A genome-wide association study suggests contrasting associations in ACPA-positive versus ACPA-negative rheumatoid arthritis

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ABSTRACT

Background Rheumatoid arthritis (RA) can be divided into two major subsets based on the presence or absence of antibodies to citrullinated peptide antigens (ACPA). Until now, data from genome-wide association studies (GWAS) have only been published from ACPA-positive subsets of RA or from studies that have not separated the two subsets. The aim of the current study is to provide and compare GWAS data for both subsets.

Methods and results GWAS using the Illumina 300K chip was performed for 774 ACPA-negative patients with RA, 1147 ACPA-positive patients with RA and 1079 controls from the Swedish population-based case–control study EIRA. Imputation was performed which allowed comparisons using 1 723 056 single nucleotide polymorphisms (SNPs). No SNP achieved genome-wide significance (2.9 × 10⁻⁸) in the comparison between ACPA-negative RA and controls. A case–case association study was then performed between ACPA-negative and ACPA-positive RA groups. The major difference in this analysis was in the HLA region where 768 HLA SNPs passed the threshold for genome-wide significance whereas additional contrasting SNPs did not reach genome-wide significance. However, one SNP close to the RPS12P4 locus in chromosome 2 reached a p value of 2 × 10⁻⁶ and this locus can thus be considered as a tentative candidate locus for ACPA-negative RA.

Conclusions ACPA-positive and ACPA-negative RA display significant risk allele frequency differences which are mainly confined to the HLA region. The data provide further support for distinct genetic aetiologies of RA subsets and emphasise the need to consider them separately in genetic as well as functional studies of this disease.

INTRODUCTION

Rheumatoid arthritis (RA) is a common inflammatory joint disease caused by a complex interplay of genetic variants and environmental exposures.1–3 Disease outcomes in RA are highly variable, and the presence or absence of antibodies to citrullinated peptide antigens (ACPA) has proved to be one of the best clinical predictors of the severity of disease course.4 5 In addition, ACPA-positive patients with unspecified arthritis respond differently from ACPA-negative patients with RA to early methotrexate therapy.6

In recent years a number of candidate genes have been shown to associate differently with ACPA-positive and ACPA-negative RA. Several genetic variants within the HLA region, specifically the shared epitope-containing HLA-DRB1 alleles,7–9 PTNP22 alleles,10 11 as well as a variant in the CS-TRAFL region,12 13 TNFAIP3,14 15 CD40, CCL21 and many other loci16 17 have been shown to be associated with ACPA-positive RA but have not been tested for ACPA-negative RA. By contrast, variations in IRF518 and C-type lectin genes19 appear to be associated with ACPA-negative RA. Association of ACPA-negative disease with HLA-DRB1*03 haplotype was previously suggested20 21 but has not been replicated in a larger study.22 In at least one study23 an indication for an association of PTNP22 marker with ACPA-negative RA was presented based on 65 cases of RA. On the other hand, STAT4 variant has been shown in a meta-analysis to be a risk factor for both subgroups of RA.24 Smoking is the only environmental risk factor unambiguously associated with the risk of RA, but it too appears to affect risk only for ACPA-positive patients.8

These data on different risk factors for ACPA-positive and ACPA-negative RA have been used to propose a new aetiological model for ACPA-positive RA, whereas no such model yet exists for ACPA-negative disease.18 25 26 A major implication of these observations is that genetic and immunological studies of RA should consider this heterogeneity of RA.

So far, the most powerful technique to analyse the effects of genetic variation on disease susceptibility—that is, the genome-wide association study (GWAS)—has not addressed this heterogeneity and genome-wide data published on RA to date have either considered ACPA-positive disease alone15 17 27 or grouped both subtypes together.14 28

In order to provide a more complete picture of genetic risk factors for RA, we have performed genome-wide association analyses in both RA subsets in two different collections of RA cases and controls defined by ACPA status (Swedish Epidemiological Investigation of Rheumatoid Arthritis (EIRA) and North American RA Consortium (NARAC)), and in data from the Wellcome Trust Case–Control Consortium (WTCCC) which contains patients from both subsets but where subdivision according to ACPA status has not yet been performed.

METHODS

Subjects

EIRA is a population-based case–control study enrolling incident (predominantly <1 year after
RESULTS

GWAS of ACPA-negative RA

We conducted a GWAS for ACPA-negative patients with RA with 774 cases and 1079 controls selected from the EIRA study. Both genotyped and imputed single nucleotide polymorphisms (SNPs) were included in the analysis. No single SNP reached genome-wide significance (figure 2). A Q-Q plot for observed versus expected p values is shown in figure 3A and shows no significant deviation from the expected distribution. As shown in table 1, five SNPs from three genetic loci had p values <10^{-5}. One out of five was not associated with ACPA-positive RA while the other four (from two independent loci at chromosome 7) had only nominal association. These results indicate little or no overlap between the two RA subgroups for the five tentative SNPs that may associate with ACPA-negative RA in this GWAS.

GWAS of ACPA-positive RA

We have previously reported GWAS data on ACPA-positive RA based on a fraction of the EIRA study in combination with NARAC. In addition to the previously used 627 ACPA-positive RA cases and 641 controls from Sweden, we now selected 520 new ACPA-positive RA cases and 438 controls from the EIRA study for extension of the GWAS for ACPA-positive RA. Because all cases and controls were taken from the same study population, we combined all EIRA samples into a single analysis which included both genotyped and imputed SNPs. The diagram of genome-wide association for this analysis is shown in figures 4 and 5 and Q-Q plots are shown in figure 3B. Out of 1 723 056 analysed SNPs, we found clinical onset) cases of RA. The study base comprises residents aged 18–70 years in a geographically-defined area in the central and southern parts of Sweden. Details of the study design have been reported elsewhere. For each case a control was randomly selected from the study base by matching age, sex and residential area. For the present study we selected 3176 individuals (829 ACPA-negative cases of RA, 1218 ACPA-positive cases of RA and 1129 controls) for genome-wide genotyping. Informed consent was obtained from all participants and the ethical review board at the Karolinska Institutet approved the study. A portion of the data was included in a previously published GWAS of ACPA-positive RA (see table 1 in online supplement), but here we enlarge the GWAS dataset for ACPA-positive patients with RA and controls and include genome-wide data on ACPA-negative patients for the first time.

NARAC provided genotypes for 889 ACPA-positive patients and 1232 controls. The patients of self-reported white ancestry were recruited as prevalent (69.6%) or incident RA cases from several sites throughout North America. Nearly half of the cases (51.1%) reported a positive family history. Control subjects were selected on the basis of similar self-reported ancestry from 20 000 persons who were part of the New York Cancer Project. Written informed consent was obtained from all subjects who provided blood samples in accordance with protocols approved by the local institutional review boards.

The British RA population comprised 1860 patients and 3000 controls. Recruitment procedures have been described previously, together with frequencies of genetic variations. Demographic characteristics of patients and controls and the study logistics are shown in table 1 in the online supplement and in figure 1 where corresponding numbers after quality control procedures (see below) are shown. Genotyping, serological analysis and statistical evaluation are shown in the online supplement.

Figure 1 Work flow for genome-wide analysis (GWAS) of two subgroups of rheumatoid arthritis (RA). Three different Caucasian study populations represented in different colours (blue, green and red: Swedish, US, UK). Selection of data from previously published studies indicated by dashed rectangles with subsequent reference. Difference in sums is due to QC procedures at each stage of analysis. ACPA, antibodies to citrullinated peptide antigens.
1.96, p=9.77E-09). After relaxing the threshold for significance up to 10^{-6}, an additional 196 SNPs were found to be significant from the HLA locus and seven non-HLA SNPs from the cluster of a ‘gene desert’ at chromosome 13 (see table 2 in online supplement). These seven SNPs are all in a recombination block according to HapMap data.\textsuperscript{31}

719 SNPs which passed a genome-wide significance threshold (see table 2 in online supplement). Of note, 718 of these SNPs were located within the HLA locus at chromosome 6 with physical positions between 31 279 236 and 33 164 413 (1 885 177 bp). A single non-HLA SNP rs2476601 was from \textit{PTPN22} gene at chromosome 1 with OR 1.66 (95% CI 1.40 to 1.96, p=9.77E-09). After relaxing the threshold for significance.
Contrasts between ACPA-positive and ACPA-negative RA

To formally test the hypothesis of a contrast between the two disease subgroups, we used the EIRA study to perform a direct comparison between ACPA-positive and ACPA-negative RA using the full GWAS data sets for these two populations of RA patients. The threshold for genome-wide significance was estimated as $2.9 \times 10^{-8}$ (after Bonferroni correction for 1,723,056 tests). After corrections for multiple testing we found significant differences only in the HLA region of chromosome 6p with 814 SNPs spanning between 31,278,893 and 33,164,413 (see table 4 in online supplement). When we increased the threshold to $10^{-5}$ we identified an additional 352 SNPs in the HLA region targeted to physical positions in the extended HLA locus between 30,155,944 and 33,886,942 (3,730,998 bp) and three additional non-HLA SNPs (table 2): rs4305317 from chromosome 2 close to the LDHAL3 (lactate dehydrogenase A-like 3) gene, rs6448119 from chromosome 4 between the KCNIP4 (Kv channel interacting protein 4) and the GPR125 (G protein-coupled receptor...
The contrasting genetic aetiologies of ACPA-positive and ACPA-negative RA are most strikingly evident at the HLA locus, where the associations are allele-specific for ACPA-negative disease and one appeared to provide particularly strong protection. Notably, only very few genetic variations were associated with both RA subsets and those had a very minor influence on the genetic risk of RA. The described differences in the HLA region between ACPA-positive and ACPA-negative RA are well in line with previous genetic studies and concerning tentative associations described as being associated with ACPA-positive RA in previous genome-wide studies and concerning tentative associations defined by absence of ACPA reactivity, and the first comparison between the two subsets was made. When analysing the published data for association with HLA genes, and particularly with variations in HLA class II genes, are valid only for the ACPA-positive subset of RA. Overall, we found significant differences in genetic associations between the two subsets, both concerning genetic variations that are preferentially seen for the ACPA-negative subset of RA. Additionally, the association with HLA genes, and particularly with variations in HLA class II genes, is dominated by susceptibility risk alleles for ACPA-positive RA, and rs44819 seem to be in association primarily with ACPA-negative RA.

### Table 2

<table>
<thead>
<tr>
<th>Reference sequence</th>
<th>Chromosome</th>
<th>ACPA ACPA-negative versus ACPA-positive</th>
<th>ACPA ACPA-negative RA</th>
<th>ACPA ACPA-positive RA</th>
<th>Allelic frequency in cases</th>
<th>Allelic frequency in controls</th>
<th>Allelic frequency in cases</th>
<th>Allelic frequency in controls</th>
<th>Allelic frequency in cases</th>
<th>Allelic frequency in controls</th>
<th>Allelic frequency in cases</th>
<th>Allelic frequency in controls</th>
<th>Allelic frequency in cases</th>
<th>Allelic frequency in controls</th>
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<th>Allelic frequency in controls</th>
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<th>Allelic frequency in controls</th>
<th>Allelic frequency in cases</th>
<th>Allelic frequency in controls</th>
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*Genotyping status varied as directly genotyped ('gen') or imputed ('imp').
†Cochran–Armitage trend test.
‡Genotyping frequency for ACPA-negative RA group presented for opposite allele due to different direction of association.
ACPA, antibodies to citrullinated peptide antigens; EIRA, Swedish Epidemiological Investigation of Rheumatoid Arthritis; GWAS, genome-wide association studies; NARAC, North American RA Consortium; RA, rheumatoid arthritis; SNP, single nucleotide polymorphism; WTCCC, Wellcome Trust Case-Control Consortium.

Extended report


The described differences in the HLA region between ACPA-positive and ACPA-negative disease are well in line with previous genetic studies and concerning tentative associations described as being associated with ACPA-positive RA, and rs44819 seem to be in association primarily with ACPA-negative RA.
results have to be interpreted with caution given the limited power of our investigations. Nevertheless, we can be confident that the major discrepancies described by GWAS—that is, the differential associations in the HLA region—are indeed true differences between the ACPA-positive and ACPA-negative RA subsets.

Concerning the non-HLA genes associated with the different subsets of RA, we performed additional genotyping to confirm the accuracy of imputation of SNPs using real genotyping data, when possible, to evaluate differences between the two RA subsets in order to decrease the risk of false positive findings due to use of imputations. Using this methodology we were not able to detect any strong genetic risk factors for ACPA-negative RA, whereas we found suggestive evidence—for two new candidate loci in ACPA-negative disease that the major discrepancies described by GWAS—that is, the power of our investigations. Nevertheless, we can be confident that the major discrepancies described by GWAS—that is, the differential associations in the HLA region—are indeed true differences between the ACPA-positive and ACPA-negative RA subsets.

Deciphering the pathogenesis of ACPA-negative RA remains a major challenge for genetic studies. In this study we found suggestive evidence—but not genome-wide significance-based evidence—for two new candidate loci in ACPA-negative disease (ie, RPS12P4 and IGFBP1). We also found suggestive evidence for the previously described IRF5 locus as susceptibility genes for ACPA-negative RA. Thus, most of the difference in genetic factors between ACPA-negative and ACPA-positive RA is seen in the HLA region, close to the HLA-DRB1 locus. The non-HLA variant rs4305317, close to RS12P4 at chromosome 2, is the best candidate for association with ACPA-negative RA but not with ACPA-positive RA. It should be emphasised, however, that this association as well as other data related to associations with ACPA-negative RA need independent replication owing to the limited size of the present study.

GWAS provide new potentials to determine genetic variations and molecules pathways that are shared between different inflammatory diseases. The associations of several diseases and disease subsets with PTPN22, CD40, TRAF1-C5 and STAT4 are typical examples of this sharing. The present study illustrates the other complementary perspective—namely, the potential also to use GWAS to subdivide criterion-based diseases such as RA into new entities. As exemplified here, one subset of a disease may then share certain risk genes and possibly pathogenic pathways with some other autoimmune entities, as is the case for PTPN22 and ACPA-positive RA and type I diabetes, whereas the other subset of the same criterion-based disease may share genetic linkages and pathogenetic pathways with still other autoimmune entities. We can expect refined classifications of criterion-based diseases such as RA to lead to the use of genetics to provide an indication of what molecular pathways are involved in the pathogenesis of different subsets of today’s criterion-based diseases. This knowledge should, in turn, be indispensable when trying to find treatments to target these pathways in patients in these different and distinct subsets of chronic autoimmune diseases.

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Competing interests None.

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Ethics approval This study was conducted with the approval of the Regional Ethical Review Board in Stockholm.

Table 3 Frequencies of previously detected genetic variants for RA: comparison of meta-analysis of ACPA-positive RA patients from three populations with ACPA-negative RA patients

<table>
<thead>
<tr>
<th>SNP</th>
<th>Chromosome</th>
<th>Gene/loci</th>
<th>Minor allele*</th>
<th>EIRA ACPA-positive MAF cases</th>
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<th>EIRA ACPA-negative MAF cases</th>
<th>EIRA ACPA-negative MAF controls</th>
<th>NARAC MAF cases</th>
<th>NARAC MAF controls</th>
<th>WTCCC MAF cases</th>
<th>WTCCC MAF controls</th>
<th>ACPA-positive RA OR (95%CI)*</th>
<th>ACPA-negative RA OR (95%CI)†</th>
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<td>0.72 (0.63 to 0.82)</td>
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<td>0.77 (0.69 to 0.85)‡</td>
<td>0.98 (0.84 to 1.14)</td>
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Statistically significant odds ratios shown in bold.

‡WTCCC excluded due to heterogeneity between ACPA positive cohorts.

* Mantel–Haenszel OR from meta-analysis of EIRA ACPA-positive RA/NARAC/WTCCC.

† Mantel–Haenszel OR for EIRA ACPA-negative RA.

1 WTCCC excluded due to heterogeneity between ACPA positive cohorts.

ACPAs, antibodies to citrullinated peptide antigens; EIRA, Swedish Epidemiological Investigation of Rheumatoid Arthritis; MAF, minor allele frequency; NARAC, North American RA Consortium; RA, rheumatoid arthritis; SNP, single nucleotide polymorphism; WTCCC, Wellcome Trust Case–Control Consortium.
Provenance and peer review  Not commissioned; externally peer reviewed.

REFERENCES