CYP21A2 polymorphisms in patients with autoimmune Addison’s disease, and linkage disequilibrium to HLA risk alleles

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Abstract

Objective: Steroid 21-hydroxylase, encoded by CYP21A2, is the major autoantigen in autoimmune Addison’s disease (AAD). CYP21A2 is located in the region of the HLA complex on chromosome 6p21.3, which harbours several risk alleles for AAD. The objective was to investigate whether CYP21A2 gene variants confer risk of AAD independently of other risk alleles in the HLA loci.

Design: DNA samples from 381 Norwegian patients with AAD and 340 healthy controls (HC) previously genotyped for the HLA-A, -B, -DRB1, and -DQB1 and MICA loci were used for genotyping of CYP21A2.

Methods: Genotyping of CYP21A2 was carried out by direct sequencing. Linkage of CYP21A2 to the HLA loci was assessed using UNPHASED version 3.0.10 and PHASE version 2.1.

Results: Heterozygotes of the single-nucleotide polymorphisms (SNPs) rs397515394, rs6467, rs6474, rs76565726 and rs6473 were detected significantly more frequently in AAD patients compared with HC (P<0.005), but all SNPs were in a linkage disequilibrium (LD) with high-risk HLA-DRB1 haplotypes. rs6472C protected against AAD (odds ratio \( Z \) 0.15, 95% CI (0.08–0.30), \( P = 3.8 \times 10^{-10} \)). This SNP was not in an LD with HLA loci (\( P = 0.02 \)), but did not increase protection when considering the effect of HLA-DRB1 alleles. Mutations causing congenital adrenal hyperplasia were found in heterozygosity in <1.5% of the cases in both groups.

Conclusion: Genetic variants of CYP21A2 associated to AAD are in LD with the main AAD risk locus HLA-DRB1, and CYP21A2 does not constitute an independent susceptibility locus.

Introduction

Autoimmune Addison’s disease (AAD) is caused by the destruction of hormone-producing cells in the adrenal cortex by autoreactive immunological mechanisms. AAD often occurs together with other organ-specific autoimmune disorders, as part of autoimmune polyendocrine syndromes types 1 and 2 (APS1 and APS2 respectively) (1, 2). APS1 is a rare monogenic autosomal recessive disease caused by mutations in the autoimmuregulator (AIRE) gene (3). Isolated AAD and APS2, however, are thought to be caused by susceptibility variants of multiple genes interacting with environmental triggers. To date, the HLA class II haplotypes DRB1*03:01 and DRB1*04:04 have been shown to be the strongest predisposing genetic factors for AAD with odds ratio (OR) of 2.9 and 3.3 (4) respectively. Risk is particularly high when these haplotypes are combined (OR = 32) (2). The HLA-class I genes HLA-A and HLA-B (OR = 2.6 of HLA-B*08) and MHC-class I-related chain A (MICA) also harbour the AAD risk alleles.
(4, 5, 6, 7). In addition, several other genes related to the immune system have been associated with AAD: cytotoxic T lymphocyte antigen-4 (CTLA-4) (8, 9), protein tyrosine phosphatase non-receptor type 22 (PTPN22) (10, 11), MHC class II transactivator (CIITA), C-type lectin domain family 16, member A (CLEC16A) (12), cytochrome P450, family 27, subfamily B, polypeptide 1 (CYP27B1) (13, 14) and programmed death ligand (PD-L1) (15).

The major autoantigen in AAD is the enzyme steroid 21-hydroxylase (21OH), which is expressed mainly in the adrenal cortex (16), and circulating autoantibodies (Ab) against 21OH are present in more than 84% of patients with AAD in various European cohorts (2, 17, 18, 19). 21OH is encoded by CYP21A2, and mutations in this gene are the main cause of congenital adrenal hyperplasia (CAH) (20). Polymorphisms and mutations in CYP21A2 are common, mainly due to the presence of the structurally related pseudogene CYP21A1P (21). The variants in CYP21A2 may potentially have an impact on the immunogenicity of 21OH and thereby influence the chance of an autoreactive response being directed towards it. The examples of such effects are seen in type 1 diabetes where autoantibody frequencies towards the zinc transporter eight (SLC30A8) are dependent on which isoform is expressed (22). Moreover, different isoforms of the thyroid-stimulating hormone receptor (TSHR) vary in their immunogenicity (23, 24). The expression of CYP21A2 in thymic medullary cells could potentially be dependent on polymorphisms, thereby influencing negative selection of 21OH-specific T cells.

We therefore investigated whether CYP21A2 is a susceptibility gene for AAD. Previously, two studies have addressed CYP21A2 polymorphisms in relationship with the risk of developing AAD without finding any disease-specific variants (25, 26). However, both studies were underpowered; the largest cohort included 24 patients with AAD. In this study, we analysed the much larger well-characterised Norwegian cohort (n=381). As CYP21A2 is located on chromosome 6p21.3 in the HLA-III locus, which is in strong linkage disequilibrium (LD) with the HLA-I and II loci, such a large sample size is required to determine whether potential CYP21A2 variants add to the risk of AAD independently of the HLA loci.

Subjects and methods

Subjects

A total of 381 patients with AAD (64% females, 36% males; mean age 58 years) were recruited from the National Norwegian Registry of patients with Addison’s disease (2) and 340 anonymous Norwegian blood donors controls (healthy controls (HC)) were available for genetic analyses. 21OH autoantibody index values as determined by RIA were available for all patients (2). AAD was diagnosed in patients with adrenal insufficiency with either a positive 21OH-Ab test, or adrenal insufficiency combined with another endocrine autoimmune disease. Of the 381 AAD patients, 92% were positive for 21OH-Ab, and 58% had APS2 (Addison’s disease plus autoimmune thyroid disease and/or type 1 diabetes), while 34% had isolated AAD.

Ethics

All included patients and blood donors signed a written consent form. The study was approved by the Regional Committee for Medical Ethics of Western Norway and carried out according to the Helsinki declaration.

Genetic analyses

DNA was isolated from whole blood using standard commercial kits. The sequence of the whole CYP21A2 gene, including ten exons and nine introns, were analysed in 85 patients with AAD. As the antigenicity of 21OH most likely would be located in the coding regions, coding polymorphisms and rare variants detected in the 85 patients were sought for in a larger material of AAD patients (n=381) and HC (n=340). The CYP21A2 gene was amplified in two different fragments using primers discriminating the pseudogene from the functional CYP21A2 gene. The primers specific for CYP21A2 were targeted to the eight base pair (bp) deletion regions in exon 3 and the exon 6 cluster regions, which are the major markers for distinguishing the pseudogene from CYP21A2. The first primer pair amplified a fragment starting with the promoter region and ending with the four-point mutation region in exon 6 (21) (fragment 1); the second primer pair amplified the gene from exon 3 spanning the eight bp deletion region (21) to 170 bp of the 3’ end from exon 10 (fragment 2). Expand high fidelity PCR system (Roche) was used for amplifying PCR fragment 1; the thermal cycling protocol consisted of an initial denaturation step at 94 °C for 2 min, followed by ten cycles of denaturation at 94 °C for 15 s, annealing at 55 °C for 30 s and elongation at 72 °C for 2.5 min. Then the cycle was repeated 20 times with an increment of 5 s for each cycle. The PCR was terminated by an elongation step at 72 °C for 7 min. AmpliTaq Gold with Gene Amp PCR system (Life Technologies) was used for amplifying PCR fragment 2; the thermal cycling conditions were initial denaturation at
96 °C for 10 min, followed by 35 cycles of 94 °C for 20 s, 54 °C for 20 s and 72 °C for 2.5 min. The final elongation step was run at 72 °C for 7 min. The variants and single-nucleotide polymorphisms (SNP) of CYP21A2 were identified by direct sequencing using standard conditions on an ABI 3730 DNA analyser. The primers (purchased from Eurogentec, Seraing, Liège, Belgium) of PCR and sequencing reactions have been described previously (27, 28, 29). Sequencing data were aligned to the CYP21A2 gene sequence (http://www.ncbi.nlm.nih.gov/nuccore/M12792.1). As a quality control to check that the pseudogene was not amplified in the PCR product, we checked that no pseudogene variants were present in the sequences. The copy number of the CYP21A2 gene was determined in AAD patients and HC by duplex real time PCR method (30). The genotyping of HLA-A, -B, -DRB1 and -DQB1, and MICA was described previously by (4).

### Statistical analyses

χ² and Fisher’s exact tests for the determination of significant differences between genotype and allele frequencies of patients and HC, grouped according to age at diagnosis, patients with or without type 1 diabetes or thyroid disease and gender; and calculations of OR with 95% CIs were performed by IBM SPSS Statistics 20 using significance level of P<0.05. The calculation of Hardy–Weinberg equilibrium (P>0.001 cutoff) and LD map of the CYP21A2 gene SNPs were performed by Haploview version 4.2 (31). Global association tests with conditional analysis for allele main effects were performed by UNPHASED version 3.0.10 (32) to determine whether the associations with CYP21A2 were independent (P<0.05) of the HLA loci or not. Haplotype frequencies were generated by PHASE version 2.1 (33). D’Agostino and Pearson omnibus normality test was used to test whether the values of 21OH index and age at diagnosis were distributed in a Gaussian manner, and Kruskal–Wallis test with Dunn’s multiple comparison was used for testing differences between CYP21A2/HLA genotypes or haplotypes and 21OH antibody index values and mean age at diagnosis, using the Graph Pad Prism version 5.02 for Windows (GraphPad Software Inc., La Jolla, CA, USA).

### Results

#### SNPs and haplotypes of CYP21A2 in AAD patients and HC

The common exon variants p.9_10insL/g.1705_1706 insCTG (rs397515394), p.K102R/g.2361A>G (rs6474), p.N493S/g.4377A>G (rs6473), the intron 2 variant g.2333C>T (rs6467) and the intron 3 variant g.2538 C>T (rs76565726) were frequently detected in both AAD and HC. Conversely, p.S268T/g.3323 G>C (rs6472) appeared rarely (Table 1). Several other silent and intron variants were also detected in both AAD patients and HC.

#### Table 1

<table>
<thead>
<tr>
<th>CYP21A2 SNP</th>
<th>Genotype</th>
<th>AAD (%)</th>
<th>HC (%)</th>
<th>P value</th>
<th>OR</th>
<th>95% CI</th>
<th>P value</th>
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<tbody>
<tr>
<td>rs397515394</td>
<td>H/H</td>
<td>129 (35)</td>
<td>161 (48.3)</td>
<td>0.001</td>
<td>1.79</td>
<td>1.31–2.46</td>
<td>0.0003</td>
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<td></td>
<td>H/K</td>
<td>204 (55.3)</td>
<td>142 (42.6)</td>
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</tr>
<tr>
<td></td>
<td>K/K</td>
<td>36 (9.8)</td>
<td>30 (9.0)</td>
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<td></td>
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</tr>
<tr>
<td>rs6467</td>
<td>H/H</td>
<td>72 (19.6)</td>
<td>107 (32.5)</td>
<td>0.0005</td>
<td>1.92</td>
<td>AA vs AC</td>
<td>0.0004</td>
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<td></td>
<td>H/K</td>
<td>198 (54)</td>
<td>153 (46.5)</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>K/K</td>
<td>97 (26.4)</td>
<td>69 (21.0)</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>rs6474</td>
<td>G/G</td>
<td>130 (35.2)</td>
<td>155 (47.0)</td>
<td>0.005</td>
<td>1.69</td>
<td>GG vs GA</td>
<td>0.001</td>
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<tr>
<td></td>
<td>G/A</td>
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<td>144 (43.6)</td>
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<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>A/A</td>
<td>35 (9.5)</td>
<td>31 (9.4)</td>
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<td></td>
<td></td>
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<tr>
<td>rs76565726</td>
<td>CC</td>
<td>118 (32.0)</td>
<td>157 (47.6)</td>
<td>0.00003</td>
<td>2.10</td>
<td>CC vs CT</td>
<td>6.1×10⁻⁶</td>
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<tr>
<td></td>
<td>CT</td>
<td>211 (57.2)</td>
<td>134 (40.6)</td>
<td></td>
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<tr>
<td></td>
<td>TT</td>
<td>40 (10.8)</td>
<td>39 (11.8)</td>
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<td></td>
<td></td>
<td></td>
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<tr>
<td>rs6472</td>
<td>G/G</td>
<td>370 (97.4)</td>
<td>277 (85.0)</td>
<td>3.3×10⁻⁹*</td>
<td>0.15</td>
<td>G vs C</td>
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<td>G/C</td>
<td>10 (2.6)</td>
<td>45 (13.8)</td>
<td>0 (0)</td>
<td></td>
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<td></td>
<td>C/C</td>
<td>0 (0)</td>
<td>4 (1.2)</td>
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<td></td>
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<tr>
<td>rs6473</td>
<td>G/G</td>
<td>131 (34.6)</td>
<td>156 (48.3)</td>
<td>0.001</td>
<td>1.83</td>
<td>GG vs GA</td>
<td>0.0002</td>
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<tr>
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<td>139 (43.0)</td>
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<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td></td>
<td>A/A</td>
<td>34 (9.0)</td>
<td>28 (8.7)</td>
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<td></td>
</tr>
</tbody>
</table>

P values were calculated by χ² test for 2×3 tables and Fisher’s exact test on 2×2 tables.

*Fisher’s exact test.
(listed in Supplementary Table 1, see section on supplementary data given at the end of this article), but were not further investigated in the large cohort.

For the rs397515394, rs6474 and rs6473 SNPs, the heterozygote genotype occurred significantly ($P \leq 0.001$) more often in patients with AAD than in HC, compared with the homozygote genotype of the major alleles (Table 1). Haplotype reconstruction of CYP21A revealed that +AA and +GG (in the order rs397515394/rs6474/rs6473, from now denoted as the +AA and +GG haplotypes) mainly occurred together (Supplementary Table 2, see section on supplementary data given at the end of this article). The frequencies of these haplotypes were significantly different between AAD patients and HC ($P=0.006$), where 35.7% AAD patients and 28.2% HC had the haplotype +AA, and 61.6% AAD patients and 67.7% HC had the haplotype +GG. Other combinations of these SNPs were seen in 2.8% of AAD patients and 4.1% of HC.

Regarding the intron variants rs6467 and rs76565726, the heterozygote genotype and the minor alleles were also more common in AAD than in HC (Table 1). The frequency of rs6467C was 53.4% in the AAD group, the heterozygote genotype occurred significantly ($P=0.001$) more often in patients with AAD than in HC, compared with the homozygote genotype of the major alleles (Table 1). Haplotype reconstruction of CYP21A revealed that +AA and +GG (in the order rs397515394/rs6474/rs6473, from now denoted as the +AA and +GG haplotypes) mainly occurred together (Supplementary Table 2, see section on supplementary data given at the end of this article), but were not further investigated in the large cohort.

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Regarding the intron variants rs6467 and rs76565726, the heterozygote genotype and the minor alleles were also more common in AAD than in HC (Table 1). The frequency of rs6467C was 53.4% in the AAD group, compared with 44.2% in HC (OR=1.10–1.72), Z=3.8, 95% CI (1.17–2.80). The allele frequencies of rs76565726C were 39.4% in AAD and 32.1% in HC (OR=1.10–1.72), P=0.005. The majority of the rs76565726T alleles were seen together with the +GG haplotype, but never with the +AA haplotype (Supplementary Table 2), and was almost in complete LD with all these three coding SNPs (D’>0.97, Fig. 1b).

The rs6472C seemed to be a protective variant to AAD, where the allele frequency of the C allele was 8.1% in HC compared with 1.3% in AAD patients (OR=0.15, 95% CI (0.08–0.30), $P=3.8 \times 10^{-10}$, Table 1). The rs6472C allele was only seen together with the +GG variant of the rs397515394/rs6474/rs6473 haplotype (Supplementary Table 2), which was in complete LD (D’=1, Fig. 1b). The rs6472C allele in the AAD patients was mainly seen (nine of ten alleles) in the haplotype +CGTCG (in order rs397515394/rs6474/rs6473/rs76565726/rs6472/rs6473). In the control group, the haplotypes +AGTCG and +AGCCCG were more frequent (22 and 23 of 53 rs6472C alleles, respectively, Supplementary Table 2).

**Are the CYP21A2 associations independent of HLA I and II loci?**

To this end, a global regression analysis was performed to determine whether AAD associations of CYP21A2 were independent ($P<0.05$) of high-risk HLA loci. Table 2 gives that all the CYP21A2 SNPs associations, except rs6472 ($P=0.02$), were lost when HLA-DRB1 was set as a conditional marker, suggesting that the HLA-type determines the AAD-risk. The SNPs rs397515394, rs6472 and rs6473 showed independence from the HLA-DQB1 locus ($P=0.02$, $P=0.0002$ and $P=0.04$, respectively), while the rs6467, rs6474 and rs76565726 SNPs were in LD with HLA-DQB1 (Table 2). All the exon variants of CYP21A2 further showed independency to the HLA-A, HLA-B and MICA, while the two intron variants were both in LD with HLA-A and MICA. The rs6467 was in LD with HLA-B, whereas rs76565726 was not ($P=0.02$) (Table 2).

We next wanted to investigate how CYP21A2 alleles are linked to the HLA-DRB1 risk alleles. Supplementary Table 3, see section on supplementary data given at the end of this article, gives the major CYP21A2 haplotypes (the SNPs rs397515394/rs6474/rs6473 with haplotype +AGA and +GGG) in combination with the most common HLA-DRB1 haplotypes generated by PHASE. The HLA-DRB1*0301 mainly occurred together with the +GGG haplotype (i.e. 95.5% and 98.2% of AAD and HC respectively), while the HLA-DRB1*0404 haplotype was most commonly seen with the +AGA variant (81.8% and 85.3% of AAD and HC cases respectively). The HLA-DRB1*15 and *01 haplotypes also occurred most frequently together with the +GGG CYP21A2 haplotype, while the HLA-DRB1*0404 haplotypes were also seen together with the +AGA allele (Supplementary Table 3). Furthermore, the individuals with heterozygous HLA-DRB1*0301/*0404 high-risk genotype were also heterozygote for CYP21A2 +AA/+GG in 81.7% AAD patients ($n=98$) and 83.3% HC ($n=6$) respectively.

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**Figure 1**

$r^2$ linkage plot (a) and D’ linkage plot (b) of common variants of CYP21A2.
Table 2

<table>
<thead>
<tr>
<th>Test locus</th>
<th>HLA-A</th>
<th>HLA-B</th>
<th>HLA-C</th>
<th>HLA-DQA1</th>
<th>HLA-DQB1</th>
<th>rs397515394</th>
<th>rs6467</th>
<th>rs6474</th>
<th>rs6472</th>
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<tbody>
<tr>
<td>n=53</td>
<td>4.3 × 10⁻⁹</td>
<td>3.0 × 10⁻⁹</td>
<td>3.0 × 10⁻⁹</td>
<td>6.6 × 10⁻⁹</td>
<td>6.6 × 10⁻⁹</td>
<td>3.0 × 10⁻⁹</td>
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<td>3.0 × 10⁻⁹</td>
</tr>
</tbody>
</table>

For rs6467, the HLA-DRB1*03:01 haplotype was most frequently reconstructed together with the minor C allele, while the majority of HLA-DRB1*04:04, –*15 and –*01 haplotypes were seen together with the A allele. For HLA-DRB1*04:01, both rs6467 alleles were more equally distributed (Supplementary Table 3). For rs76565726 SNP, the minor T allele was mainly seen together with the HLA-DRB1*03:01 haplotype (Supplementary Table 3).

The majority of the rs6472C alleles in AAD (six of ten) were reconstructed by PHASE together with the high-risk HLA-DRB1*03:01, while the rest with HLA-DRB1*07:01 (two of ten) and HLA-DRB1*13:01 (two of ten). For the HC group, the rs6472C allele was mainly seen together with the haplotypes HLA-DRB1*13:01 (19 of 53) –*01 (6 of 53) and –*07:01 (11 of 53). The protective effect of rs6472C was lost (P > 0.05) when considering the effect of the HLA-DRB1 haplotypes (Table 3).

CYP21A2 variants related to biochemical and clinical parameters

Although all of the patients in this study were diagnosed with AAD, 8% lacked 21OH-Ab at the time of testing. Our analyses revealed that the frequencies of heterozygous variants of CYP21A2 were higher in the 21OH-Ab positive group (Supplementary Table 4, see section on supplementary data given at the end of this article). The mean 21OH-Ab levels at diagnosis were also higher in patients with the AAD-associated genotypes of CYP21A2, although not statistically significant (Supplementary Table 4).

Furthermore, the HLA-DRB1*03:01 allele was found in 36.5 and 12.1% of 21OH-Ab positives and negatives respectively. Likewise, for HLA-DRB1*04:04, the allele frequency was 18.2 and 8.6% for 21OH-Ab positives and negatives. HLA-DRB1*04:01 and –*15 were more common in the 21OH-Ab negative group at 19 and 20.7%, respectively, compared with 9.6 and 11.9% in the 21OH-Ab positive group. Finally, the HLA-DRB1*03:01*/04:04 genotype was found only in 21OH-Ab positives. The mean 21OH-Ab levels at diagnosis were significantly higher in patients with the HLA-DRB1*03:01 and –*04:04 haplotypes compared with other haplotypes, and similarly for the HLA-DRB1*03:01*/04:04 genotype (P < 0.0005). Patients with the HLA-B*08 had significantly higher 21OH Ab indices at diagnoses compared with patients with other HLA-B haplotypes (P = 0.028), while the 21OH Ab indices were significantly higher in patients with the HLA-A*01 compared with HLA-A*02 (P = 0.0031). The results are summarised in Supplementary Table 4.

The AAD-associated CYP21A2 variants were more frequent in patients with onset of the disease before...
Table 3  Haplotype reconstruction of protective and high risk alleles of HLA-DRB1 and rs6472.

<table>
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<tr>
<th>HLA-DRB1</th>
<th>rs6472</th>
<th>AAD</th>
<th>HC</th>
<th>Odds ratio</th>
<th>95% CI</th>
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<td>19</td>
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<tr>
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<td>*0701</td>
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</table>

P values were calculated by Fisher’s exact test.

40 years of age than in those with later onset. In addition, the protective variant rs6472C was not detected in patients with disease onset before 20 years (Supplementary Table 5, see section on supplementary data given at the end of this article).

There was no association between autoimmune thyroid disease of the APS2 patients and the CYP21A2 variants. The rs76565726T allele was, however, more frequent in APS2 patients with type 1 diabetes than in AAD patients without type 1 diabetes (OR=1.517, 95% CI (1.027-2.240), P=0.04), but there was no such association with the other CYP21A2 variants. There was no association between gender and CYP21A2 variants.

Rare variants of CYP21A2 in AAD patients and HC

A rare heterozygous coding variant, p.A159T/g.2637G>A, was found in 3/370 patients with AAD and in 1/330 HC. All four were also heterozygous for the rare haplotype HLA-B*4801 which was absent in other patients and controls. Known disease causing mutations frequently reported in patients with CAH (34) were also found as heterozygous in both AAD patients and HC. The I2 splice variant (rs6467G) was detected in 2/370 AAD patients and 1/331 HC. The eight bp deletion in exon 3 (rs387906510) was found in one AAD patient and in one HC. The non-classical CAH variant p.V281L (rs6471) was found in 3/380 AAD patients and 5/326 HC, while p.P453S (rs6445) was found in 3/379 AAD patients and 4/322 HC. No copy number variations were detected in AAD patients or HC; they all had two copies of CYP21A2.

Discussion

It is not known why certain proteins, such as 21OH, become autoantigens in organ-specific autoimmune diseases. However, common features are that autoantigens are intracellular enzymes with restricted tissue expression. One possibility is that only altered or modified self-proteins can induce autoreactive immune responses, and that genetic polymorphisms may represent such alterations. By direct sequencing of CYP21A2 in AAD patients, we did not find any disease-specific risk alleles, but heterozygous genotypes of common CYP21A2 variants were significantly more frequent in AAD patients than in HC. However, we found that all the CYP21A2 SNPs associations, except for rs6472, were dependent on the HLA-DRB1 locus, which is the strongest single genetic risk factor of AAD (2, 4, 35, 36). Therefore, the higher heterozygous genotype frequency of the two main haplotypes of CYP21A2 alleles, +AA and +GG, merely reflects the high-risk genotype of HLA-DRB1*03:01/*04:04 (2). The protective rs6472C association could also be explained by the linkage with the HLA protective variants.

The non-coding AAD-associated CYP21A2 variants rs6467 and rs76565726 were also dependent on MICA and HLA-A or -B. The rs76565726T allele was further associated with type 1 diabetes of the APS2 patients included in the study. Interestingly, the rs6467C and rs76565726T alleles have both shown to be in LD with components of the 8.1 ancestral haplotype (37).

Our data indicated that all of our patients with the DRB1*03:01/*04:04 genotype were positive for 21OH Ab and had the highest 21OH Ab indices compared with other genotypes. This is consistent of HLA-DRB1*03:01/*04:04 genotype association with expression of 21OH Ab (38). The corresponding CYP21A2 genotype did not add to the high 21OH Ab association of HLA-DRB1*03:01/*04:04, which underlines the strength of HLA-DRB1 risk factors. Similarly, we here found a trend for association between CYP21A2 genotypes and age of disease onset. This is in agreement with previous findings of a significant lower mean age of onset in patients who carries the HLA-DRB1*03:01/*04:04 genotype (2).

A hypothesis proposes that low protein expression due to genetic polymorphisms might increase the probability of autoreactive T cells to escape from the thymus during negative selection. This has been suggested for the variable number of tandem repeats polymorphism in the gene encoding insulin and its association with the production of Ab and autoreactive T cells to insulin in type 1 diabetes (39, 40). Although the HLA-DRB1 locus proves to be the highest predisposing factor of AAD, the significance of CYP21A2 heterozygote genotypes is not clear because it is not known if the gene is inherited co-dominantly like the HLA genes.
In conclusion, sequencing of the exons and introns of CYP21A2 did not reveal any disease-specific risk variants associated with AAD. Instead, CYP21A2 polymorphisms are in LD with the high-risk haplotypes of the HLA-DRB1 loci, and do not independently add to increased risk or protection, but merely reflects the effect of HLA-DRB1.

Declaration of interest
The authors declare that there is no conflict of interest that could be perceived as prejudicing the impartiality of the research reported.

Supplementary data
This is linked to the online version of the paper at http://dx.doi.org/10.1530/EJE-12-0891.

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