

A Genetic Locus on Chromosome 2q24 Predicting Peripheral Neuropathy Risk in Type 2 Diabetes: Results From the ACCORD and BARI 2D Studies

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Genetic factors have been postulated to be involved in the etiology of diabetic peripheral neuropathy (DPN), but their identity remains mostly unknown. The aim of this study was to conduct a systematic search for genetic variants influencing DPN risk using two well-characterized cohorts. A genome-wide association study (GWAS) testing 6.8 million single nucleotide polymorphisms was conducted among participants of the Action to Control Cardiovascular Risk in Diabetes (ACCORD) clinical trial. Included were 4,384 white case patients with type 2 diabetes (T2D) and prevalent or incident DPN (defined as a Michigan Neuropathy Screening Instrument clinical examination score >2.0) and 784 white control subjects with T2D and no evidence of DPN at baseline or during follow-up. Replication of significant loci was sought among white subjects with T2D (791 DPN-positive case subjects and 158 DPN-negative control subjects) from the Bypass Angioplasty Revascularization Investigation in Type 2 Diabetes (BARI 2D) trial. Association between significant variants and gene expression in peripheral nerves was evaluated in the Genotype-Tissue Expression (GTEx) database. A cluster of 28 SNPs on chromosome 2q24 reached GWAS significance ($P < 5 \times 10^{-8}$) in ACCORD. The minor allele

of the lead SNP (rs13417783, minor allele frequency = 0.14) decreased DPN odds by 36% (odds ratio [OR] 0.64, 95% CI 0.55–0.74, $P = 1.9 \times 10^{-9}$). This effect was not influenced by ACCORD treatment assignments (P for interaction = 0.6) or mediated by an association with known DPN risk factors. This locus was successfully validated in BARI 2D (OR 0.57, 95% CI 0.42–0.80, $P = 9 \times 10^{-4}$; summary $P = 7.9 \times 10^{-12}$). In GTEx, the minor, protective allele at this locus was associated with higher tibial nerve expression of an adjacent gene (*SCN2A*) coding for human voltage-gated sodium channel NaV1.2 ($P = 9 \times 10^{-4}$). To conclude, we have identified and successfully validated a previously unknown locus with a powerful protective effect on the development of DPN in T2D. These results may provide novel insights into DPN pathogenesis and point to a potential target for novel interventions.

Diabetic peripheral neuropathy (DPN)—the most common cause of neuropathy worldwide—is a frequent complication of diabetes that significantly contributes to the increased morbidity and mortality associated with this disease (1). Up to one-fourth of the annual U.S. expenditure on diabetes is due to DPN, a large proportion of

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which is secondary to type 2 diabetes (T2D) (2,3). The most common presentation of DPN is a distal symmetric polyneuropathy resulting from small and large fiber dysfunction leading to loss of sensory, proprioception, temperature, and pain discrimination, along with symptoms of numbness, tingling, burning, and shooting pain (1,4). Signs and symptoms begin distally and spread proximally.

Known risk factors for DPN include duration and severity of hyperglycemia, age, dyslipidemia, hypertension, obesity, height, and smoking (1,5–9). Because these exposures fail to fully explain interindividual differences in the risk of developing DPN, genetic factors have been postulated to be involved in the etiology of DPN (10), although formal heritability estimates, such as those available for other diabetic complications, including cardiovascular autonomic neuropathy (narrow-sense heritability up to 39%) (11–13), are not available for DPN. Knowledge of the genetic factors that modulate DPN risk may provide insights into the molecular pathways linking the diabetic milieu to nerve damage, which may in turn suggest new pharmacological targets for preventing or treating DPN. However, although many genetic studies have been performed for other diabetic complications (14), data on the genetic determinants of DPN are scant. A few candidate gene studies have been performed, but these were small and not followed by replication attempts (10). A locus on chromosome 8p21.3 was recently found to be associated with painful DPN in a genome-wide association study (GWAS), but this finding did not reach genome-wide significance and is still to be replicated (15).

Here we report the results of a GWAS for DPN conducted among participants with T2D in the Action to Control Cardiovascular Risk in Diabetes (ACCORD) clinical trial. Our findings, which were replicated in the population of the Bypass Angioplasty Revascularization Investigation 2 Diabetes (BARI 2D) trial, point to a locus on chromosome 2q24 as a powerful determinant of DPN risk that may act by affecting a nearby voltage-gated sodium channel, NaV1.2, expressed in peripheral nerves. This is the first GWAS of DPN yielding a genome-wide significant signal with independent replication and biological plausibility of the leading candidate gene in the associated region.

RESEARCH DESIGN AND METHODS

Study Population

Discovery Set: ACCORD Study

The ACCORD clinical trial investigated whether cardiovascular event rates could be reduced by intensively targeting hyperglycemia to HbA_{1c} <6.0% (42 mmol/mol) compared with a standard target of HbA_{1c} between 7 and 7.9% (53–63 mmol/mol). For this purpose, 10,251 participants with T2D and high cardiovascular risk were randomized in a 1:1 ratio to receive intensive or standard glycemic control

therapy at 77 clinical sites across the U.S. and Canada (16). The study also investigated the effect of intensive versus standard blood pressure control and fibrate versus placebo therapy on cardiovascular events through the ACCORD blood pressure and lipid subtrials in a double two-by-two factorial design (16). In addition, ACCORD had a rich follow-up of study participants and collected data on other diabetic complications, including DPN, at baseline and during follow-up. Of the 10,251 ACCORD participants, 8,174 consented to genetic studies. To minimize confounding by race, our GWAS for discovery of genetic predictors of DPN was restricted to 5,360 whites. Among them, DPN data were collected from 5,168 participants at baseline and/or during follow-up by means the Michigan Neuropathy Screening Instrument (MNSI) clinical examination score.

Validation Set: BARI 2D Study

BARI 2D was a two-by-two factorial clinical trial enrolling 2,368 participants with T2D and established coronary artery disease (17). For glycemic control, participants were randomly assigned to insulin sensitization or insulin provision strategy to reach the same HbA_{1c} target of <7.0% (53 mmol/mol). For coronary artery disease, participants were randomly assigned to undergo coronary revascularization procedures (percutaneous coronary intervention or coronary artery bypass graft surgery) or medical therapy. The aim was to investigate the cardiovascular event reduction by both treatment strategies. As in ACCORD, other secondary outcomes were obtained in BARI 2D, including DPN, which was evaluated with the same MNSI clinical examination score at baseline and follow-up (18). A total of 1,030 whites consented to genetic studies in BARI 2D; 949 had genetic data that passed internal quality control (QC) and also had information about the presence of DPN at baseline and follow-up. Because participants were recruited in the two studies during the same time period (January–June 2001 and February 2003–October 2005 for ACCORD, and January 2001–March 2005 for BARI 2D) and both studies upheld participation in another clinical trial as an exclusion criterion (16,19), the chances of a person being included in both studies were deemed to be negligible.

Outcome Definition

The ACCORD and BARI 2D trials both defined neuropathy as an MNSI clinical examination score >2.0 (18,20)—a criterion that has been extensively validated as being highly sensitive and specific for the diagnosis of DPN (21,22). The MNSI clinical examination includes a focused examination of the feet to assess skin and structural abnormalities, along with assessment of distal vibration perception with a 128-Hz tuning fork and ankle reflexes. For the purpose of the genetic association study, DPN case subjects were defined as participants having an MNSI >2.0 at study entry and/or at any time during follow-up (4.9 and 5.3 years on average in ACCORD and BARI 2D, respectively), whereas DPN control subjects were defined

as participants having an MNSI ≤ 2.0 at study entry and for the entire duration of follow-up.

DNA Extraction and Genotyping

Discovery Set: ACCORD Study

Detailed DNA extraction, genotyping, QC methods, and imputation in ACCORD can be found in the supplementary material of the article in which the GWAS was first reported (23). In brief, genotyping was performed in two centers using different platforms and chips: 6,085 DNA samples (ACCORD UVA Set) were genotyped at the University of Virginia (UVA) on Illumina HumanOmniExpressExome-8 (v1.0) chips containing 951,117 SNPs; 8,174 samples (ACCORD UNC Set) were genotyped at the University of North Carolina (UNC), on Affymetrix Axiom Biobank1 chips containing 628,679 probes. The ACCORD UVA set included subjects who had given consent to genetic studies by any investigator; the ACCORD UNC included the subjects in the ACCORD UVA set plus those who had given consent only to studies by ACCORD investigators. After extensive QC of the individual genotyping sets and harmonization of genotypes for those samples and SNPs that were in common between the two genotyping sets, data were organized in two nonoverlapping data sets: ANYSET ($n = 5,971$), including subjects from the ACCORD UVA set, genotyped at either UVA or UNC at a total of 1,263,585 individual SNPs, and ACCSET ($n = 2,113$), including subjects from the ACCORD UNC set minus those in the ACCORD UVA set, genotyped only at UNC at a total of 572,192 SNPs. Imputation was conducted independently in the ANYSET and ACCSET data sets by means of IMPUTEv2.3.1 (24) using the full 1000 Genomes Phase 3 (October 2014) panel as the reference. After discarding imputed SNPs with an information content < 0.3 , the total (genotyped + imputed) SNPs were 25,017,489 in ANYSET and 25,012,865 in ACCSET.

Validation Set: BARI 2D Study

DNA was isolated and purified from whole blood using the Qiagen QIAamp DNA purification kit (Qiagen, Germantown, MD), as previously described (25). Genotyping was performed using the Infinium Multi-Ethnic Global Array (Illumina, San Diego, CA) according to the manufacturer's instructions. After indels, SNPs with call rates < 0.99 , and multiallelic sites were filtered out, the samples were prephased with SHAPEIT and imputed toward the Phase 3 Cosmopolitan Reference panel of 1000 Human Genomes project using IMPUTE2 software. Imputed genotypes were then converted into dosages using FCGENE software. Imputation quality ranged from 85 to 100% for the 40 variants available for validation in BARI 2D (variants listed in Table 2 and Supplementary Table 6).

Data Analysis

Descriptive Statistics

Analyses were run in SAS 9.4 software (SAS Institute, Cary, NC). Normally distributed continuous variables are

presented as mean \pm SD and were analyzed by independent t test for difference in means between groups. Nonnormally distributed continuous variables are presented as median (interquartile range) values and were analyzed by t test after log transformation. Categorical variables are presented as counts (percentages) and were analyzed by χ^2 tests to examine differences among groups.

GWAS

A GWAS for DPN was performed in 5,168 white ACCORD participants. GWAS analyses were conducted separately in ACCSET (3,554 case subjects/830 control subjects) and ANYSET (600 case subjects/184 control subjects) using SAS 9.4 software on the Harvard Medical School computing cluster, Orchestra. After filtration for minor allele frequency (MAF) $\geq 5\%$, 6,847,206 genotyped or imputed SNPs formed the GWAS panel in each data set. For each common variant, minor allele dosage (ranging from 0 to 2) was inferred from the genotypes or computed from the imputed posterior probabilities. The association between minor allele dosage of each variant and DPN was tested by logistic regression, assuming an additive genetic model and adjusting for assignment to interventions, seven clinical center networks, and top three principal components (PC1–PC3). After using genomic control corrections ($\lambda = 1.014$ for ANYSET and $\lambda = 1.032$ for ACCSET), the GWAS results from the ACCSET and ANYSET sets were meta-analyzed in METAL (Abecasis Laboratory, University of Michigan, Ann Arbor, MI) (26), through a fixed-effects inverse-variance approach. Genome-wide significance was defined as a P value $< 5 \times 10^{-8}$, and suggestive (notable) significance as $P < 1 \times 10^{-6}$. Manhattan and quantile-quantile (QQ) plots were generated to illustrate the GWAS results.

Further analyses of SNPs reaching genome-wide significance were carried out by 1) testing whether the SNP had similar effects on prevalent DPN (MNSI > 2.0 at study entry) and incident DPN (MNSI ≤ 2.0 at baseline and MNSI > 2.0 during follow-up); 2) testing for interaction with baseline characteristics or, for incident DPN, with trial treatments (intensive vs. standard glycemic control, intensive vs. standard blood pressure control, fenofibrate + statin vs. placebo + statin for hyperlipidemia control) by adding appropriate interaction terms; 3) evaluating the association between SNP and baseline characteristics, individual MNSI components, and other diabetic complications, including cardiovascular autonomic neuropathy and incident DPN and diabetic retinopathy; 4) evaluating the association between DPN and SNPs in African American participants; and 5) evaluating the association between DPN and genotyped low-frequency variants (MAF 0.01–0.05) placed in the linkage disequilibrium (LD) block as the top common SNP in the GWAS.

Continuous and dichotomous outcomes were tested by linear and logistic regression models, respectively. Incident outcomes were tested by means of Cox regression models.

Validation

All GWAS-significant SNPs (28 SNPs at locus 2q24) and lead variants at loci that reached a P value of $<1 \times 10^{-5}$ in the discovery set (ACCORD) were tested for association with DPN in a validation set derived from the BARI 2D study. Logistic regression was used for this purpose with adjustments by the following covariates: country of origin, top three principal components, assignments to cardiovascular treatment strata (early medical therapy vs. early revascularization with percutaneous coronary intervention or coronary artery bypass grafting), and assignments to glycemic control strata (insulin sensitization vs. insulin provision). Given that replication was attempted for 13 variants, the significance threshold was set to $P < 0.004$ based on a Bonferroni correction (0.05/13). Variants that were successfully validated in BARI 2D were tested for their effects on prevalent DPN (MNSI >2.0 at the study entry) and incident DPN (MNSI turned >2.0 during the follow-up), as described for the discovery set.

Meta-analysis of BARI 2D and ACCORD

Results in BARI 2D were meta-analyzed with those in ACCORD by means of METAL (Abecasis Laboratory, University of Michigan) using a fixed-effects inverse-variance approach.

Power of Genetic Analyses

The discovery set (ACCORD) provided 80% power ($\alpha = 5 \times 10^{-8}$) to detect genetic effects corresponding to a relative risk of 1.20 and 1.24 for effect allele frequencies of 0.50 and 0.15, respectively. The validation set (BARI 2D) provided 80% power ($\alpha = 0.0038$, adjusting for the 13 loci for which replication was sought) to detect genetic effects corresponding to a relative risk of 1.26 and 1.32 for effect allele frequencies of 0.50 and 0.15, respectively.

Expression Quantitative Trait Loci Analysis

The top variant from the GWAS was tested for association with tibial nerve-specific gene expression through in silico analyses using the Genotype-Tissue Expression (GTEx) v7 database (27). GTEx is an online database containing tissue-specific gene expression data obtained from 620 donors (34% females, 85% whites, 68% >50 years of age) by means of Illumina TrueSeq RNA sequencing and the Affymetrix Human Gene 1.1 ST Expression Array and linked to GWAS data obtained from the same individuals by whole-genome sequencing, whole-exome sequencing, or Illumina SNP arrays (www.gtexportal.org). Expression quantitative trait loci (eQTL) analyses of genes within ± 2 mega base pairs (Mbp) from the lead SNP were conducted among 361 genotyped individuals for which tibial nerve tissue expression profiles were available. Normalized effect sizes and their 95% CIs were obtained from linear regression models testing the association of the minor allele of the lead SNP with gene expression adjusted by the top three genotyping principal components, sex, genotyping platform, and a set of other covariates described in the GTEx documentation (27).

Gene Expression Analysis for SCN2A

SCN2A is expressed in the human peripheral nervous system in dorsal root ganglia (28). To quantify the level of gene expression for SCN2A in the tibial nerve, RNA sequencing (RNA-seq) samples from several human tissues were contrasted: tibial nerve, hippocampus, and skeletal muscle samples from the GTEx database (27) and dorsal root ganglia samples from the study by North et al. (29). Because library preparation, mapping, and relative abundance quantification in transcripts per million (TPM) were performed differently for these two studies, the meta-analysis was performed as follows: Coding gene relative abundances for 18,876 quantified coding genes were extracted from the North et al. (29) study, and for each sample with nonzero SCN2A abundance, the percentile of SCN2A expression with respect to all coding genes in that sample were calculated. For the GTEx data sets, the uniformly processed RNA-seq abundances for coding genes were extracted from the GTEx companion website database (GTEx_Analysis_2016-01-15_v7_RNASeQCv1.1.8_gene_tpm.gct.gz) and renormalized by constraining the TPMs of all the 19,260 coding genes quantified in the study to sum to 1 million. For each sample with nonzero SCN2A abundance, the percentile of SCN2A expression with respect to all coding genes in that sample was calculated.

RESULTS

Clinical Characteristics of DPN Case Subjects and Control Subjects

The clinical characteristics of the discovery and validation sets are reported in Table 1. To minimize ethnic confounding, both sets included only self-reported whites. The discovery set consisted of 5,168 ACCORD participants: 4,384 who showed signs of DPN at study entry and/or during follow-up (DPN case subjects) and 784 who did not show signs of DPN at any time during the study (DPN control subjects). Compared with the latter, DPN case subjects were significantly older and taller, had longer duration of diabetes, higher HbA_{1c}, BMI, and urinary albumin-to-creatinine ratio (UACR), and lower HDL cholesterol, were more frequently treated with insulin, and had a higher prevalence of self-reported retinopathy. For many of these variables, differences with control subjects were more pronounced for prevalent than incident case subjects (Supplementary Table 1). The validation set consisted of 949 BARI 2D participants, including 791 DPN case subjects and 158 DPN control subjects, defined as above. Overall, the clinical characteristics of the validation set were similar to those of the discovery set, except for lower HbA_{1c} and cholesterol levels (Table 1). Within the validation set, DPN case subjects had lower total and LDL and HDL cholesterol and were more frequently treated with insulin compared with DPN control subjects.

GWAS of DPN

A total of 6,847,206 common variants (MAF >0.05), genotyped or imputed, were tested for association with

Table 1—Characteristics of DPN case and control subjects

Baseline characteristic	Discovery set (ACCORD)			Validation set (BARI 2D)		
	DPN case subjects (n = 4,384)	DPN control subjects (n = 784)	P value	DPN case subjects (n = 791)	DPN control subjects (n = 158)	P value
Female	1,538 (35.1)	289 (36.9)	0.34	204 (25.8)	51 (32.3)	0.09
Age (years)	63.2 ± 6.5	61.6 ± 6.4	<0.0001	63.33 ± 8.47	62.09 ± 9.29	0.10
T2D duration (years)	10.9 ± 7.5	9.1 ± 6.9	<0.0001	10.5 ± 8.38	9.06 ± 8.71	0.05
BMI (kg/m ²)	33.2 ± 5.2	31.9 ± 4.8	<0.0001	31.8 ± 5.41	32.33 ± 5.97	0.27
Waist circumference (cm)	110.0 ± 12.9	105.3 ± 12.0	<0.0001	108.99 ± 13.08	108.42 ± 13.97	0.62
Height (cm)	171.7 ± 9.5	170.0 ± 9.4	<0.0001	NA	NA	NA
HbA _{1c} (%)	8.22 ± 0.93	8.11 ± 0.90	0.02	7.54 ± 1.54	7.66 ± 1.63	0.40
Fasting glucose (mmol/L)	9.93 ± 2.82	9.75 ± 2.76	0.09	NA	NA	NA
SBP (mmHg)	135.2 ± 16.7	134.7 ± 16.4	0.42	131.65 ± 20.6	128.75 ± 16.32	0.05
DBP (mmHg)	74.1 ± 10.4	75.0 ± 10.7	0.03	73.82 ± 11.92	73.54 ± 11.22	0.78
LDL (mmol/L)	2.67 ± 0.84	2.68 ± 0.83	0.52	2.43 ± 0.83	2.59 ± 0.85	0.03
HDL (mmol/L)	1.04 ± 0.27	1.06 ± 0.29	0.0047	0.95 ± 0.23	0.98 ± 0.23	0.13
Women	1.16 ± 0.29	1.22 ± 0.29	0.0009	1.06 ± 0.24	1.02 ± 0.22	0.19
Men	0.97 ± 0.23	0.98 ± 0.23	0.54	0.91 ± 0.21	0.96 ± 0.24	0.02
Total cholesterol (mmol/L)	4.74 ± 1.05	4.76 ± 1.04	0.33	4.35 ± 1.05	4.56 ± 1.16	0.03
Triglycerides (mmol/L)†	1.95 (1.37–2.81)	1.91 (1.29–2.76)	0.14	1.76 (1.24–2.58)	1.90 (1.28–2.7)	0.46
eGFR (mL/min/1.73 m ²)	87.8 ± 21.7	90.4 ± 20.4	0.0016	NA	NA	NA
UACR (mg/mmol)†	1.4 (0.7–4.2)	1.1 (0.6–2.8)	<0.0001	NA	NA	NA
Previous CV event*	1,556 (35.5)	264 (33.7)	0.33	318 (40.2)	69 (43.7)	0.42
Report of retinopathy	439 (11.3)	40 (5.6)	<0.0001	NA	NA	NA
Current smoker	496 (11.3)	84 (10.7)	0.8	63 (8)	19 (12.1)	0.09
Previous smoker	2,194 (57.0)	390 (56.2)	0.8	456 (57.8)	88 (56.1)	0.69
Insulin therapy	1,598 (36.5)	220 (28.1)	<0.0001	212 (26.8)	27 (17.1)	0.01
ACCORD Glycemia trial						
Standard	2,227 (50.8)	371 (47.3)	0.07	—	—	—
Intensive	2,157 (49.2)	413 (52.7)		—	—	—
ACCORD BP trial	1,862 (42.5)	361 (46.1)	0.06	—	—	—
Standard	926 (21.1)	182 (23.2)	0.81	—	—	—
Intensive	936 (21.4)	179 (22.8)		—	—	—
ACCORD Lipid trial	2,522 (57.5)	423 (54.0)	0.06	—	—	—
Fibrate	1,294 (29.5)	219 (27.9)	0.86	—	—	—
Placebo	1,228 (28.0)	204 (26.0)		—	—	—
BARI 2D CV intervention						
Medical therapy	—	—	—	398 (50.3)	67 (42.4)	0.07
Early revascularization	—	—	—	393 (49.7)	91 (57.6)	
BARI 2D diabetic therapy						
Insulin provision	—	—	—	394 (49.8)	71 (44.9)	0.26
Insulin sensitization	—	—	—	397 (50.2)	87 (55.1)	

Except where noted, data are means ± SD for continuous variables and counts (%) for categorical data. BP, blood pressure; CV, cardiovascular; DBP, diastolic blood pressure; NA, not available; SBP, systolic blood pressure. †Median (interquartile range). *Prior CV event: In ACCORD, this includes secondary prevention status or history of myocardial infarction, stroke, angina, and/or ischemic changes (electrocardiogram) on graded exercise tolerance test or positive imaging, coronary revascularization procedures, or other revascularization procedures at baseline; in BARI 2D, this includes history of myocardial infarction, congestive heart failure, stroke, or transient ischemic attack.

DPN in the discovery set. Of these, 28 reached genome-wide significance ($P < 5 \times 10^{-8}$), as summarized in the Manhattan and QQ plots shown in Fig. 1. These variants lie in the same region of chromosome 2q24 and are in strong LD with each other in whites (Fig. 2A). When the analysis was conditioned on the lead SNP (rs13417783),

the effects of all the other genome-wide significant variants disappeared (Supplementary Fig. 1), indicating that all 28 variants captured the same genetic effect. The lead SNP had a MAF of 0.15 and was associated with a 36% decrease in the odds of DPN per minor allele copy (odds ratio [OR] 0.64, 95% CI 0.55–0.74; $P = 1.9 \times 10^{-9}$) (Table

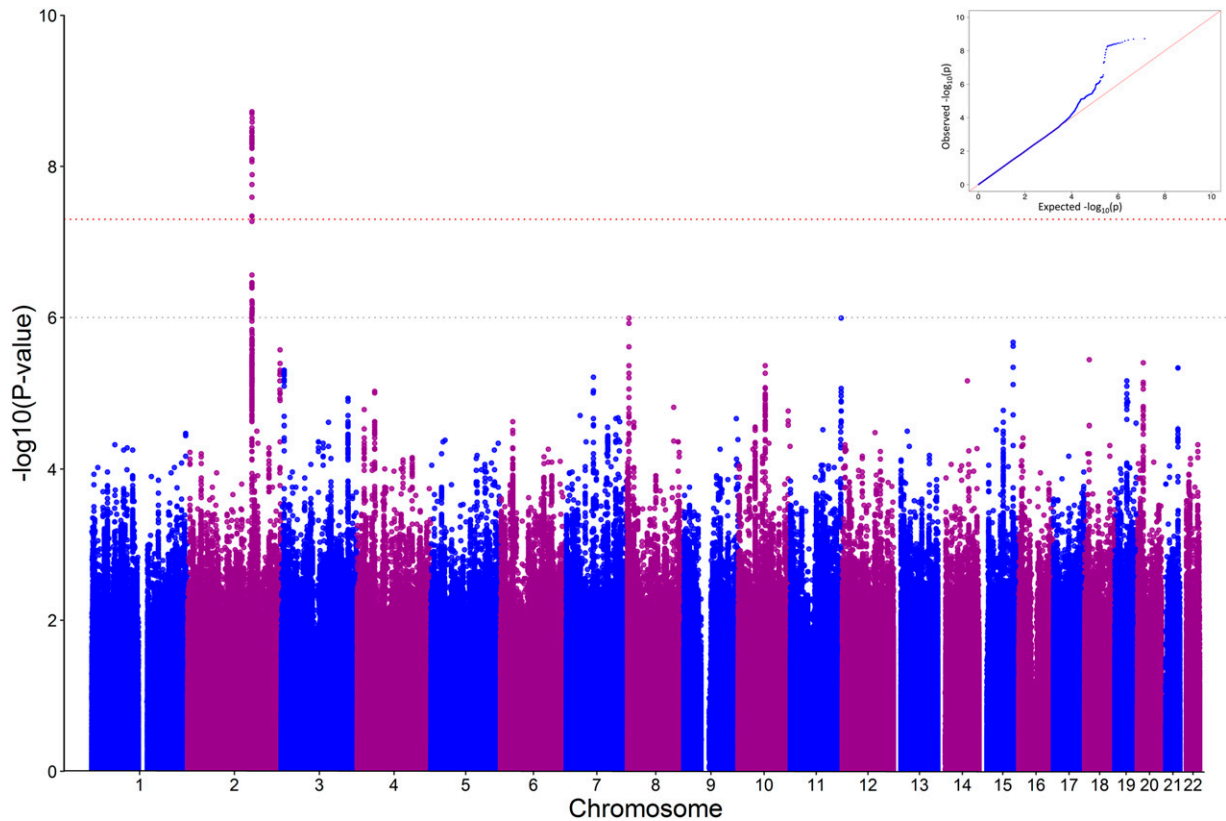


Figure 1—GWAS results. A: Manhattan plot. Each dot represents a polymorphism (SNP). The x -axis depicts each chromosome and the y -axis shows the negative $\log_{10} P$ value for association of each SNP with DPN. The red dotted line indicates the genome-wide significance threshold of $P = 5 \times 10^{-8}$; the gray dotted line indicates the notable genome-wide significance threshold of $P = 1 \times 10^{-6}$. B: QQ plot (inset). The black dashed line indicates the null hypothesis. The blue line represents the observed $\log_{10} P$ values corresponding to the expected P values. $\lambda = 0.994$.

2). While rs13417783 was an imputed variant (with an excellent quality of imputation), other SNPs in the genome-wide significant cluster were genotyped (Supplementary Table 2). Effects were in the same direction in both genotype sets of ACCORD (Supplementary Table 2). Two other loci, rs13265430 on chromosome 8p23 and rs77494074 on chromosome 11q25, attained P values in the notable range ($P = 1 \times 10^{-6}$ to 5×10^{-8}), and 10 more attained P values in the 1×10^{-5} to 1×10^{-6} range (Table 2). All of these associations were only modestly affected by adjustment for differences in age, diabetes duration, and/or BMI (Supplementary Table 3). No evidence of association was observed with the loci on chromosome 8 and 12, where a suggestive association with painful DPN had been detected in a previous GWAS (15) (Supplementary Table 4). Of 14 polymorphisms that were previously reported to be associated with DPN (30) and for which data were available in the ACCORD GWAS, 1 (rs1963645 at the *NOS1AP* locus) showed a significant association with DPN. However, this was in the opposite direction as that previously reported (Supplementary Table 5).

Validation of GWAS Findings

The 13 independent loci that attained $P < 1 \times 10^{-5}$ in the GWAS were investigated for their association with DPN in

the validation set. The effect of the top GWAS locus (2q24) was successfully replicated, with an OR of 0.57 per lead SNP (rs13417783) minor allele copy (95% CI 0.41–0.80, $P = 9 \times 10^{-4}$) (Table 2). One of the other 27 SNPs at 2q24 that were GWAS-significant in the discovery set (rs10200297) showed a stronger association than rs13417783 in the validation set (Supplementary Table 6). However, in a meta-analysis of the discovery and validation sets, rs13417783 remained the lead SNP at this locus (OR 0.63, 95% CI 0.55–0.72, $P = 7.9 \times 10^{-12}$). Among the other loci with $P < 1 \times 10^{-5}$ in the discovery set, one (rs10555080, aka rs72397229, on 19q12) showed a nominally significant association with DPN in the validation set ($P = 0.0098$), resulting in a P value in the notable range ($P = 2.6 \times 10^{-7}$) in the two sets combined. Another locus (rs201655918 on 14q24) was also nominally significant in the validation set, but the effect was in the opposite direction than in the discovery set. Four loci (rs1202660 on 7q11; rs2491019 on 10q22; rs11073752 on 15q25, and rs9948095 on 18p11) showed nonsignificant associations in the validation set that were in the same direction as in the discovery set. One of these SNPs (rs11073752) attained a P value in the notable range ($P = 6.5 \times 10^{-7}$) in the meta-analysis of the discovery and validation sets.

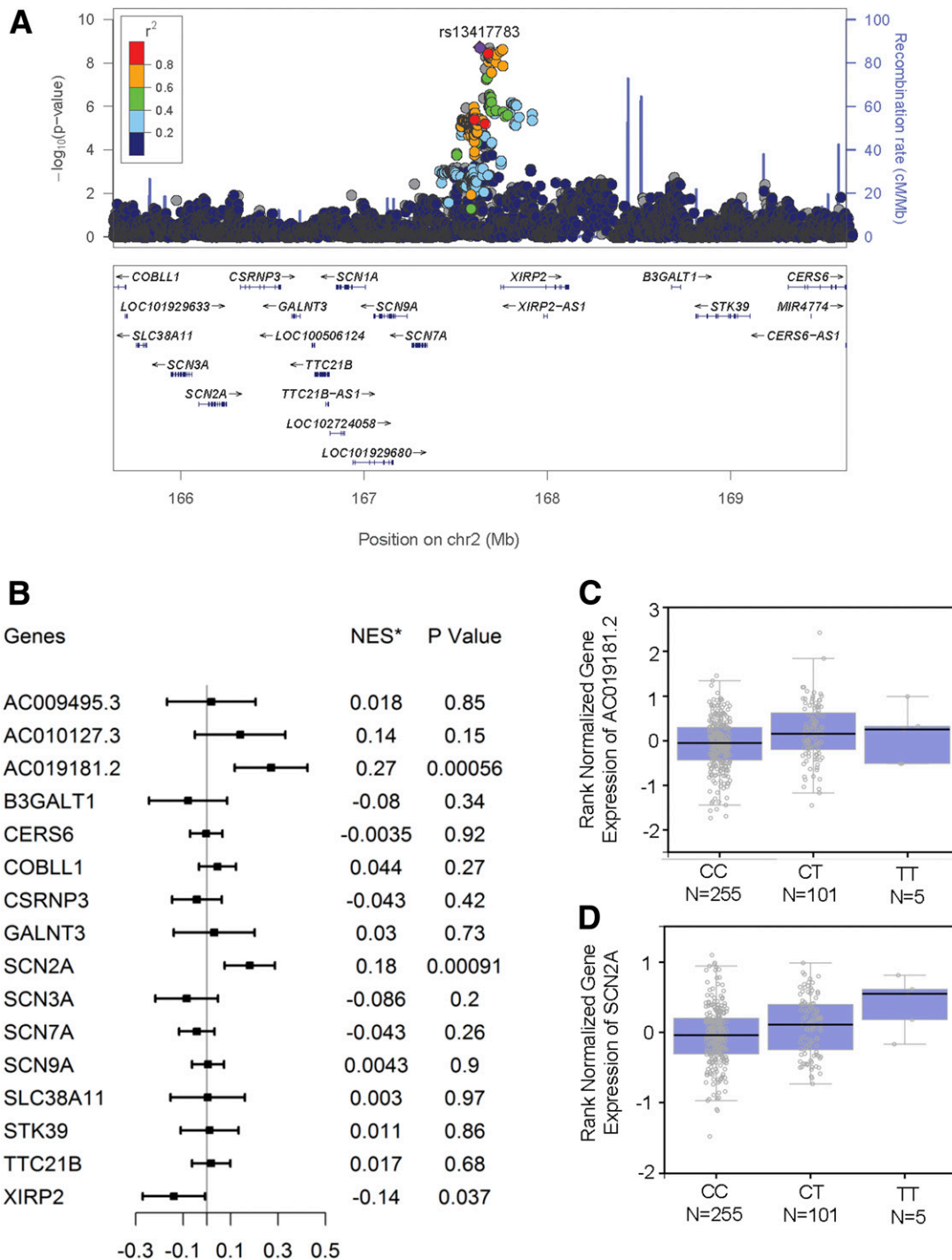


Figure 2—Characterization of locus 2q24. **A**: Regional association plot of locus 2q24. Variants are displayed ± 2 Mbp upstream and downstream of the lead SNP (rs13417783). The x-axis depicts the chromosomal positions of the SNPs according to National Center for Biotechnology Information Build 37, and the y-axis depicts the $-\log_{10} P$ values for association of these SNPs with DPN in ACCORD. SNPs in strong LD with the lead SNP (purple) are marked in red ($r^2 > 0.8$). The bottom panel depicts genes from the University of California, Santa Cruz (UCSC) Known Genes data set within the region. The locus zoom plot was generated using LocusZoom (Abecasis Laboratory, University of Michigan School of Public Health) through <http://locuszoom.sph.umich.edu/genform.php?type=yourdata>. The reference database was hg19/1000 Genomes Nov 2014 European. **B**: eQTL analysis of locus 2q24 showing the association between rs13417783 and tibial nerve-specific expression of neighboring genes. The eQTL analysis was conducted on data from the GTEx database (<http://www.gtexportal.org/home/>). Genes were those located within ± 2 Mbp from the lead SNP rs13417783. *NES is the normalized effect size, i.e., the slope of the linear regression between minor (T) allele dosage and gene expression. This effect size is computed in a normalized space where magnitude has no direct biological interpretation. **C**: Tibial nerve-specific expression of AC019181.2 stratified by rs13417783 genotypes. **D**: Tibial nerve-specific expression of SCN2A stratified by rs13417783 genotypes. Box plots were generated in GTEx.

Table 2 – Top loci ($P < 1 \times 10^{-5}$) associated with DPN: effects in ACCORD and validation in BARI 2D

SNP	Position†	Closest gene	MA**	MAF‡ 1000G	Discovery set (ACCORD)			Validation set (BARI 2D)			ACCORD + BARI 2D*			
					MAFS case subjects	MAFS control subjects	P	OR (95% CI)	P	OR (95% CI)	P	OR (95% CI)	P	
rs13417783	2:167629849	XIRP2	T	0.14	0.14	0.20	0.64 (0.55–0.74)	1.9×10^{-9}	0.14	0.20	0.57 (0.41–0.80)	0.0009	0.63 (0.55–0.72)	7.9×10^{-12}
rs12988669	2:240275570	HDAC4	C	0.15	0.16	0.20	0.71 (0.62–0.82)	2.7×10^{-6}	0.16	0.13	1.22 (0.83–1.78)	0.32	0.76 (0.66–0.87)	5.1×10^{-5}
rs60770880	3:8037416	LOC101-927394	A	0.21	0.21	0.26	0.75 (0.66–0.84)	5.0×10^{-6}	0.20	0.21	0.93 (0.68–1.26)	0.62	0.77 (0.68–0.86)	1.0×10^{-5}
rs11932946	4:45140214	GUF1	G	0.12	0.12	0.16	0.69 (0.59–0.82)	9.6×10^{-6}	0.13	0.11	1.01 (0.68–1.49)	0.98	0.73 (0.63–0.85)	4.5×10^{-5}
rs1202660	7:70658177	WBSR17	T	0.22	0.20	0.25	0.74 (0.65–0.84)	6.2×10^{-6}	0.23	0.26	0.81 (0.60–1.09)	0.16	0.75 (0.67–0.85)	2.5×10^{-6}
rs13265430	8:4165607	CSMD1	A	0.09	0.09	0.13	0.64 (0.52–0.76)	1.0×10^{-6}	0.11	0.09	1.35 (0.84–2.15)	0.21	0.70 (0.59–0.83)	4.3×10^{-5}
rs2491019	10:70776987	KIAA1279	A	0.45	0.47	0.40	1.31 (1.17–1.47)	4.4×10^{-6}	0.45	0.46	1.02 (0.79–1.32)	0.86	1.25 (1.13–1.39)	2.0×10^{-5}
rs77494074	11:132794801	OPCML	T	0.08	0.07	0.10	0.61 (0.50–0.74)	1.0×10^{-6}	0.07	0.06	1.28 (0.71–2.29)	0.41	0.66 (0.54–0.79)	1.3×10^{-5}
rs201655918	14:76791306	ESRRB	C	0.28	0.26	0.32	0.75 (0.66–0.85)	6.9×10^{-6}	0.30	0.24	1.41 (1.02–1.96)	0.04	0.81 (0.72–0.91)	5.3×10^{-4}
rs11073752	15:88423051	NTRK3	C	0.33	0.32	0.38	0.76 (0.67–0.85)	2.1×10^{-6}	0.33	0.36	0.80 (0.61–1.05)	0.11	0.76 (0.68–0.85)	6.5×10^{-7}
rs9948095	18:12018665	IMPA2	C	0.14	0.15	0.20	0.71 (0.61–0.82)	3.6×10^{-6}	0.14	0.16	0.88 (0.63–1.24)	0.46	0.73 (0.64–0.84)	5.4×10^{-6}
rs10555080 (aka rs72397229)	19:32043170	THEG5	A	NA	0.36	0.30	1.32 (1.17–1.49)	6.9×10^{-6}	0.38	0.32	1.46 (1.10–1.94)	0.0098	1.34 (1.20–1.50)	2.6×10^{-7}
rs34948558	21:42825856	MX1	A	0.28	0.27	0.32	0.76 (0.67–0.85)	4.7×10^{-6}	0.30	0.31	1.01 (0.77–1.33)	0.95	0.79 (0.71–0.88)	3.0×10^{-5}

In ACCORD, the primary model was adjusted by assignment to interventions, seven clinical center networks, and top three principal components. In BARI 2D, adjustments included assignment to interventions, country of origin, and top three principal components. *Meta-analysis of results in the discovery and validation sets. †Position is chromosome:bp according to the National Center for Biotechnology Information assembly build GRCh37/hg19. **MA is minor or effect allele. †MAF in the discovery set is the average of minor allele frequencies in the two ACCORD genotyping sets (ANYSET and ACCSET). †MAF in 1000 Genomes Project Phase 3 European populations was derived from Ensembl GRCh37 Release 93 (<http://grch37.ensembl.org/index.html>).

Characteristics of the Association Between 2q24 Locus and DPN

The magnitude of the genetic effect at 2q24 in whites was similar if the analysis was restricted to prevalent or incident cases both in ACCORD and BARI 2D (Table 3). In ACCORD, no significant differences in the strength of the association were observed in relation to clinical characteristics, except for a significantly stronger effect among participants with self-reported diabetic retinopathy than in those without this trait ($P = 0.02$) (Supplementary Fig. 2). No interaction was found with the intervention tested in ACCORD (i.e., intensive vs. standard glycemic control, intensive vs. standard blood pressure control, and fenofibrate vs. placebo) (Supplementary Fig. 3). When the MNSI score components were analyzed individually, the strongest association was seen with alterations of foot appearance (OR 0.71, $P = 2 \times 10^{-7}$) and ankle jerk (OR 0.76, $P = 2 \times 10^{-5}$), followed by loss of vibration perception (OR 0.88, $P = 0.04$), whereas no association could be observed with foot ulcer (OR 1.00, $P = 0.99$). Nominally significant associations were observed between 2q24 locus and triglycerides, estimated glomerular filtration rate (eGFR), and UACR at baseline (Supplementary Table 7). As reported in the Type 2 Diabetes Knowledge Portal (<http://www.type2diabetesgenetics.org>), an association between triglycerides and the index SNP (rs13417783) as well as the other GWAS-significant SNPs in LD with it had been previously detected in the Genetics of Diabetes Audit and Research in Tayside Scotland (GoDARTS) study ($P = 0.00011$ for rs13417783). However, adjustment for this variable or for the other two associated with 2q24 (eGFR and UACR) did not attenuate the association of this locus with DPN (Supplementary Table 8). Similarly, adjustment for age and duration of diabetes, which showed significant differences between case subjects and control subjects, had no effect (Supplementary Table 8). In addition, the association between the 2q24 locus and DPN was unaffected (OR 0.64, 95% CI 0.54–0.77) by selecting control subjects who had a longer duration of diabetes (longer than the median of 7 years), and was only modestly reduced (OR 0.73, 95% CI 0.60–0.89) by selecting older control subjects (older than the median age of 61 years). No association was detected between the 2q24 locus and risk of cardiac autonomic neuropathy or risk of micro- and/or macrovascular complications (Supplementary Tables 9 and 10).

2q24 Locus and DPN in African Americans

None of the 28 SNPs at the 2q24 locus showing GWAS-significant association with DPN in whites were associated with DPN in African Americans from ACCORD ($n = 1,345$), as judged on the basis of a two-sided $P < 0.05$. However, 15 of these SNPs had two-sided $P < 0.20$, with effects going in the same direction as in whites (OR 0.75–0.85) (Supplementary Table 6). The strongest association was observed with rs16852735 (OR 0.75, two-sided $P = 0.069$, one-sided $P = 0.034$), which in African Americans was not in LD ($r^2 = 0.02$) with the top SNP in whites (rs13417783). The number of African Americans in BARI 2D was too small for a meaningful analysis.

Low-Frequency Variants at 2q24 and DPN

On the basis of the findings with the common variants, five low-frequency variants (MAF 0.01–0.05), which were placed in the same LD block as the lead SNP (rs13417783) and had been genotyped in ACCORD, were tested for association with DPN among white participants. All five variants, which were in high LD with each other ($r^2 = 0.82$ –1.00), showed a significant association with DPN ($P < 0.01$, based on a Bonferroni adjustment for five comparisons) (Table 4). This association was somewhat attenuated but remained significant after adjustment for rs13417783 (Table 4). Conversely, adjustment for any of these low-frequency variants had minimal impact on the magnitude of the association between the common variant (rs13417783) and DPN (Table 4). Two of these variants (rs1509652 and rs6755015) were genotyped in BARI 2D and did not show any association with DPN (OR 0.94 and OR 1.07, respectively, $P > 0.05$ for both), although power for the analysis of low-frequency variants was limited in this data set due to the smaller sample size.

Association Between 2q24 Locus and Gene Expression

The common variants associated with DPN at 2q24 span 80 kb of noncoding sequence placed between a cluster of genes coding for NaVs (*SCN1A*, *SCN2A*, *SCN3A*, *SCN7A*, and *SCN9A*) on the centromeric side and *XIRP2* (xin actin binding repeat containing 2) on the telomeric side (Fig. 2A). In an eQTL analysis of GTEx data concerning 16 genes placed in a 2-Mbp radius from the lead SNP, carriers of the rs13417783 minor allele had significantly higher tibial nerve expression of *SCN2A*, coding for NaV α subunit 2, and *AC019181.2* (*LOC101929633*),

Table 3—Association between top loci and prevalent/incident DPN in ACCORD and BARI 2D

	ACCORD			BARI 2D		
	N case/N control subjects	OR (95% CI)	HR (95% CI)	N case/N control subjects	OR (95% CI)	HR (95% CI)
Case vs. control subjects						
Prevalent	2,547/784	0.64 (0.55–0.75)	—	518/158	0.59 (0.42–0.83)	—
Incident	1,837/784	0.65 (0.56–0.77)	0.80 (0.73–0.88)	271/158	0.59 (0.40–0.87)	0.69 (0.55–0.88)

Table 4—Association between low-frequency variants at 2q24 and DPN

Low-frequency variant	Position	Alleles*	MAF	r^2 †	Univariable				Multivariable			
					Low-frequency variant		rs13417783		Low-frequency variant		rs13417783	
					OR	P	OR	P	OR	P	OR	P
rs16852465	2:167524744	G/A	0.036	0.009	1.94	3.8E-04	0.64	1.9E-09	1.80	1.7E-03	0.66	2.1E-08
rs1509652	2:167589745	C/T	0.038	0.01	1.76	1.1E-03	0.64	1.9E-09	1.63	5.3E-03	0.66	2.0E-08
rs11884905	2:167611786	C/T	0.037	0.009	1.84	6.7E-04	0.64	1.9E-09	1.70	3.1E-03	0.66	2.1E-08
rs6721669	2:167636784	T/C	0.035	0.009	1.98	2.9E-04	0.64	1.9E-09	1.84	1.3E-03	0.66	2.2E-08
rs6755015	2:167666021	T/C	0.040	0.008	1.68	2.5E-03	0.64	1.9E-09	1.56	1.0E-02	0.66	1.6E-08

*Minor allele/major allele. †Results of regression models including one of the low-frequency variants along with rs13417783 as DPN predictors. ‡ r^2 with rs13417783.

coding for an uncharacterized noncoding RNA ($P = 9 \times 10^{-4}$ and $P = 6 \times 10^{-4}$, respectively) (Fig. 2B–D). A nominally significant association ($P = 0.03$) was also detected with lower expression of the immediately adjacent *XIRP2* gene.

To gain further insight into *SCN2A* gene expression in peripheral nerves, we contrasted *SCN2A* gene expression in the hippocampus (a central nervous system tissue, serving as a positive control), with dorsal root ganglion (DRG), which contains the cell bodies of the neurons supplying the axons to the sensory portion of the tibial nerve, tibial nerves, and skeletal muscle, an excitable nonnervous system tissue, serving as negative control. Coding gene relative abundances (in TPMs) and their corresponding percentiles are provided for all four tissues in Table 5, which includes samples from both sexes. Abundant RNA signal for *SCN2A* was found in both the hippocampus and in the DRG. Although at lower levels, *SCN2A* was also consistently expressed (in all but one sample) in the tibial nerve. By contrast, it was undetectable in 80% of the samples of the skeletal muscle samples and, in the remaining 20% of the samples, was among the lowest in abundance across all tissues.

DISCUSSION

Through a GWAS of the ACCORD cohort, we have identified a previously unrecognized locus on chromosome 2q24 having a powerful effect on the risk of DPN in T2D. An association of similar strength was found between this locus and DPN in BARI 2D. In both cohorts, the 2q24 minor allele conferred protection from DPN, being more frequent in DPN-negative control subjects than in DPN case subjects and the general population. In further support of these findings, the same allele was found to be associated with higher tibial nerve expression of a nearby gene (*SCN2A*) coding for the α subunit of NaV1.2, providing a possible functional basis for the genetic effect observed at the population level. This is the first report of a DPN locus that reaches genome-wide significance in a GWAS and is replicated in an independent study.

The fact that almost identical effects on DPN were found for this locus in the discovery (OR 0.63) and replication (OR 0.57) is remarkable and makes this finding especially robust. Such a high degree of concordance reflects the use of the same DPN definition (clinical examination MNSI >2) in studies and the high sensitivity, specificity, and correlation with abnormal nerve conduction characteristic of this DPN outcome (21,22). Other contributing factors include the similar clinical characteristics of the two cohorts with regard to height, BMI, diabetes duration, blood pressure, and smoking status, and the similar incidence of DPN, despite the administration of different interventions.

There are scant data in the literature to which our findings can be compared because only one other GWAS of DPN has been published to date. That study, based on the

Table 5—Relative *SCN2A* abundance (in TPM) and corresponding percentiles across coding genes

Tissue	Fraction of samples with detectable (TPM >0) <i>SCN2A</i> expression	Mean <i>SCN2A</i> TPM (\pm SD) among coding genes in samples with TPM >0	Mean <i>SCN2A</i> percentile (\pm SD) among coding genes in samples with TPM >0
Hippocampus	123 of 123	18.8 \pm 15.8	71.7 \pm 14.9
DRG	21 of 21	18.1 \pm 6.0	49.0 \pm 6.6
Tibial nerve	413 of 414	2.0 \pm 1.8	30.8 \pm 5.7
Skeletal muscle	112 of 564	0.13 \pm 0.08	22.8 \pm 3.3

GoDARTS data sets, found suggestive evidence ($P = 1.8 \times 10^{-7}$) for a DPN locus on chromosome 8p21 near *GFRA2* (15). We could not replicate that finding in our study, and conversely, no significant evidence for the locus 2q24 that we identified in ACCORD and BARI 2D was reported in the GoDARTS study. In addition to the possibility of the 8p21 locus being a false positive, given the lack of genome-wide significance and previous replication, there are important differences between the two GWASs that could explain these discrepancies. First, the outcome considered by the GoDARTS study was painful DPN, defined as a prescription history of at least one of five drugs indicated for the treatment of neuropathic pain along with a positive monofilament test for sensory neuropathy, which is known to have low specificity. By contrast, in our GWAS, DPN was defined by means of a validated instrument (MNSI clinical examination) that does not include pain in its assessment. Thus, the two studies captured different aspects of DPN involving different components of the peripheral nervous system (predominantly small fibers in the case of painful DPN vs. large fibers in the case of MNSI-diagnosed DPN).

Second, both ACCORD and BARI 2D were clinical trials, with close follow-up, standardized outcome acquisition by trained professionals, and strict adjudication, whereas the GoDARTS study was based on medical record data collected as part of routine medical care.

Finally, ACCORD and BARI 2D participants were characterized by a long duration of diabetes (15 years on average by the end of the study), which helped minimize misclassification of control subjects—an essential feature for the identification of protective effects on DPN, such as that associated with the 2q24 locus. Although diabetes duration was not specified in the GoDARTS report, it was likely to be shorter owing to the population-based nature of that cohort.

The DPN locus that we have identified may allow clinicians to focus prevention efforts on patients at higher risk of DPN. However, the real relevance of this finding lies in the great potential for improving our understanding of DPN biology and for identifying novel targets for preventive interventions. It is noteworthy in this regard that the newly identified DPN locus is located in close vicinity to a cluster of genes coding for the α subunits of NaVs, which are responsible for multiple aspects of neuron excitability, including thresholds for depolarizing responses and the amplitude of action potentials (31). From the most proximal

to the most distal from the top variant, these genes include *SCN7A*, *SCN9A*, *SCN1A*, *SCN2A*, and *SCN3A*, which code for NaVx, NaV1.7, NaV1.1, NaV1.2, and NaV1.3, respectively. In the GTEx database, the protective allele of the 2q24 locus was significantly associated with higher expression of one of these genes (*SCN2A*) in the tibial nerve, supporting the hypothesis that increased activity of the corresponding NaV1.2, which is expressed in DRG and tibial nerve, may guard against the detrimental effects of the diabetic milieu on peripheral nerves. *SCN2A* mRNA is expressed by human and murine DRG neurons but not by Schwann cells or other cell types that are found in the tibial nerve (mousebrain.org), which suggests that the *SCN2A* mRNA in the tibial nerve is contributed by sensory nerve axons.

Rare mutations in the *SCN2A* gene have been implicated in the etiology of neurodevelopmental diseases such as autism spectrum disorder (loss of function mutations) and infantile seizures (gain of function mutations) (32), but the effect of these variants on susceptibility to DPN has never been investigated due to their rarity, nor has the effect of NaV1.2 loss or gain of function been studied in animal models of DPN. A relationship with DPN etiology has been instead clearly established for NaV1.3 and NaV1.7 (coded by *SCN3A* and *SCN9A*, respectively) (33–36), but no differences in their expression were found among 2q24 genotypes in the GTEx database. Whether this was due to the small size and/or the lack of exposure to diabetes of the samples in the GTEx database, or is related to the fact that NaV1.3 and NaV 1.7 are preferentially expressed in small fibers mediating pain transmission, whereas the MNSI score mainly tests large fibers mediating vibration sense and tendon reflexes, remains to be determined.

Altogether, these findings highlight the need for further studies of the SCN genes in the 2q24 region as functional mediators of the DPN locus and potential targets of novel preventive interventions. These studies would include testing of the association between the 2q24 genotype and the expression of these genes in peripheral nerve samples specifically collected from subjects with diabetes, along with studies assessing the impact of overexpressing or knocking down these genes in peripheral nerves of animal models of DPN (37). The noncoding gene *AC019181.2* (*LOC101929633*), which also showed evidence of association with the 2q24 locus in the GTEx database, should be included in these studies given the

potential role of noncoding RNAs as regulators of gene expression (38,39).

The genomic mechanisms linking this locus to differences in gene expression are unclear at this time. The index SNP and the other 27 variants reaching GWAS significance are in a noncoding region with quite subtle epigenetic marks. The index SNP was found by ENCODE to be located in a weak enhancer (as indicated by an H3K4m1 mark) in human embryonic stem cells, but whether this regulatory element is also active in neural cells remains to be determined. Of the other 27 SNPs, the 2 highest ranking in RegulomeDb are rs12993796 and rs16852735. The first SNP is located in a DNA segment that binds BATF (a transcription factor involved in the differentiation of immune cells) in a lymphoblastoid cell line (GM12878). The second SNP is placed in a region showing evidence of binding to REST (RE1 silencing transcription factor) in a neuroectodermic cell line (PFSK-1). REST is a transcription factor that represses neuronal genes, including NaVs (40). Because REST is expressed in peripheral nerves (as shown by GTEX data) and in DRG, one can speculate that the higher expression of *SCN2A* associated with the 2q24 protective allele in these tissues may be due to decreased binding of this repressor to the DNA segment where rs16852735 is located. The other 25 SNPs showed minimal evidence of being functional in the summary provided by RegulomeDb. Resequencing of the LD block in which the GWAS-significant SNPs are located in large series of case and control subjects, followed by ad hoc functional studies, will be necessary to identify the causal variant(s) and understand its (their) impact on genomic function.

Although the association with DPN was strongest at 2q24, another locus placed on chromosome 15q25 yielded notable GWAS significance in the ACCORD GWAS as well as in the meta-analysis with BARI 2D. Especially interesting is the vicinity of this locus to the *NTRK3* gene coding for the receptor of neurotrophin 3, which, by prompting the extension of fibers from proprioceptive DRGs to the muscle spindle and the ventral horn of the spinal cord, is responsible for inducing the synaptic connection between sensory and motor neurons (41). On the basis of this evidence, this locus should be considered as a prime candidate for future studies, although the available GTEX data do not suggest an association between the index SNP at 15q25 and *NTRK3* expression.

Strengths of our study include the advantages of clinical trials, such as the rigorous and standardized protocols for data acquisition, the regular follow-up, and access to rich phenotype data, as well as the systematic GWAS approach based on genotyped and imputed data of excellent quality and wide coverage. As discussed above, the use of a validation cohort having very similar clinical characteristics to the discovery cohort was another critical strength.

Nonetheless, some limitations should be acknowledged. Because ACCORD and BARI 2D were both designed to include participants with T2D at high risk of cardiovascular disease, whether our findings could be generalized to

individuals with different characteristics or with type 1 diabetes remains to be determined. Similarly, our study was limited to white subjects, and it is not known whether these findings also apply to individuals of other races, although the limited data on African American individuals from ACCORD suggest that this might be the case. Also, our study, while larger than most of the genetic studies of DPN published thus far, was powered to detect only relatively large genetic effects and the fact that control subjects were slightly younger and had slightly shorter diabetes duration than case subjects may have biased results toward the null hypothesis. Therefore, other loci having smaller yet functionally relevant effects may have gone undetected. Finally, because the GWAS was limited to common polymorphisms (MAFs >5%), the existence of additional genetic effects due to less frequent variants cannot be excluded.

In summary, we have identified and successfully validated a locus on chromosome 2q24 having a powerful protective effect on the development of DPN in T2D. Tissue expression analysis suggests that this effect may be mediated by higher expression of the NaV1.2 in the tibial nerve, which is known to increase neuronal excitability. These results may provide novel insights into the pathogenesis of DPN and point to a potential new target for interventions aimed at preventing or treating this complication of diabetes.

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Author Contributions. Y.T., H.S., and A.D. designed the study; acquired, analyzed, and interpreted the data from ACCORD; wrote the initial draft of the manuscript; and revised the manuscript to its final form. P.A.L., H.C., and S.C. acquired, analyzed, and interpreted the data from BARI 2D and revised the manuscript to its final form. R.P.-B., B.A.P., and B.C. contributed to the study design, interpreted the data, and revised the manuscript to its final form. P.R.R. and T.J.P. performed the RNA-seq meta-analysis for *SCN2A* gene expression, wrote the corresponding sections of the manuscript, and revised the manuscript to its final form. M.J.W., A.A.M.-R., J.B.B., and J.C.M. acquired, analyzed, and interpreted the data and revised the manuscript to its final form. H.S. and A.D. are the guarantors of this work and, as such, had full access to all the data in the study and take responsibility for the integrity of the data and the accuracy of the data analysis.

Data and Resource Availability. The ACCORD database is available upon request from the National Heart, Lung, and Blood Institute Biologic Specimen and Data Repository (<https://biolinc.nih.gov/studies/accord/>). The ACCORD GWAS data have been deposited in the database of Genotypes and Phenotypes (dbGAP, Study Accession: phs001411.v1.p1).

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