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Exclusion of Polymorphisms in Carnosinase Genes (CNDP1 and CNDP2) as a Cause of Diabetic Nephropathy in Type 1 Diabetes

Results of Large Case-Control and Follow-Up Studies

Krzysztof Wanie,1,2 Grzegorz Placha,1,2,3 Jonathon Dunn,1 Adam Smiles,1 James H. Warram,1 and Andrzej S. Krolewski1,2

OBJECTIVES—Recently, an association was found between diabetic nephropathy and the D18S880 microsatellite, located in the carnosinase gene (CNDP1) on chromosome 18q. Alleles of this microsatellite encode for a variable number of leucine residues (from four to seven) in the leader peptide of the carnosinase precursor. The frequency of subjects homozygous for the five leucines was higher in control subjects than in case subjects in studies focusing on type 2 diabetic patients. To test whether this finding can be extended to type 1 diabetic patients, we carried out a comprehensive study on association between diabetic nephropathy and the D18S880 microsatellite and 21 additional SNPs that tagged the genomic region containing CNDP1 and CNDP2.

RESEARCH DESIGN AND METHODS—Overall, 1,269 Caucasian patients with type 1 diabetes were included in the study, including 613 patients with normoalbuminuria and a long duration of diabetes, 445 patients with persistent proteinuria, and 211 patients with end-stage renal disease (ESRD). All patients were genotyped for selected polymorphisms, the associations with diabetic nephropathy were tested by a χ² test, and odds ratios were calculated.

RESULTS—We did not find any significant association between diabetic nephropathy and any examined genetic markers. The negative findings of the case-control study were supported further by negative findings obtained from the 6-year follow-up study of 445 patients with persistent proteinuria, during which 135 patients developed ESRD.

CONCLUSIONS—Our large, comprehensive study did not find an association between the D18S8880 microsatellite or any other polymorphisms in the CNDP2–CNDP1 genomic region and susceptibility for diabetic nephropathy in type 1 diabetes. Diabetes 57:2547–2551, 2008

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Diabetic nephropathy is the most severe complication resulting from type 1 diabetes. Approximately 30 to 40% of type 1 diabetic patients develop this complication, which leads to end-stage renal disease (ESRD) and increases the risk of cardiovascular morbidity and mortality (1–3). Epidemiologic and family studies have demonstrated that in addition to levels of glycemic control, genetic factors play an important role in the development of diabetic nephropathy (4–6). Many groups have been searching for genes that make individuals susceptible to diabetic nephropathy using linkage studies or candidate gene approaches (7).

Recently, Freedman et al. (12) published data from a case-control study in which the authors selected case (patients with type 2 diabetes and ESRD) and control (individuals with type 2 diabetes but without diabetic nephropathy) subjects from among Caucasians in North Carolina. The cases were ascertained through dialysis centers, and the control subjects were recruited as volunteers for the Diabetes Heart Study. This study supported Janssen et al.’s (5) findings that subjects with diabetes but without diabetic nephropathy were more frequently ho-
mozygous for the five-leucine repeat genotype than those who had ESRD. Although both studies concluded that the five-leucine repeat was protecting against diabetic nephropathy, the effect of duration of diabetes on frequency of this genotype in control and case subjects was not examined in either study (13).

In this report, we attempted to extend the findings of Janssen et al. and Freedman et al. (9,12) to patients with type 1 diabetes. We examined the association between the number of leucine repeats in \textit{CNDP1} and other tagging single nucleotide polymorphisms (SNPs) in the \textit{CNDP2}-\textit{CNDP1} genomic region and the risk of various stages of diabetic nephropathy in a population of Caucasian patients with type 1 diabetes living in the eastern part of Massachusetts and attending a large diabetes center. Large case-control as well as follow-up study designs were used.

### RESEARCH DESIGN AND METHODS

 Patients for this investigation were selected from the Joslin Study on Genetics of Diabetic Nephropathy in type 1 Diabetes. The detailed description of the Joslin clinic population and the method of selection of patients for the study can be found in the online appendix (available at http://dx.doi.org/10.2373/dh07-1303). The Committee on Human Subjects of the Joslin Diabetes Center approved the protocol and informed consent procedures for the study.

**Diagnosis of type 1 diabetes and diabetic nephropathy.** Patients were considered type 1 diabetic if hyperglycemia was diagnosed before age 40 years, its control required insulin treatment within 1 year of diagnosis, and such treatment could not be interrupted thereafter. Only patients aged 15–50 years at examination were eligible for enrollment into these studies. The diabetic nephropathy status of each patient was determined on the basis of medical records and measurements of the urinary albumin-to-creatinine ratio. Methods for measuring the albumin-to-creatinine ratio and classification criteria have previously been described (14). At the time of enrollment, patients were classified into the following study groups (detailed description of the criteria can be found in the online appendix): 1) Control subjects were considered to have normoalbuminuria if they had diabetes duration of \(\geq15\) years and had persistent normoalbuminuria; 2) Case subjects were considered to have persistent microalbuminuria if they had diabetes duration \(\geq3\) years and had persistent microalbuminuria; 3) Case subjects were considered to have persistent proteinuria if they had diabetes duration \(\geq7\) years and had persistent proteinuria; and 4) Case subjects were considered to have ESRD if they had begun dialysis or received a renal transplant as a result of diabetic nephropathy. Patients with proteinuria at the enrollment were followed until 2005 to determine who progressed to ESRD.

DNA was extracted using a standard phenol-chloroform protocol. For the current study, we used only patients classified as control subjects \((n = 613)\) or case subjects with advanced diabetic nephropathy \((445\) with proteinuria and \(211\) with ESRD). Patients with microalbuminuria were not examined in the current investigation. In total, 1,269 patients from the Joslin Study on Genetics of Diabetic Nephropathy in type 1 Diabetes were used in this investigation.

D18S880 microsatellite was genotyped using previously described primers (9) and standard PCR protocols. The PCR products were separated using the ABI 377 Sequencer (Perkin Elmer, Foster City, CA). All samples were successfully genotyped for microsatellite markers. All selected SNPs were genotyped using Sequenom MassArray Platform (Broad Institute Center for Genotyping and Analysis, Cambridge, MA). The maximum SNP-specific missing data rate was 4.7%.

**Selection of SNPs.** We identified haploblocks in the \textit{CNDP2} gene locus with the D’ 90% confidence bounds method of Gabriel et al. (15) using haplview software (16). We selected tagging SNPs (htSNPs) needed to tag frequent haplotypes in a block (frequency \(\geq0.05\)) using the method of Stram et al. (17). The minimum set of htSNPs within each block was selected to ensure an \(R^2\) of at least 0.80 for all haplotypes observed at a frequency of at least 5%. In this set of htSNPs, the minimum \(R^2\) was always \(\geq0.80\). For the \textit{CNDP2} locus, we selected 12 htSNPs, which cover two haploblocks denoted as A and B and one inter-block denoted as C. Because of less clear haploblock structure in the

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**FIG. 1.** Approximate genomic location and \(P\) values for selected single SNP comparisons for the \textit{CNDP1} and \textit{CNDP2} genomic regions assuming additive mode of inheritance. Nominal \(P\) values for \(x^2\) tests with 2 d.f. are also provided. Haploblocks are shown schematically as gray rectangles. SNPs 1–12 are considered tagging SNPs for particular haplo- and interblocks. *2 d.f.; **additive mode of inheritance.
TABLE 2
Distribution of genotypes for D18S880 microsatellite according to study groups

<table>
<thead>
<tr>
<th>Genotype</th>
<th>Control subjects with normoalbuminuria</th>
<th>Case subjects with proteinuria</th>
<th>Case subjects with ESRD</th>
</tr>
</thead>
<tbody>
<tr>
<td>D18S880</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>n</td>
<td>613</td>
<td>445</td>
<td>211</td>
</tr>
<tr>
<td>5_5</td>
<td>33.0</td>
<td>29.4</td>
<td>32.2</td>
</tr>
<tr>
<td>5_6</td>
<td>43.6</td>
<td>45.2</td>
<td>47.9</td>
</tr>
<tr>
<td>5_7</td>
<td>6.0</td>
<td>5.4</td>
<td>6.2</td>
</tr>
<tr>
<td>6_6</td>
<td>12.6</td>
<td>15.5</td>
<td>11.8</td>
</tr>
<tr>
<td>X_X</td>
<td>4.9</td>
<td>4.5</td>
<td>1.9</td>
</tr>
</tbody>
</table>

Genotype frequency data are percent. Genotypes with frequencies <5% were combined to X_X. Control subjects with diabetes duration <25 and ≥25 years had similar distribution of the D18S880 genotype. Total χ² = 7.50; 8 d.f.; P = 0.48.

RESULTS

Characteristics of the study groups are shown in Table 1. They reflect the study design. Age at diagnosis of type 1 diabetes was similar in all groups, all patients had long duration of diabetes, all were treated with insulin (data not shown), and all had similar A1C and BMI. However, patients with proteinuria and ESRD had longer duration of diabetes (and therefore were older) and higher blood pressure than control subjects.

Figure 1 shows the genomic region that contains CNDP2 and CNDP1. Both genes are located on the long arm of chromosome 18 (18q22.3) in a tail-to-head orientation. CNDP2 spans 24.8 kb and has 12 exons. CNDP1 is 13 kb telomeric from CNDP2, which spans 50.6 kb and also has 12 exons. The linkage disequilibrium (LD) structure of CNDP2 allows us to distinguish two haploblocks (A and B) followed by an interval (C) without haploblock structure. CNDP1 is characterized by a less clear haploblock structure, and the selected SNPs were grouped into three intervals: D, E, and F. Overall, in the CNDP2-CNDP1 genomic region, we selected and genotyped 21 SNPs and the D18S880 microsatellite. All SNPs were in Hardy-Weinberg equilibrium.

The results of single SNP analysis are shown in the bottom part of Fig. 1 and in an online appendix. None of the examined SNPs appeared to be significantly differently distributed between control and case subjects with proteinuria or ESRD except for SNPs located in the interval D, which contains a proximal and distal promoter of CNDP1. Genotype frequencies of three of these three SNPs were different at P < 0.05 between control and case subjects with ESRD. However, the differences became insignificant after Bonferroni adjustment. Haplotype analysis of these three SNPs did not yield a more significant difference between control and case subjects with ESRD (data not shown).

The results for the D18S880 microsatellite were analyzed separately. Five alleles corresponding to repeats of four, five, six, seven, and eight leucines were found. The first and last alleles were very rare (<1%). The frequency of the allele encoding the five leucines, the protective allele from the Janssen et al. report, was very similar. In all three groups, 57.8% in patients with normoalbuminuria and long-duration type 1 diabetes (control subjects) and 54.8 and 59.2% for patients with proteinuria and ESRD, respectively. Overall, the distribution of the alleles did not differ among the three study groups (P = 0.2) (Table 2A in the online appendix).
The frequencies of the D18S880 genotypes in the study groups are presented in Table 2. In this table, the genotypes less frequent than 5% were combined into one group referred to as the X_X genotype. The frequency of subjects homozygous for five leucines was very similar in the three study groups. The frequencies of other genotypes were also similar (P = 0.5). Combined analysis of the D18S880, in which control subjects were compared with case subjects (patients with proteinuria or ESRD), also failed to replicate results published by Janssen et al. The OR in our study was 1.13 (95% CI 0.89–1.43).

To further study the associations between ESRD and the three SNPs located in interval D with the D18S880 microsatellite, as well as 21 SNPs that tagged the genomic region containing CNDP2 and CNDP1. Unfortunately, we did not find any significant association between diabetic nephropathy and any of the examined genetic markers. Noteworthy, three SNPs in the promoter region of CNDP1 (rs12954438, rs8903332, and rs11151964) could be considered associated with ESRD, assuming the additive inheritance model at the nominal P = 0.05 significance level. However, those SNPs have never been studied before. Moreover, based on our data, those SNPs are not in LD with any of the D18S880 alleles. Therefore, we considered our examination of the SNPs in the promoter region of the CNDP1 gene as exploratory study and employed stringent Bonferroni correction. The negative findings of the case-control study were supported further by negative findings obtained in the 6-year follow-up study of 445 patients with persistent proteinuria, during which 135 patients developed ESRD. In conclusion, our large comprehensive study did not support the role of D18S880 microsatellite or any other polymorphisms of CNDP2 and CNDP1 in the development of diabetic nephropathy in type 1 diabetes. Following, we discuss our results in comparison with findings from the other studies.

Table 4 shows the frequency of CNDP1 five leucine/five leucine repeat genotype in case (patients with diabetic nephropathy) and control (individuals with diabetes) subjects in the three studies.

<table>
<thead>
<tr>
<th>Study</th>
<th>n</th>
<th>Percent of 5–5 in control subjects</th>
<th>Percent of 5–5 in case subjects</th>
<th>OR* (5–5 as reference)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Janssen et al. (9): type 1 and type 2 diabetes**</td>
<td>242</td>
<td>43</td>
<td>27</td>
<td>2.0 (1.17–3.42)</td>
</tr>
<tr>
<td>Freedman et al. (12): type 2 diabetes</td>
<td>600</td>
<td>39</td>
<td>29</td>
<td>1.5 (1.07–2.13)</td>
</tr>
<tr>
<td>Wanic et al. (current study): type 1 diabetes</td>
<td>1,269</td>
<td>33</td>
<td>30</td>
<td>1.1 (0.89–1.43)</td>
</tr>
</tbody>
</table>

*95% CIs are provided in parenthesis, and ORs calculated for the protective effect. **Including 57 patients with type 1 and 185 with type 2 diabetes. 5–5, five leucine/five leucine repeat genotype.
evaluated the combined frequencies among both type 1 diabetic and type 2 diabetic patients. Interestingly, the frequency of the five/five homozygotes in case subjects is very similar in the three studies (differences were not statistically significant: \( \chi^2 = 0.5; P = 0.8 \)). The frequency of the five/five homozygotes seems to be different among the control subjects, being most frequent in the Janssen et al. study, intermediate in the Freedman et al. study, and lowest in the current study (\( \chi^2 = 5.6; P = 0.06 \)). The first study was the smallest and used patients from four different countries, including one Arabic country. The study by Freedman et al. (12) selected case and control subjects from among European-Americans residing in North Carolina but did so through completely different mechanisms. The case subjects were found through dialysis centers. The control subjects were recruited as volunteers for the Diabetic Heart Study. Only the current study drew case and control subjects from the same clinic population, and it included more case and control subjects than the two other studies combined.

At present, there is no clear explanation for the discrepant findings summarized in Table 4. One possibility is that they result from improper selection of control subjects in some of the studies. However, because the differences in the previous studies were observed in patients with type 2 diabetes, one cannot exclude the possibility that the five leucine/five leucine genotype of the D18S880 microsatellite plays a role in protection against diabetic nephropathy in patients with type 2 diabetes but not type 1 diabetes. Therefore, the discrepant findings may simply indicate differences in genetic susceptibility to diabetic nephropathy in type 1 and type 2 diabetes (21).

Additionally, we examined the possibility that the D18S8880 microsatellite alleles are not causally related to diabetic nephropathy but are in LD with other DNA sequence differences that are causal. To test this possibility, we examined 21 SNPs that encompass most of the genetic variation in the CNDP2-CNDP1 genomic region. Neither single-SNP nor haplotype analysis showed any significant association with proteinuria or ESRD. However, these negative findings should be qualified because the haploblock structure, particularly for CNDP1 locus, is poorly defined in the current HapMap data. Furthermore, we had only limited information to estimate LD between the D18S8880 microsatellite and other SNPs in the CNDP2-CNDP1 genomic region.

Some other qualifications of our findings should be discussed. First, although our study is large, it is too small to detect significant ORs below 1.2. To demonstrate such a small effect, one would need several thousand case and control subjects, as was demonstrated recently in studies on type 2 diabetes (22,23). The cross-sectional part of our study might have been underpowered to detect ORs reported by Freedman et al. (12). However, this deficiency was overcome by implementing the follow-up study, which had sufficient power to detect a genotype RR of 1.5. Second, it is well known that patients with ESRD have very high mortality, and some of the associations may not be related to risk of the development of ESRD but may instead determine survival of such patients. In our study, we excluded such a possibility by examining the risk of development of ESRD according to specific genotypes in the prospective study. Finally, spurious associations or lack thereof can result from poor quality of genotyping. In our study, we used manual genotyping, which can be susceptible to errors, for D18S8880 microsatellite. However, we had only a few errors when we repeated genotyping in 10% of the study population. On the other hand, tagging SNPs were genotyped on the Sequenom platform with almost perfect genotyping.

ACKNOWLEDGMENTS

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