with increased transcription of the BAFF cytokine.19 Unfortunately, we could not detect a functional effect of the genotypic combination using the BAFF level at initiation, as the association did not reach statistical significance. This may be due to the small number of included patients as only 90 patients had a BAFF level available for the analysis. Since we could not confirm the functional effect of the combination in our study, replication in independent populations is required to support our results.

Because the genotypic combination was strongly associated to the RTX treatment efficacy, it may also affect the
safety profile to RTX. Indeed, a better efficacy to RTX may be due to a stronger B-cell depletion, which could be correlated to more side effects in particular infectious events. Our study did not assess the safety profile of the patients, and studies with a longer follow-up should be done in order to better characterise the safety profile of the patients depending on their genotype.

**CONCLUSIONS**

In conclusion, our results support the contribution of IRF5, SPP1 and TNFSF13B in the response to RTX treatment in RA at W24. However, an independent replication is required to establish the exact contribution of the alleles rs2004640, rs9138 and rs9514828 in the RTX response. Identifying individual genetic risk factors would increase our understanding of the mechanisms underlying variation in response to RTX. If validated, our model could help to define a personalised strategy for patients with RA.

**Author affiliations**

1Department of Rheumatology, Assistance Publique—Hôpitaux de Paris, Bichat-Hospital, Université Paris Diderot, Paris, France
2Plateforme de Génomique Constitutionnelle, Assistance Publique—Hôpitaux de Paris, Bichat Hospital, Université Paris Diderot, Paris, France
3UMR 1027, INSERM, Toulouse III University, Toulouse, France
4Department of Rheumatology, Hôpital Purpan, CHU Toulouse, Toulouse, France
5Department of Rheumatology, Université Paris-Sud, Assistance Publique—Hôpitaux de Paris, Paris, France
6INSERM U1184, Université Paris-Sud, Paris, France
7Department of Rheumatology, Service d’Immunéo-Rhumatologie, Montpellier, France
8Department of Rheumatology, Hôpital Lyon-sud, Pierre-Béline, France
9Department of Rheumatology, Université Paris Descartes, Hôpital Cochin, Assistance Publique—Hôpitaux de Paris, Paris, France
10INSERM U1153, PRES Sorbonne Paris-Cité, Paris, France
11Centre de Référence des Maladies Auto-immune Rares, Hôpitaux Universitaires de Strasbourg, Strasbourg, France
12Department of Rheumatology, Rouen University Hospital, Rouen, France
13INSERM U099, Université Paris Diderot, PRES Sorbonne Paris-Cité, Paris, France

**Acknowledgements** We thank all the SMART investigators and Laura Smales (Toronto, Ontario, Canada) for editing the manuscript.

**Contributors** P-AJ and PD designed the study. All authors collected the patients’ data, SG and PD carried out the statistical analyses. P-AJ and PD wrote the first version of the manuscript. All authors read and approved the final version of the manuscript.

**Funding** SMART study was sponsored by ROCHE, France.

**Competing interests** PD is supported by an unrestricted grant from ROCHE.

**Patient consent** Obtained.

**Ethics approval** The main SMART study was approved by the local ethics committee (Groupe Hospitalier Pitòi-Salpêtrière, Paris).

**Provenance and peer review** Not commissioned; externally peer reviewed.

**Data sharing statement** Data are available on demand by emailing the corresponding author.

**Open Access** This is an Open Access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY-NC 4.0) licence, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: http://creativecommons.org/licenses/by-nc/4.0/

**REFERENCES**

Variants of genes implicated in type 1 interferon pathway and B-cell activation modulate the EULAR response to rituximab at 24 weeks in rheumatoid arthritis

Pierre-Antoine Juge, Steven Gazal, Arnaud Constantin, Xavier Mariette, Bernard Combe, Jacques Tebib, Maxime Dougados, Jean Sibilia, Xavier Le Loet and Philippe Dieudé

*RMD Open* 2017 3:
doi: 10.1136/rmdopen-2017-000448

Updated information and services can be found at:
[http://rmdopen.bmj.com/content/3/2/e000448](http://rmdopen.bmj.com/content/3/2/e000448)

These include:

**References**

This article cites 19 articles, 6 of which you can access for free at: [http://rmdopen.bmj.com/content/3/2/e000448#BIBL](http://rmdopen.bmj.com/content/3/2/e000448#BIBL)

**Open Access**

This is an Open Access article distributed in accordance with the Creative Commons Attribution Non Commercial (CC BY-NC 4.0) license, which permits others to distribute, remix, adapt, build upon this work non-commercially, and license their derivative works on different terms, provided the original work is properly cited and the use is non-commercial. See: [http://creativecommons.org/licenses/by-nc/4.0/](http://creativecommons.org/licenses/by-nc/4.0/)

**Email alerting service**

Receive free email alerts when new articles cite this article. Sign up in the box at the top right corner of the online article.

**Notes**

To request permissions go to: [http://group.bmj.com/group/rights-licensing/permissions](http://group.bmj.com/group/rights-licensing/permissions)

To order reprints go to: [http://journals.bmj.com/cgi/reprintform](http://journals.bmj.com/cgi/reprintform)

To subscribe to BMJ go to: [http://group.bmj.com/subscribe/](http://group.bmj.com/subscribe/)