Association Testing of Previously Reported Variants in a Large Case-Control Meta-analysis of Diabetic Nephropathy

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Association Testing of Previously Reported Variants in a Large Case-Control Meta-analysis of Diabetic Nephropathy

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We formed the GEnetics of Nephropathy—an International Effort (GENIE) consortium to examine previously reported genetic associations with diabetic nephropathy (DN) in type 1 diabetes. GENIE consists of 6,366 similarly ascertained participants of European ancestry with type 1 diabetes, with and without DN, from the All Ireland-Warren 3-Genetics of Kidneys in Diabetes U.K. and Republic of Ireland (U.K.-R.O.I.) collection and the Finnish Diabetic Nephropathy Study (FinnDiane), combined with reanalyzed data from the Genetics of Kidneys in Diabetes U.S. Study (U.S. GoKinD). We found little evidence for the association of the EPO promoter polymorphism, rs161740, with the combined phenotype of proliferative retinopathy and end-stage renal disease in U.K.-R.O.I. (odds ratio [OR] 1.14, P = 0.19) or FinnDiane (OR 1.06, P = 0.60). However, a fixed-effects meta-analysis that included the previously reported cohorts retained a genome-wide significant association with that phenotype (OR 1.31, P = 2 × 10\(^{-8}\)). An expanded investigation of the ELMO1 locus and genetic regions reported to be associated with DN in the U.S. GoKinD yielded only nominal statistical significance for these loci. Finally, top candidates identified in a recent meta-analysis failed to reach genome-wide significance. In conclusion, we were unable to replicate most of the previously reported genetic associations for DN, and significance for the EPO promoter association was attenuated.


Type 1 diabetes has continuously increased worldwide, and the highest incidence is found in Finland (1). Diabetic nephropathy (DN) is a complication that develops in approximately 25–40% of patients with type 1 and type 2 diabetes. DN is the leading cause of end-stage renal disease (ESRD) in the developed world. Currently, 44% of the new cases of ESRD in the U.S. annually are attributable to DN (2). A better understanding of the causal factors of DN and its pathogenesis may lead to new strategies to decrease its incidence, preemptively treat the disorder, attenuate morbidity and mortality, and would be a valuable contribution to global public health.

Several observations suggest that DN, one of the major complications of type 1 and type 2 diabetes, has an inherent genetic susceptibility. Familial clustering of DN is evident for both type 1 and type 2 diabetes (3–6), and genetic risk factors are being sought in multiple populations (7–9). Unfortunately, robust replication of many initial associations has not been forthcoming (10).

This study recruited a large collection of individuals with type 1 diabetes as part of the GENetics of Nephropathy—an International Effort (GENIE) consortium and examined selected candidate loci associated with DN from genome-wide case-control studies or other association studies that reported high levels of statistical significance. The variants examined and the rationale for their inclusion are as follows:

1. A single nucleotide polymorphism (SNP) (rs1617640) within the promoter region of the EPO gene (encoding erythropoietin) was identified as having a genome-wide significant (P = 5 × 10\(^{-8}\)) association with ESRD and
proliferative diabetic retinopathy (PDR) (11). Interestingly, erythropoietin levels were elevated sevenfold in the human vitreous fluid of nondiabetic individuals with the risk genotype TT compared with those with the wild-type GG genotype. In addition, EPO expression levels were significantly elevated above control in the tissues and vitreous fluid of animal models of DN (DN in db/db mice) and in proliferative retinopathy (murine oxygen-induced retinopathy model), respectively (11).

2) The engulfment and cell motility 1 gene (ELMO1) has been reported to be associated with DN in Japanese patients with type 2 diabetes (12). Recently, Pezzolesi et al. (13), using the Genetics of Kidneys in Diabetes U.S. study (U.S. GoKinD) cohorts, also examined ELMO1 for association with DN and presented evidence of association of variants within this gene for the development of DN. However, the risk alleles for ELMO1 identified in their study differed from those reported in the original Japanese investigation. In the context of a genome-wide association study (GWAS), 118 SNPs were assessed in 1,705 individuals of European ancestry with type 1 diabetes (885 control subjects and 820 DN case subjects). The strongest associations in ELMO1 in the U.S. study occurred at rs11769038 (odds ratio [OR] 1.24; \(P = 1.7 \times 10^{-3}\)) and rs1882090 (OR 1.23; \(P = 3.2 \times 10^{-3}\)), located in intron 16. Two additional SNPs, located in introns 18 and 20, were also nominally associated with DN. In total, eight ELMO1 SNPs were reported to confer risk for DN, although none reached genome-wide significance (13). Supportive evidence was also found in African Americans with type 2 diabetes and ESRD (14).

3) The U.S. GoKinD GWAS analyzed 359,193 SNPs in 820 case subjects (284 with proteinuria and 536 with ESRD) and 885 control subjects with type 1 diabetes but no evidence of DN. Although no risk variant achieved genome-wide significance, the primary association analysis identified 11 SNPs representing four distinct chromosomal regions (\(P < 1 \times 10^{-3}\)). The strongest association with DN reported in this study was on chromosome 9q with rs10868025 (OR 1.45; \(P = 5.0 \times 10^{-7}\)) (15).

4) Finally, in an effort to systematically explore and comprehensively capture common genetic variations that might be associated with DN, we reviewed the largest meta-analysis published to date studying genetic associations with the DN phenotype (7). In GENIE, we examined the top-reported SNP (or proxy) for each gene in that report for an association with DN.

In this study, we have assembled the largest reported case-control sample of DN in type 1 diabetes to evaluate the previously reported genetic associations in newly genotyped samples from the U.K., Republic of Ireland (R.O.I.), and Finland, plus pre-existing data from the U.S. GoKinD.

### RESEARCH DESIGN AND METHODS

#### Cohorts

**U.K.-R.O.I. collection.** Recruited individuals were part of the All Ireland-Warren 5-Geneetics of Kidneys in Diabetes U.K. collection (U.K.-R.O.I.). All were self-reported as white, with grandparents born in the U.K. or Ireland, and type 1 diabetes diagnosed before the age of 31 years requiring uninterrupted insulin treatment. Case subjects (n = 903) with DN had persistent proteinuria (>0.5 g/24 h), hypertension (>135/85 mmHg and/or treatment with antihypertensive medication), and diabetic retinopathy. ESRD (28%) was defined as requiring renal replacement therapy or having received a kidney transplant. Individuals in the control group (n = 1,001) had had type 1 diabetes for at least 15 years, had no evidence of microalbuminuria on repeated testing, and were not receiving antihypertensive medication (Table 1).

**Finnish Diabetic Nephropathy Study (FinnDiane).** The FinnDiane study is a nationwide multicenter study of >4,800 adult participants with type 1 diabetes (16). This study comprises genotype data for 2,914 patients with type 1 diabetes diagnosed before age 35 years and insulin treatment started within 1 year of diagnosis. The disease status was defined by urine albumin excretion rate (AER) or urine albumin-to-creatinine ratio (ACR) in at least two of three consecutive urine collections at local centers. Macroalbuminuria (n = 686) was defined as AER >200 mg/min or >300 mg/24 h or an ACR >25 mg/mmol for men and >35 mg/mmol for women in overnight, 24-h, or spot urine collections, respectively. Similarly, the limit for normal AER (n = 1,601) was <20 \(\mu\)g/min or <30 mg/24 h or an ACR <25 mg/mmol for men and <35 mg/mmol for women. Control patients with normal AER were required to have type 1 diabetes before age 35 years and insulin treatment started within 1 year of diagnosis. The disease status was defined by urine albumin excretion rate (AER) or urine albumin-to-creatinine ratio (ACR) in at least two of three consecutive urine collections at local centers. Macroalbuminuria (n = 686) was defined as ongoing dialysis treatment or receipt of a kidney transplant. From the total, 505 participants were included from an independent Finnish cohort collected by the National Institute for Health and Welfare (17). These participants met the FinnDiane diagnosis and selection criteria and were analyzed together with the FinnDiane cohort (Table 1).

**U.S. GoKinD.** The U.S. GoKinD study consists of a DN case-control cohort of individuals diagnosed with type 1 diabetes before age 31 years, who were between 18 and 59 years of age at enrollment, and who began insulin treatment within 1 year after diagnosis (18). The 905 case subjects were defined as people aged 18–54, with type 1 diabetes for at least 10 years, and DN. The 898 control subjects were aged 18–59, had type 1 diabetes for at least 15 years, but did not have DN. The DN definition includes individuals with ESRD (on dialysis or having received a kidney transplant) or persistent macroalbuminuria (at least two of three tests positive for albuminuria by dipstick ≥1+ or ACR >300 \(\mu\)g albumin/mg of urine creatinine). The U.K. GoKinD inclusion criteria were used to recruit individuals to the control group. Individuals were recruited at two study centers, George Washington University (GWU) and the Joslin Diabetes Center.

### TABLE 1

Phenotypic characteristics of the GENIE cohorts (U.K.-R.O.I., FinnDiane, and U.S. GoKinD)

<table>
<thead>
<tr>
<th>Cohorts</th>
<th>Case subjects</th>
<th>Control subjects</th>
<th>Case subjects</th>
<th>Control subjects</th>
<th>Case subjects</th>
<th>Control subjects</th>
</tr>
</thead>
<tbody>
<tr>
<td>U.K.-R.O.I.</td>
<td>903</td>
<td>1,001</td>
<td>1,289</td>
<td>1,577</td>
<td>774</td>
<td>821</td>
</tr>
<tr>
<td>Sex (n)</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Male</td>
<td>531</td>
<td>438</td>
<td>764</td>
<td>651</td>
<td>402</td>
<td>342</td>
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<tr>
<td>Female</td>
<td>372</td>
<td>563</td>
<td>525</td>
<td>926</td>
<td>372</td>
<td>479</td>
</tr>
<tr>
<td>Type 1 diabetes</td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>Duration (years)</td>
<td>32.9 ± 9.5</td>
<td>27.2 ± 8.7</td>
<td>32.8 ± 9.1</td>
<td>27.9 ± 9.5</td>
<td>31.4 ± 7.8</td>
<td>25.4 ± 7.7</td>
</tr>
<tr>
<td>Age at diagnosis (years)</td>
<td>14.6 ± 7.7</td>
<td>14.5 ± 7.8</td>
<td>12.8 ± 7.6</td>
<td>15.1 ± 8.3</td>
<td>11 ± 6.6</td>
<td>13 ± 7.3</td>
</tr>
<tr>
<td>HbA1c (%)</td>
<td>9.0 ± 1.9</td>
<td>8.7 ± 1.6</td>
<td>8.8 ± 1.6</td>
<td>8.0 ± 1.2</td>
<td>7.5 ± 1.9</td>
<td>7.5 ± 1.2</td>
</tr>
<tr>
<td>BMI (kg/m²)</td>
<td>26.2 ± 4.7</td>
<td>26.2 ± 4.2</td>
<td>25.5 ± 4.2</td>
<td>25.2 ± 3.4</td>
<td>25.7 ± 5.2</td>
<td>26.1 ± 4.3</td>
</tr>
<tr>
<td>ESRD (%)</td>
<td>28.0</td>
<td>0</td>
<td>48.2</td>
<td>0</td>
<td>65.6</td>
<td>0</td>
</tr>
</tbody>
</table>

Categoric data are shown as indicated; continuous data as mean ± SD. †Reanalysis of the U.S. GoKinD dataset using new quality control filters to account for published plate effects (see RESEARCH DESIGN AND METHODS for complete details).
Center (JDC) using differing methods of ascertainment and recruitment (see Pezzolesi et al. [15] for details). Analysis of the U.S. GoKinD cohort was limited to individuals whose reported primary ethnicity was white.

**Phenotype definition: DN and EPO study outcomes.** DN was the primary outcome and determined independently of ESRD status. For this analysis, case subjects had clinical evidence of PDR, whereas control subjects had none (irrespective of DN status). Cohorts analyzed in the original EPO study (Fig. 1) were composed of European-American cases, and control subjects were collected from distinct geographic areas in the U.S. These included the GoKinD cohort (Boston, Pittsburgh, and Minneapolis), the Utah cohort (Salt Lake City), and the Boston cohort (Boston Joslin Center for Diabetes) (11).

**SNP selection.** SNP markers with evidence for association with DN susceptibility in reference studies (11) were selected for genotyping in GENIE. Where more than one SNP was associated at a particular locus with DN, the most strongly associated variant was selected for genotyping in the DN case-control cohorts. Where no genotyping assay could be developed for the index SNP, a proxy in strong linkage disequilibrium (LD) was genotyped using the CEU HapMap population. CEU is the official three letter code for the HapMap map (http://www.hapmap.org) for the Utah residents with ancestry from Northern and Western Europe (see http://hapmap.ncbi.nlm.nih.gov/citinghapmap.html). For the original U.S. GoKinD reported results and ELMO1, additional SNPs within 20-kb upstream and downstream of the locus (or index SNP) were selected using the SNP Annotation and Proxy Search (http://www.broadinstitute.org/mpg/snp/prox), specifying chromosome position, CEU samples, and 1000 Genome Pilot 1 data. The expanded SNP list was extracted from GWAS results for 3,570 FinnDiane samples, 791,687 SNPs in 1,726 U.K.-R.O.I. samples, and 2,809 SNPs in 1,505 U.S. GoKinD samples.

**SNP imputation.** MACH 1.0 software (http://www.sph.umich.edu/csg/abecasis/MACH) with the HapMap phase II CEU reference panel was used to perform SNP imputation for GWAS results in each cohort. Estimates of the crossover and error rates were obtained via 50 iteration runs in ~300 randomly selected samples per cohort. A greedy algorithm was used for imputation, and the maximum likelihood method was specified to yield allele dosages. A filter was applied to exclude SNPs with low imputation quality (0.7 < 0.6), resulting in ~2.4 million SNPs per cohort.

**Statistical analysis.** Association tests were conducted using PLINK v1.07 (20) (http://pngu.mgh.harvard.edu/purcell/plink), with logistic regression adjusted for sex and age. U.K.-R.O.I. was adjusted for recruitment center, but the two U.S. GoKinD centers, GWU and JDC, were analyzed separately as reported by Pezzolesi et al. (15). Data from the GWAS genotyping was adjusted additionally for duration of type 1 diabetes and principal components from Eigenstrat analysis. The EPO locus was analyzed with the Pearson χ² test in the FinnDiane dataset without adjusting for any covariates. Fixed-effects meta-analyses were conducted with the software package Comprehensive Meta-Analysis (Version 2.2040, Englewood, NJ) and the software package METAL (http://www.sph.umich.edu/csg/abecasis/Metal/) (21) under the additive genetic model. To determine the appropriate significance threshold for combination for multiple testing, we calculated the total number of effective tests (because a large portion of SNPs were in LD), using SNPSpD (http://gump.qimr.edu.au/general/dane/NS/NNSpD.html). SNPSpD uses correlation between analyzed SNPs to calculate the total number of independent tests (22). The total number of tests tested is 2,199, with 113.7 effect-independent tests. Thus the experiment-wise cutoff for statistical significance was set at 4.4 × 10⁻⁸ (0.05/113.7).

**RESULTS**

**EPO promoter polymorphism.** The association of the EPO promoter polymorphism, rs1617640, with DN was evaluated by de novo genotyping of the SNP in GENIE. For this analysis, case subjects were defined as having both ESRD and PDR because the initial report showed the polymorphism was robustly associated with DN when both of these “extreme” phenotypes were coexpressed. Significant association was not observed in the U.K.-R.O.I. (P = 0.19) or FinnDiane collections (P = 0.60), although the directions of effect were consistent with the original report. Fixed-effects meta-analysis of the association of rs1617640 with ESRD/PDR, including the previously reported cohorts (a total of 3,162 case and 3,845 control subjects across five separate cohorts of European and European-American ancestry) retained genome-wide statistical significance (OR 1.31 [95% CI 1.20–1.44], P = 2 × 10⁻⁸, Fig. 1). As an additional experimental control, we examined the potential association of the EPO promoter polymorphism with the development of PDR in case subjects, irrespective of ESRD status. No association was observed between EPO and PDR for the individual cohorts or in the meta-analysis of the combined results for FinnDiane (OR 0.95 [95% CI 0.85–1.04], P = 0.25) or and U.K.-R.O.I. (0.96 [0.88–1.04], P = 0.29). Furthermore, no association was observed after inclusion of the restricted phenotype, PDR, in U.S. GoKinD case and control subjects, separately, or in the meta-analysis of all cohorts combined (results not shown).

**ELMO1.** Neither single-center nor meta-analysis of de novo genotyping in U.K.-R.O.I., nor GWAS data for FinnDiane, revealed a significant association in subjects with type 1 diabetes between rs741301, the previously reported risk variant within ELMO1, and DN (OR 1.04 [95% CI 0.95–1.13], P = 0.46; Supplementary Fig. 1). Pezzolesi et al. (15) also tested rs741301 but did not replicate the reported association. They went on to test other SNPs in the region and reported nominal associations (P = 0.002–0.05) with eight other SNPs. We examined LD between rs741301 and the
**EPO rs1617640 and Risk of Combined PDR/ESRD**

<table>
<thead>
<tr>
<th>Study name</th>
<th>SNP</th>
<th>Odds ratio</th>
<th>Lower limit</th>
<th>Upper limit</th>
<th>Z-Value</th>
<th>p-Value</th>
<th>Odds ratio and 95% CI</th>
</tr>
</thead>
<tbody>
<tr>
<td>Utah</td>
<td>rs16176401.446</td>
<td>1.146</td>
<td>1.046</td>
<td>1.254</td>
<td>3.107</td>
<td>0.002</td>
<td></td>
</tr>
<tr>
<td>US GoKinD</td>
<td>rs16176401.535</td>
<td>1.320</td>
<td>1.228</td>
<td>1.419</td>
<td>5.566</td>
<td>0.000</td>
<td></td>
</tr>
<tr>
<td>Boston</td>
<td>rs16176401.382</td>
<td>1.050</td>
<td>0.952</td>
<td>1.156</td>
<td>2.308</td>
<td>0.021</td>
<td></td>
</tr>
<tr>
<td>Finn Diane</td>
<td>rs16176401.055</td>
<td>0.866</td>
<td>0.760</td>
<td>0.980</td>
<td>0.532</td>
<td>0.595</td>
<td></td>
</tr>
<tr>
<td>UK ROI</td>
<td>rs16176401.140</td>
<td>0.938</td>
<td>0.860</td>
<td>1.018</td>
<td>1.315</td>
<td>0.188</td>
<td>2 x 10^{-9}</td>
</tr>
</tbody>
</table>

<table>
<thead>
<tr>
<th>Minor Allele</th>
<th>Major Allele</th>
</tr>
</thead>
<tbody>
<tr>
<td>1</td>
<td>2</td>
</tr>
</tbody>
</table>

Meta Analysis

FIG. 1. Previously published and new results from this study provide an estimate of the effect of the EPO promoter SNP (rs1617640) on the risk of the combined phenotype of PDR and ESRD in type 1 diabetes in five cohorts (3,162 case subjects and 3,845 control subjects) in a fixed-effects meta-analysis.

SNPs reported to be associated with DN by these investigators. The $r^2$ statistic between rs741301 and the other SNPs revealed only low to moderate LD, ranging from 0.38 to 0.65 (Supplementary Table 1).

As an additional and more extensive test of variants in this region, we performed an expanded analysis capturing all available SNPs 20 kb upstream and downstream of the ELMO1 locus to account for LD differences presumably due to ancestry. Results of the expanded analysis did not reveal any significant SNPs for either cohort individually or for the two cohorts meta-ana lysed after correcting for multiple testing ($P < 4.3 \times 10^{-5}$). Furthermore, no SNP achieved significance with inclusion of the U.S. GoKinD results in the meta-analysis (Supplementary Table 2).

Risk variants reported from U.S. GoKinD for DN in type 1 diabetes. Eleven DN susceptibility SNPs that were first reported by the U.S. GoKinD investigators as highly associated with the risk of developing DN in type 1 diabetes were parsed into eight candidate loci. We selected one representative SNP for each region of strong LD in which multiple SNPs represented the same association signal. After performing additional QC checks (see RESEARCH DESIGN AND METHODS), we first tested the eight U.S. GoKinD potential DN susceptibility SNPs by reanalyzing the U.S. GoKinD dataset downloaded from dbGAP (19). As in the original report, none of the eight SNPs were associated with DN at genome-wide statistical significance (Table 2). The two SNPs in the FERM (F [Band 4.1], E [Ezrin], R [Radixin], M [Moesin]) domain 3 (FRMD3) region showed similar $P$ values as in the original report ($2.1 \times 10^{-7}$ and $1.6 \times 10^{-6}$, respectively; Table 2). In our analysis, the statistical significance of the $P$ values for SNPs in the CPVL/CHN2 and CARS regions was reduced from $6.5 \times 10^{-5}$ to $2 \times 10^{-3}$ and $6.4 \times 10^{-6}$ to $2.2 \times 10^{-3}$, respectively. $P$ values for the 6 SNPs in the 13q region were also changed from $1.8-7.0 \times 10^{-6}$ to $1.4-9.5 \times 10^{-3}$.

We next examined these SNPs in our newly genotyped samples. Case-control analysis was performed for these loci in the U.K.-R.O.I. and FinnDiane samples revealed no significant associations in either cohort. The strongest signal was observed at rs39075 near CPVL/CHN2 in U.K.-R.O.I., (OR 1.12, $P = 0.08$) and in meta-analysis of the two replication cohorts (U.K.-R.O.I. and FinnDiane; OR 1.06, $P = 0.06$; Table 2). In expanded locus-region analyses (plus or minus 20 kb of the locus of interest), no SNP reached significance after adjustment for multiple testing (one-tailed $P = 0.03$, experiment-wise threshold $P = 4.3 \times 10^{-5}$) for the two cohorts separately or via meta-analysis. The combined meta-analysis including U.S. GoKinD revealed two SNPs downstream of FRMD3, rs1888747 ($P = 1.5 \times 10^{-3}$) and rs13288659 ($P = 9.7 \times 10^{-5}$), which showed significance after adjusting for experiment-wise multiple testing ($P < 4.3 \times 10^{-5}$). However, neither SNP achieved genome-wide significance ($P < 5 \times 10^{-8}$; Supplementary Table 3).

Pooled meta-analyses examining variants associated with DN in type 1 and type 2 diabetes. In the most comprehensive literature search for DN associated genetic variants to date, Mooyaart et al. (7) identified 24 loci. In GENIE, we examined all the available top-reported SNPs (or their proxies) for each gene in that report. Three SNPs were nominally associated ($P < 0.05$) with DN: rs13293564 at UNCl3B ($P = 0.01$) and rs179075 at the ACE ($P = 0.03$) in FinnDiane, and rs39075 at CPVL/CHN2 ($P = 0.05$) in the U.K.-R.O.I. samples. In a meta-analysis of the two cohorts, the ACE polymorphism remained nominally significant ($P = 0.04$). Including the U.S. GoKinD results, the FRMD3 signal at rs1888747 emerged as noted above; no other signals were significant after adjusting for multiple comparisons (see Supplementary Table 4 for full details).

DISCUSSION

Using a large, homogeneous population sample of European ancestry subjects with type 1 diabetes in the GENIE consortium, we were unable to replicate most of the previously reported genetic associations with DN that we examined.

Our findings do not support previously reported genetic associations with DN in type 1 diabetes in the largest GWAS published to date (15). None of these signals reached genome-wide statistical significance with the addition of larger, similarly ascertained datasets. Using ORs at the lower limit of the 95% CI from the original publication, our
### Table 2: Results in the reanalyzed U.S. GoKinD and additional GENIE cohorts for eight SNPs with strongest reported associations to DN in U.S. GoKinD samples with GENIE, we were unable to achieve genome-wide significance. Further, after performing additional QC checks, a substantially larger collection of U.K.-R.O.I. and FinnDiane cohorts in the combined sample of U.K.-R.O.I. and FinnDiane represents a substantially larger collection of case and control subjects than U.S. GoKinD and is well powered to detect the original U.S. GoKinD risk variants reported from U.S. GoKinD. We investigated other previously reported genetic associations with DN reported positive findings (type I error). From the foregoing observations, we conclude that there is a high likelihood that many of the previously reported positive associations with DN registered previously reported effect sizes thereby decreasing the likelihood that these associations represent genuine genetic effects.

<table>
<thead>
<tr>
<th>SNP</th>
<th>Gene</th>
<th>Risk variant</th>
<th>OR (95% CI) U.S. GoKinD</th>
<th>OR (95% CI) U.S. GoKinD</th>
<th>OR (95% CI) Updated U.S. GoKinD</th>
<th>OR (95% CI) Published U.S. GoKinD</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs1041466</td>
<td>ELMO1</td>
<td>A (G)</td>
<td>1.14 (0.94–1.37)</td>
<td>1.19 (0.94–1.52)</td>
<td>1.11 (0.94–1.31)</td>
<td>1.07 (0.89–1.29)</td>
</tr>
<tr>
<td>rs1888747</td>
<td>ELMO1</td>
<td>G (A)</td>
<td>1.12 (0.91–1.38)</td>
<td>1.19 (0.95–1.49)</td>
<td>1.16 (0.92–1.45)</td>
<td>1.12 (0.94–1.32)</td>
</tr>
<tr>
<td>rs13289150</td>
<td>ELMO1</td>
<td>G (C)</td>
<td>1.14 (0.94–1.38)</td>
<td>1.19 (0.95–1.49)</td>
<td>1.16 (0.92–1.45)</td>
<td>1.12 (0.94–1.32)</td>
</tr>
<tr>
<td>rs6492208/rs2391777</td>
<td>No gene</td>
<td>A (G)</td>
<td>1.08 (0.86–1.35)</td>
<td>1.09 (0.85–1.39)</td>
<td>1.11 (0.87–1.41)</td>
<td>1.08 (0.85–1.38)</td>
</tr>
<tr>
<td>rs1411765</td>
<td>FRMD3</td>
<td>T (C)</td>
<td>1.16 (0.95–1.42)</td>
<td>1.19 (0.95–1.49)</td>
<td>1.19 (0.94–1.42)</td>
<td>1.15 (0.92–1.41)</td>
</tr>
<tr>
<td>rs1411766</td>
<td>FRMD3</td>
<td>A (G)</td>
<td>1.20 (0.98–1.44)</td>
<td>1.23 (1.01–1.49)</td>
<td>1.21 (0.98–1.47)</td>
<td>1.17 (0.94–1.42)</td>
</tr>
<tr>
<td>rs1741288</td>
<td>FRMD3</td>
<td>T (C)</td>
<td>1.03 (0.81–1.32)</td>
<td>1.05 (0.83–1.31)</td>
<td>1.08 (0.84–1.38)</td>
<td>1.04 (0.81–1.32)</td>
</tr>
<tr>
<td>rs741301</td>
<td>EPO</td>
<td>C (T)</td>
<td>1.19 (0.95–1.48)</td>
<td>1.22 (1.00–1.47)</td>
<td>1.20 (0.97–1.48)</td>
<td>1.17 (0.94–1.42)</td>
</tr>
</tbody>
</table>

### Results in the reanalyzed U.S. GoKinD and additional GENIE cohorts for eight SNPs with strongest reported associations to DN in U.S. GoKinD samples with GENIE, we were unable to achieve genome-wide significance. Further, after performing additional QC checks, a substantially larger collection of U.K.-R.O.I. and FinnDiane cohorts in the combined sample of U.K.-R.O.I. and FinnDiane represents a substantially larger collection of case and control subjects than U.S. GoKinD and is well powered to detect the original U.S. GoKinD risk variants reported from U.S. GoKinD. We investigated other previously reported genetic associations with DN reported positive findings (type I error). From the foregoing observations, we conclude that there is a high likelihood that many of the previously reported positive associations with DN registered previously reported effect sizes thereby decreasing the likelihood that these associations represent genuine genetic effects.
of a false-negative finding (type II error), even accounting for the likely overestimation of effect sizes due to the winner’s curse phenomenon (25). We also harmonized the ascertainment criteria for case-control definitions across all the study populations (including U.S. GoKinD), making it unlikely that phenotypic heterogeneity across study populations explains the lack of replication.

A crucial issue that bears on the interpretation of case-control studies of the genetics of DN concerns the adequacy of phenotype definitions. In this and most studies cited to date, there is the presumption that long-duration diabetes exposure and the presence of frank protein in the urine—macroalbuminuria—defines DN and that phenotypic heterogeneity has been well controlled through this classification. These definitions are derived in large measure from the classic studies of Parving et al. (26), Viberti et al. (27), and Mogensen and Christensen (28), who documented 30 years ago a virtually inexorable progression to ESRD in patients who developed microalbuminuria after approximately 2 decades of exposure to the diabetic metabolic milieu. However, these longitudinal findings were based on small numbers of patients. The plasticity of DN phenotypes is reflected in more recent and much larger longitudinal studies showing that most patients with type 1 diabetes, categorized initially as having microalbuminuria, undergo regression to normoalbuminuria with preservation of renal function (29). It is not entirely clear that microalbuminuria versus macroalbuminuria, stage of chronic kidney disease and attendant renal function, the rate of renal decline, or the occurrence of extreme phenotypes, such as ESRD/PDR, represent one disease process along a continuum or many distinct disease states, each of which may be under distinct genetic control. As pointed out recently (24), genetic variants, such as those in MYH9 and APOL1 that are common in certain ethnic groups, may mask the effects at other loci unless methods such as multilocus modeling and interaction analyses are used to control for these effects.

In addition, phenotypic variation may be a function of ethnicity and disease-specific gene expression. For example, Pima Indians with type 2 diabetes have very early-onset DN, characterized by an accelerated loss of renal function and progression to ESRD despite lower blood pressures and lipid levels, factors thought to be protective (30). This has been postulated to be due to structural differences in the glomerulus ("podocyte insufficiency"), a decrease in net nephron mass (glomerulopenia) resulting in glomerulomegaly, increased intraglomerular capillary pressure, and ultimately, hyperfiltration injury (30). Whether these structural and intrarenal hydraulic changes could be genetically regulated is ultimately a testable hypothesis; they warrant further investigation to continue the inquiry why certain populations have an apparent disproportional susceptibility to ESRD and, particularly, DN.

In summary, we have presented evidence that several previously reported genetic associations with DN in type 1 diabetes could not be replicated in a large, homogeneous sample of subjects with type 1 diabetes. Our failure to replicate these associations underscores the need to apply stringent statistical thresholds of significance, maximize power through meta-analysis of all available data, and seek replication in independent samples, as has been proposed by a number of different authors (31,32). Finally, the applicability and generalizability of DN risk loci from type 1 diabetes to type 2 diabetes, and the related question of shared genetic susceptibility for nephropathy between type 1 and type 2 diabetes, remain unresolved.

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REFERENCES


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