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EXTENDED REPORT

Genome-wide association analysis of anti-TNF drug response in patients with rheumatoid arthritis

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ABSTRACT

Background Treatment strategies blocking tumour necrosis factor (anti-TNF) have proven very successful in patients with rheumatoid arthritis (RA). However, a significant subset of patients does not respond for unknown reasons. Currently, there are no means of identifying these patients before treatment. This study was aimed at identifying genetic factors predicting anti-TNF treatment outcome in patients with RA using a genome-wide association approach.

Methods We conducted a multistage, genome-wide association study with a primary analysis of 2 557 253 single-nucleotide polymorphisms (SNPs) in 882 patients with RA receiving anti-TNF therapy included through the Dutch Rheumatoid Arthritis Monitoring (DREAM) registry and the database of Apotheekzorg. Linear regression analysis of changes in the Disease Activity Score in 28 joints after 14 weeks of treatment was performed using an additive model. Markers with $p<10^{-3}$ were selected for replication in 1821 patients from three independent cohorts. Pathway analysis including all SNPs with $p<10^{-3}$ was performed using Ingenuity.

Results 772 markers showed evidence of association with treatment outcome in the initial stage. Eight genetic loci showed improved p value in the overall meta-analysis compared with the first stage, three of which (rs1568885, rs1813443 and rs4411591) showed directional consistency over all four cohorts studied. We were unable to replicate markers previously reported to be associated with anti-TNF outcome. Network analysis indicated strong involvement of biological processes underlying inflammatory response and cell morphology.

Conclusions Using a multistage strategy, we have identified eight genetic loci associated with response to anti-TNF treatment. Further studies are required to validate these findings in additional patient collections.

INTRODUCTION

Rheumatoid arthritis (RA) is a chronic, systemic inflammatory disease characterised by polyarthritis, joint damage and functional disability.[1] It cannot be cured, and treatment is directed towards reducing the symptoms associated with the disease.

Tumour necrosis factor α (TNFα) is a pleiotropic, proinflammatory and immunoregulatory cytokine that plays a crucial role in RA.[2 3] The introduction of TNF-blocking agents, such as infliximab, etanercept and adalimumab, revolutionised the treatment of RA, most notably because of the excellent clinical efficacy and ability of these agents to prevent further structural damage in patients who failed to respond to treatment with conventional disease-modifying antirheumatic drugs (DMARDs).[4 5] Despite this success, a substantial proportion of patients with RA (~30%) treated with TNF inhibitors do not display any significant clinical improvement.[6 7] Given the expensive treatment regimen and the potential side effects associated with the treatment, the idea of a priori prediction of response to anti-TNF agents in patients with RA is a highly relevant topic.[8 9]

Studies of clinical parameters and biomarkers have identified several factors that influence anti-TNF treatment outcome, including concurrent use of DMARDs, lower baseline Health Assessment Questionnaire score, gender, smoking, serological status, TNF levels at the site of inflammation, and the synovial microarchitecture. However, these factors explain only a relatively small proportion of the observed variance in response (R^2=17–29%) and are therefore not suitable to be used as predictors in a clinical setting.[9–12] In addition, effort has been put into the identification of genetic markers predicting anti-TNF treatment outcome. Most of these studies are candidate gene based, focusing on polymorphisms in genes known to be involved in RA pathogenesis and genes implicated in TNFα signalling pathways.[13] The most thoroughly investigated gene is *TNFA,* encoding TNFα, the target of anti-TNF treatment. Initial studies suggested a role for a variant in the promoter of the gene (−308G>A) in anti-TNF response, although recent meta-analyses do not support this association.[14 15]

So far, using the candidate gene approach, the most convincing evidence of association with response to anti-TNF therapy in patients with RA is found for an RA risk allele at the *PTPRC* gene locus.[16 17]

A number of additional potential candidate loci have been suggested on the basis of results from three genome-wide association studies (GWAS).[18–20] In a GWAS of 566 patients with RA, Plant *et al*[19] found evidence of association at seven genetic loci with response to TNF blockade, two of which mapped within genes: PDZ domain-containing protein 2 (*PDZD2*) and eyes absent homologue 4 (*EYA4*). In a small study (n=89) by Liu *et al*,[18] association was reported for markers in the *MAFB* and *PON1* gene regions as well as in a region of chromosome 9 that contains the interferon kappa (*IFN-κ*), *MOBKL2B* and *C9orf72* loci. The most compelling candidate for involvement in anti-TNF treatment response in this study is *IFN-κ*, since type I IFNs play a definite role in inflammatory disease and autoimmunity.[21] However, these results could not be replicated by others.[20 22] Krintel *et al*[20] reported associations of single-nucleotide polymorphisms (SNPs) within a non-coding region surrounded by the *TLR4* gene and the *DBC1* gene and a marker within the *FOXP1* gene with treatment outcome in a cohort of 196 Danish patients.

To determine whether the reported loci reflect true associations, and to search for novel loci that influence differential response to anti-TNF therapy, we performed a GWAS in a cohort of 882 Dutch patients with RA receiving anti-TNF therapy.

MATERIALS AND METHODS

Patients and study design

A multistage GWAS was performed including 984 patients with RA receiving anti-TNF medication (stage 1) with subsequent follow-up of the most significant signals in two replication cohorts (stage 2 (n=954) and 3 (n=867)).

For the initial genome-wide association analysis, patients were recruited through a collaborative effort in which 669 patients were included as part of the Dutch Rheumatoid Arthritis Monitoring (DREAM) registry (http://www.dreamregistry.nl) and 315 patients were enrolled through the database of ApotheekZorg, which facilitates the Dutch distribution of adalimumab. All patients were diagnosed with RA according to the 1987 revised American College of Rheumatology (ACR) criteria and were treated with anti-TNF according to the indications in the Netherlands: Disease Activity Score 28 (DAS28) >3.2; previous failure on at least two DMARDs, one of which has to be methotrexate; biological naïve.[23] We used the DAS28 change at 3 months as outcome for our analysis. Patients who stopped treatment within the first 3 months were not included in the study. All patients gave written informed consent, and the study was approved by the ethics committees of the participating hospitals.

For stage 2, data from 954 RA cases treated with anti-TNF were selected from nine different cohorts as part of the ACR Research and Education Foundation (REF) 'Within Our Reach' project: Autoimmune Biomarkers Collaborative Network (ABCoN), Academic Medical Center Amsterdam (AMC), Behandelstrategieen voor Rheumatoide Arthritis (BeSt), Biological in Rheumatoid arthritis Genetics and Genomics Study Syndicate (BRAGGSS), Brigham Rheumatoid Arthritis Sequential Study (BRASS), Epidemiological Investigation of Rheumatoid Arthritis (EIRA), Immunex Early Rheumatoid Arthritis (ERA) study, Karolinska Institutet (KI) study, READE, formerly Jan van Breemen Institute (READE) study, Treatment of Early Aggressive RA (TEAR)—this collection has been reported on previously.[16 24]

Finally, stage 3 included two previously described cohorts: (1) Wellcome Trust Case Control Consortium (WTCCC) comprising 595 patients with RA from the UK[19]; (2) 272 patients with RA from France ascertained through ReAct.[25]

Genotyping and preimputation quality control (QC)

For stage 1, genotyping was performed using the Illumina HumanHap550-Duo Bead Chip or the Human660W-Quad BeadChips, according to the instructions of the manufacturer (Illumina, San Diego, California, USA).

Preimputation QC procedures were applied using PLINK software.[26] SNPs that had minor allele frequency (MAF) <0.05 and call rates <95% were excluded, as well as SNPs with extreme departures from Hardy–Weinberg equilibrium ($p<1\times10^{-5}$). Subsequently, QC filtering was performed at the sample level. Four samples were excluded because of gender mismatch with phenotypic data, and 21 samples because of a genotyping rate <95%. Cryptic relatedness between study participants was examined by estimating identity by descent (IBD). Seven DNA samples were excluded based on a proportion of IBD (PI-HAT)>0.125. Lastly, principal components were computed to adjust for population stratification using the EIGENSTRAT package[27]; 59 individuals were removed as outliers, based on the EIGENSTRAT default filter. After QC, 882 individuals were left for analysis. For the replication cohorts, the same QC criteria were used.

Imputation

To obtain a marker set common to all studies and to increase overall coverage of the genome, imputation was performed using HapMap2 release 21 (downloaded from http://www.sph.umich.edu/csg/abecasis/MACH/download/HapMap-r21.html). Haplotype phasing using MaCH software (http://www.sph.umich.edu/csg/abecasis/MACH/index.html)[28] was followed by genotype imputation by Minimac (http://genome.sph.umich.edu/wiki/Minimac).

Post-imputation QC criteria were MAF ≥1% and good imputation quality, which was defined as RSQR≥0.3. In total, 2 557 253 SNPs were included in the analysis.

Stage 1 GWAS

The additive genetic effect of each SNP allele on change in DAS28 at 3 months of treatment was estimated using linear regression analysis with adjustment for baseline DAS28 and the first three principal components derived using EIGENSTRAT. These analyses were performed using the Mach2qtl software package[29] (downloaded from http://www.sph.umich.edu/csg/abecasis/MACH/download/HapMap-r21.html).

The Dutch samples were not genotyped in one run and therefore the results were analysed using a meta-analysis approach that combines study-specific β estimates based on the fixed-effects model and using the inverse of the variance of the study-specific β estimates to weigh the contribution of each study. Calculations were performed in the METAL package (http://www.sph.umich.edu/csg/abecasis/metal). Within-study genomic control correction was applied to the variance of β estimates using λ factors specific to each study ($\lambda_1=1.013$, $\lambda_2=1.016$, $\lambda_3=0.996$).

SNP selection for replication in stages 2 and 3

Markers demonstrating association with DAS28 change ($p<10^{-3}$) in stage 1 were selected for replication. Pruning of hits based on linkage disequilibrium (LD) was performed before replication: all SNPs with a HapMap Utah residents with

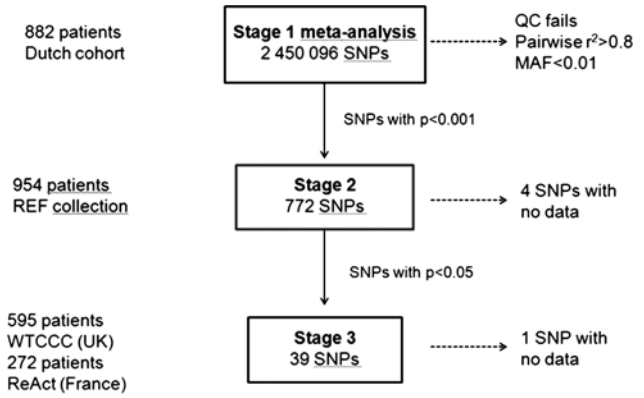

Figure 1 Study design of a multistage genome-wide association studies (GWAS) of response to anti-tumour necrosis factor (TNF) medication in patients with rheumatoid arthritis (RA). We started out with meta-analysis of GWAS data from a Dutch cohort comprising 882 patients with RA treated with anti-TNF medication. We selected 772 single-nucleotide polymorphisms (SNPs) that reached $p<0.001$, which were further followed-up in stage 2 samples (N=954 individuals). Thirty-eight SNPs out of 768 investigated in stage 2 passed $p<0.05$ and were further investigated in two separate cohorts in stage 3 (N=595 and N=272 individuals). MAF, minor allele frequency; QC, quality control.

ancestry from northern and western Europe (CEU) pair-wise correlation coefficient (r^2) >0.8 with the most strongly associated SNPs in a locus were eliminated. A total of 772 independent loci were left for replication. Replication analysis in stage 2 was carried out using existing GWAS scan data from the REF collection. Those SNPs that passed the $p<0.05$ threshold in stage 2 were further evaluated using GWAS data from two collections (WTCCC and ReAct) in stage 3. A meta-analysis using the METAL package was performed.

Explorative analysis for functional relation between genes identified in stage 1

All markers showing association with DAS change ($p<10^{-3}$) in stage 1 were investigated for functional interactions by Ingenuity Pathway Analysis (IPA) software (Ingenuity Systems, www.ingenuity.com) using an unsupervised analysis. IPA computes a score for each network accordingly to the fit of the user's set of input genes. The score, representing the –log (p value), indicates the likelihood of focus genes (genes harbouring associated SNPs) in a network being found together due to random chance.

RESULTS

Figure 1 presents an overview of our study approach. The baseline characteristics of the patients included in the study are summarised in table 1.

Genome-wide association analysis

In stage 1, 2 448 996 SNPs were tested for association with anti-TNF outcome in the Dutch population. Of these SNPs, 2359 showed evidence of association with treatment response ($p<10^{-3}$, online supplementary table 1). LD pruning reduced the number of SNPs prioritised for replication analysis to 772.

We aimed to replicate the findings in 954 patients from the REF collection for stage 2 of our study. A total of 768 SNPs passed the QC in the second stage replication cohort. Thirty-nine markers showed nominally significant ($p<0.05$) association with treatment outcome under an additive model, 20 of which demonstrated directionally consistent association and a resulting improvement in the association signal in a stage 1 and 2 combined meta-analysis (online supplementary table 2).

In stage 3, the 39 SNP stage 2 markers were further inspected for replication in two independent GWAS, comprising 595 patients from the UK and 272 patients from France (ReAct), separately. One SNP (rs11642036) failed QC criteria in both replication cohorts, leaving 38 SNPs for analysis. None of the tested SNPs showed nominal association with treatment outcome in these cohorts (table 2). However, the meta-analysis including all cohorts showed improved association signals for eight SNPs compared with our stage 1 results, three of which, rs1568885, rs1813443 and rs4411591, demonstrate directional consistency over all four cohorts studied (table 2).

None of the SNPs previously reported to be associated with treatment outcome showed evidence of association in the Dutch stage 1 cohort (table 3).[16–20]

Explorative pathway analysis of stage 1

We explored the stage 1 dataset for potential functional relationship between genes that showed evidence of association at $p<10^{-3}$ with treatment outcome using the IPA. This resulted

Table 1 Study population characteristics

	Stage 1			Stage 2	Stage 3	
	Combined	Dream	ApotheekZorg	REF Col*	WTCCC	ReAct
Number	984	669 (69.7)	315 (30.3)	954	595	272
Gender female (%)	68.6	67.8	70.4	75.6	77.3	77.9
Anti-TNF agent						
Infliximab	225 (22.9)	225 (33.7)		415 (43.5)	268 (45.0)	
Adalimumab	638 (64.8)	323 (48.2)	315 (100)	174 (18.2)	68 (11.4)	272 (100)
Etanercept	121 (12.3)	121 (18.1)		365 (38.3)	259 (43.6)	
MTX co-medication (%)	73.4	69.2	82.2	65.6	85.6	50
DAS28						
Baseline	5.5±1.2	5.3±1.3	5.8±1.0	5.5±1.2	6.7±0.9	5.9±1.0
DeltaDAS (14 weeks)	3.6±1.3	3.9±1.3	3.1±1.1			

*The American College of Rheumatology Research and Education Foundation (REF) collection used for stage 2 is composed of nine different cohorts: Autoimmune Biomarkers Collaborative Network (ABCoN), Academic Medical Center Amsterdam (AMC), Behandelstrategieen voor Rheumatoide Arthritis (BeSt), Biological in Rheumatoid arthritis Genetics and Genomics Study Syndicate (BRAGGSS), Birgham Rheumatoid Arthritis Sequential Study (BRASS),Epidemiological Investigation of Rheumatoid Arthritis (EIRA), Immunex Early Rheumatoid Arthritis (ERA) study, Karolinska Institutet (KI) study, Jan van Breemen Institute (READE) study, Treatment of Early Aggressive RA(TEAR).
Numbers are depicted as n (%) or mean±SD.
DAS, Disease Activity Score; MTX, methotrexate; TNF, tumour necrosis factor.

Table 2 Association results for replicated SNPs in all cohorts and final meta-analysis

				Stage 1 (n=882)		Stage 2 (n=954)		Stage 3 (n=867)				Combined meta-analysis	
								WTCCC		ReAct			
SNP	Chr	Position	Allele	P_{GC}	β	P_{GC}	β	P_{GC}	β	P_{GC}	β	P	β
rs4411591	18	6540117	C	7.33×10^{-4}	0.248	0.02206	0.208	0.483	0.097	0.461	0.114	5.14×10^{-5}	0.202
rs7767069	6	68827284	A	3.41×10^{-4}	−0.188	0.02839	−0.161	0.532	0.057	0.086	−0.203	8.34×10^{-5}	−0.144
rs4651370	1	185505715	A	2.54×10^{-4}	0.256	5.28×10^{-3}	0.271	0.867	−0.021	0.921	0.015	1.09×10^{-4}	0.190
rs1813443	11	99516221	C	3.50×10^{-4}	−0.195	0.04021	−0.155	0.605	−0.048	0.403	−0.097	1.37×10^{-4}	−0.148
rs1447722	3	141037143	C	5.46×10^{-4}	0.193	7.63×10^{-4}	0.185	0.881	−0.014	0.573	−0.064	1.62×10^{-4}	0.134
rs1568885	7	13604056	A	5.93×10^{-4}	0.255	0.0306	0.201	0.594	0.061	0.5	0.095	1.69×10^{-4}	0.185
rs12142623	1	185557029	A	4.19×10^{-4}	0.248	7.68×10^{-3}	0.267	0.484	−0.087	0.398	0.126	2.04×10^{-4}	0.185
rs2378945	14	31370541	A	8.61×10^{-4}	−0.166	0.01313	−0.171	0.489	0.061	0.905	0.013	6.88×10^{-4}	−0.115

All SNPs that have improved their p value in meta-analysis compared with the initial genome-wide association studies are listed. rs4411591, rs1813443 and rs1568885 demonstrated directional consistency over all four cohorts studied.
Chr, chromosome; P_{GC}, p values with genomic control correction applied; SNP, single-nucleotide polymorphism.

Table 3 Initial genome-wide association studies association results for loci previously reported to be associated with anti-tumour necrosis factor treatment response

SNP	Chr	MAF	Gene	P_{GC}	β
SNPs from Liu *et al*[18]					
rs983332	1	0.18	–	0.603	0.031
rs928655	1	0.23	GBP6	0.051	0.109
rs13393173	2	0.19	LASS6	0.71	−0.006
rs437943	4	0.34	–	0.93	0.0006
rs10945919	6	0.32	AK093144	0.44	0.03
rs854555	7	0.33	PON1	0.61	0.018
rs854548	7	0.25	PON1	0.61	0.0102
rs854547	7	0.35	PON1	0.52	0.0225
rs868856	9	0.31	MOBKL2B	0.65	−0.0218
rs2814707	9	0.26	MOBKL2B	0.95	−0.002
rs3849942	9	0.26	C9orf72	0.98	−0.0069
rs774359	9	0.27	C9orf72	0.89	−0.0159
rs6138150	20	0.18	–	0.66	0.0329
rs6028945	20	0.14	–	0.78	−0.0635
rs6071980	20	0.12	–	0.74	−0.0026
SNPs from Plant *et al*[19]					
rs12081765	1	0.39	–	0.73	−0.024
rs4694890	4	0.49	TEC	0.4	0.042
rs1532269	5	0.43	PDZD2	0.92	0.051
rs17301249	6	0.18	EYA4	0.36	−0.05
rs1350948	11	0.14	–	0.38	0.0642
rs7305646	12	0.50	–	0.39	0.05
rs7962316	12	0.40	BC118985	0.92	−0.026
SNPs from Krintel *et al*[20]					
rs10520789	15	0.13	NR2F2	0.47	0.071
rs11870477	17	0.13	MAP2K6	0.67	0.073
rs16973982	15	0.14	NR2F2	0.60	0.072
rs8046065	16	0.10	CREBBP	0.12	0.146
rs885814	1	0.32	ALPL	0.49	0.053
rs869179	1	0.34	ALPL	0.75	0.016
rs2722824	9	0.30	TLR4	0.33	−0.053
rs885813	1	0.43	ALPL	0.30	0.049
rs1875620	9	0.46	C9orf47	0.26	0.051
rs11525966	9	0.45	C9orf47	0.19	0.051
PTPRC					
rs10919563	1	0.13	PTPRC	0.384	−0.079

Chr, chromosome; MAF, minor allele frequency; P_{GC}, p values with genomic control correction applied; SNP, single-nucleotide polymorphisms.

in the identification of eight networks. The highest scoring network ($p=10^{-41}$) included 26 genes identified in the genome-wide association analysis stage 1, and nine additional interacting genes (figure 2). Importantly, this network is predicted to be involved in metabolic disease and biological processes underlying inflammatory response and cell morphology and contains genes implicated in TNF signalling (*NFκB)* and antibody formation (*IgG*).

DISCUSSION

In this report, we described the results of the largest GWAS of response to anti-TNF treatment in patients with RA conducted to date.

Using a multistage study design, we identified eight genetic loci showing suggestive evidence of association (improved p values) with treatment outcome in our overall meta-analysis, with three markers (rs4411591, rs1813443 and rs1568885) showing directional consistency over all four cohorts studied. In the combined cohort, eight identified loci together explain 3.8% of the variance in the treatment response. Although no single SNP reached a genome-wide level of significance ($p<5\times10^{-8}$), these variants represent excellent candidates for further investigation.

Of the eight markers with suggestive evidence of association, two map to an intergenic region in which the nearest gene is interesting in terms of its biological function. The SNPs, rs12142623 and rs4651370, are located ~400 kb downstream from the phospholipase A2, group IVA *(PLA2G4A)* gene. The protein encoded by *PLA2G4A* is a phospholipase enzyme involved in generation of eicosanoids, molecules with regulative function in inflammatory responses. TNFα is one of the first known stimuli for PLA2G4A activation, through the action of both TNF receptor subtypes.[30] It might be possible that the identified SNPs influence long-range regulatory elements.

In addition, three of the eight identified SNPs map within genes. The marker rs4411591 maps to the *Loc100130480*, encoding a hypothetical protein, while rs2378945 is located in the nucleotide-binding protein-like (*NUBPL*) gene. *NUBPL* encodes a protein required for the assembly of the respiratory chain NADH dehydrogenase (complex I). Finally, rs1813443 is located in the intronic region of contactin 5 (*CNTN5*), a member of the immunoglobulin superfamily, which is thought to have a role in the formation of axon connections in the developing nervous system.[31] Little is known about the possible

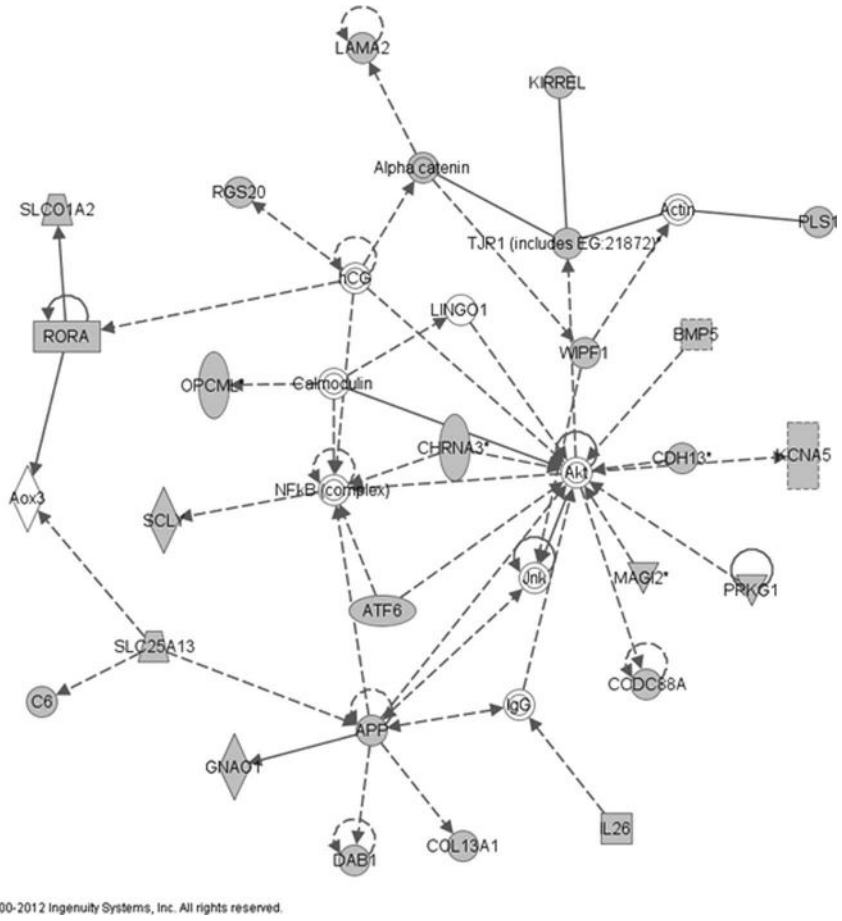

Figure 2 Top gene network derived from Ingenuity Pathway Analysis. Genes/gene products are represented graphically as nodes, and the biological relationship between two nodes is represented as an edge (line). Grey colour of the node indicates genes that were identified in the stage 1 genome-wide association studies ($p<0.001$), and white indicates that the molecule was added from the Ingenuity Knowledge Base. Dashed lines indicate indirect interactions; solid lines indicate direct interactions. The style of the arrows indicates specific molecular relationships (A acts on B, A binds to B), and dotted lines indicate an indirect interaction. All edges are supported by at least one reference from the literature or from canonical information stored in the Ingenuity Knowledge Base. Nodes are displayed using various shapes that represent the functional classes of the gene product (square, cytokines; diamond, enzyme; circle in a circle, complex/group; trapezium, transporter; ellipse lying, transcription regulator; ellipse standing, transmembrane receptor; dotted rectangle, ion channel; rectangle, ligand-dependent nuclear receptor; triangle, kinase; dotted square, growth factor; circle, other).

involvement of these genes in inflammatory disease, and there are no apparent functional links to anti-TNF treatment outcome, yet. If association with anti-TNF response can be confirmed in additional replication studies, future functional studies are needed to prove the biological link with anti-TNF response.

We did not find any evidence for association for the loci identified from previously published GWAS on anti-TNF response[18–20] or for the *PTPRC* gene (table 3)[16 17] in the Dutch patients included in our stage 1 GWAS, suggesting that these genes do not play a major role in anti-TNF treatment outcome in our population. However, the power of our study to detect an association with PTPRC loci at $p<0.0005$ in a set size of 882 patients was 26%.

However, the top network constructed with IPA indicated involvement of the genes showing suggestive association in stage 1 GWAS in the following processes: cell morphology, metabolic disease and inflammatory response. This is in line with the expected biological function of anti-TNF; TNFα is an important mediator of insulin resistance and it also impedes insulin-mediated glucose uptake.[32] More importantly, other studies showed a positive long-term effect of TNF antagonists on insulin resistance, which correlated with improvement in disease activity.[33 34] The identified network also harbours two interesting interacting molecules: NFκB and IgG. NFκB is a transcription regulator that is preferentially activated by TNF and is the main downstream target of the TNF signalling pathway.[35] The finding that the genes identified through the GWAS interact with IgG is particularly interesting, since response failure and side effects of anti-TNF due to immunogenicity are not rare and it has been found that infliximab antibodies are exclusively of IgG isotype.[36] Both molecules might have a central role in determining the outcome of treatment with anti-TNF agents. Besides this network, we could map the most prominent associations from stage 1 to the *VAV1* and *SPRED2* genes. *VAV1* has been found to protect T cells from Fas-mediated apoptosis in Jurkat leukaemia T cells,[37] and it has been confirmed that patients with RA show differential sensitivity to apoptosis of peripheral blood lymphocytes induced by anti-TNF therapy.[38] *SPRED2* is a known RA risk locus.[39] This network might represent new leads and new additional candidates for future research.

Our study, which included 2703 patients with RA treated with anti-TNF agents, is the largest GWAS of treatment outcome to date. However, our sample size still remains modest compared with genetic studies of risk of RA[40 41] and

other complex traits.[42 43] Also, there are important aspects that may affect our results. There is considerable disease heterogeneity in RA. In our dataset, there is a difference in, for example, the number of women included in the studies, but also in type of anti-TNF treatment and co-medication use (table 1). Furthermore, the REF collection used for replication in stage 2 consists of nine smaller cohorts from several populations. Hence, combining results across four different cohorts of patients that are rather diverse in subject ascertainment and assessment and previous treatment can lead to different effect estimates among studies and false negative results. In addition, the DAS28 score, used as the measure of treatment outcome in our study, is a composite score including four measures: swollen and tender joint counts, erythrocyte sedimentation rate, and self-reported general health. This score is a powerful tool for measuring treatment response in a clinical setting. However, it is likely that this complex measure is influenced by genetic effects that are individually modest and would require large sample sizes to be detected.

In the present study, we have identified eight genetic loci that show evidence of influencing anti-TNF treatment response based on a multistage approach in a population of 2703 Caucasian patients with RA. Our findings require further validation in independent cohorts and/or at a functional level.

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Notes