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Accessibility
Haplotype Structure of the \textit{ENPP1} Gene and Nominal Association of the K121Q Missense Single Nucleotide Polymorphism With Glycemic Traits in the Framingham Heart Study

Elliot S. Stolerman,1,2,3 Alisa K. Manning,4 Jarred B. McAteer,1,2 Josée Dupuis,4 Caroline S. Fox,5,6 L. Adrienne Cupples,4 James B. Meigs,3,7 and Jose C. Florez1,2,3

OBJECTIVE—A recent meta-analysis demonstrated a nominal association of the ectonucleotide pyrophosphatase phosphodiesterase 1 (\textit{ENPP1}) K→Q missense single nucleotide polymorphism (SNP) at position 121 with type 2 diabetes. We set out to confirm the association of \textit{ENPP1} K121Q with hyperglycemia, expand this association to insulin resistance traits, and determine whether the association stems from K121Q or another variant in linkage disequilibrium with it.

RESEARCH DESIGN AND METHODS—We characterized the haplotype structure of \textit{ENPP1} and selected 39 tag SNPs that captured 96% of common variation in the region (minor allele frequency \(\geq 5\%\)) with an \(r^2\) value \(\geq 0.80\). We genotyped the SNPs in 2,511 Framingham Heart Study participants and used age- and sex-adjusted linear mixed effects (LME) models to test for association with quantitative metabolic traits. We also examined whether interaction between K121Q and BMI affected glycemic trait levels.

RESULTS—The Q allele of K121Q (rs1044498) was associated with increased fasting plasma glucose (FPG), A1C, fasting insulin, and insulin resistance by homeostasis model assessment (HOMA-IR; all \(P = 0.01–0.006\)). Two noncoding SNPs (rs7775386 and rs7773477) demonstrated similar associations, but LME models indicated that their effects were not independent from K121Q. We found no association of K121Q with obesity, but interaction models suggested that the effect of the Q allele on FPG and HOMA-IR was stronger in those with a higher BMI (\(P = 0.008\) and 0.01 for interaction, respectively).

CONCLUSIONS—The Q allele of \textit{ENPP1} K121Q is associated with hyperglycemia and insulin resistance in whites. We found an adiposity-SNP interaction, with a stronger association of K121Q with diabetes-related quantitative traits in people with a higher BMI. \textit{Diabetes} 57:1971–1977, 2008

From the 1Center for Human Genetic Research and Diabetes Unit, Department of Medicine, Massachusetts General Hospital, Boston, Massachusetts; the 2Program in Medical and Population Genetics, Broad Institute of Harvard and Massachusetts Institute of Technology, Cambridge, Massachusetts; the 3Department of Medicine, Harvard Medical School, Boston, Massachusetts; the 4Department of Biostatistics, Boston University School of Public Health, Boston, Massachusetts; the 5Division of Endocrinology, Diabetes, and Hypertension, Brigham and Women’s Hospital, Harvard Medical School, Boston, Massachusetts; the 6National Heart, Lung, and Blood Institute’s Framingham Heart Study, Framingham, Massachusetts; and the 7General Medicine Division, Massachusetts General Hospital, Boston, Massachusetts.

Corresponding author: Jose C. Florez, jcflorez@partners.org.

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RESEARCH DESIGN AND METHODS

Population samples. We used data from the Framingham Heart Study (FHS) to study associations between ENPP1 variants and quantitative glycemic traits. The FHS is a community-based, multigenerational, longitudinal study of cardiovascular disease and its risk factors, including diabetes. The FHS comprises the original cohort, offspring, and generation 3 studies. Subjects described in the present analysis include 2,511 individuals from the FHS offspring cohort. In this analysis, our principal diabetes-related quantitative traits come from offspring examination 5 (1991–1994), where data from a 75-g oral glucose tolerance test (OGTT) is available for all offspring without diagnosed diabetes. The study was approved by Boston University’s institutional review board, and written informed consent, including consent for genetic analyses, was obtained for all study participants. The demographic characteristics of the FHS participants are presented in Table 1.

An extensive array of diabetes-related quantitative traits has been collected in the FHS. Diabetes-related quantitative traits measured in this study include: A1C, fasting glucose (FPG), fasting insulin, insulin resistance by homeostasis model assessment (HOMA-IR), percent fasting insulin sensitivity index (HOMA-B) (4), waist circumference (inches) to the other covariates to examine the strength of the subsequent SNP associations when adjusted for obesity. We adjusted for both age and age^2 to allow for a nonlinear trend over time. The covariates from offspring exam 5 were used for all the traits except for mean FPG, for which we used the 16-year average of each covariate.

To assess the association of each SNP with the type 2 diabetes phenotype, we used Cox proportional hazards survival analysis with diabetes as the outcome and the survival time as the age at the exam in which diabetes was determined. The survival time of individuals without diabetes was the age at their last exam. The model was implemented with the survival package in R (18), with the same adjustments as in the LME models with covariates taken at the first exam. Trait correlation among siblings was modeled with a frailty term in the survival model (19).

To assess whether positive association signals were due to linkage disequilibrium with K121Q or another variant in linkage disequilibrium with it.

The association between each individual and each SNP was assessed using a linear mixed effects (LME) model implemented in SOLAR (17) to account for the within-family correlation. Each SNP was included in a model as a fixed effect with additive coding, although additional dominant and recessive coding were evaluated to examine the association of rs1044498 (K121Q) with the quantitative traits. The models included random effects to account for the covariance between family members, the covariance structure was determined by the degree of relatedness between each relative pair.

The role of BMI in the association between rs1044498 (K121Q) and the quantitative traits was further examined in LME models of the age-, age^2, and sex-adjusted residual with K121Q, BMI, and an interaction term between K121Q and BMI as covariates.

RESULTS

A linkage disequilibrium plot showing the completed haplotype structure of the ENPP1 locus is presented in the Supplemental Figure in the online appendix, which is available at http://dx.doi.org/10.2337/db08-0206. The ENPP1 gene region contains a high degree of linkage disequilibrium. From the initial set of 167 SNPs, 96% of the 95 common variants with a MAF ≥5% were captured with an r^2 value ≥0.8 (and 100% with an r^2 value ≥0.7) by a set of 39 tag SNPs using single-marker (pairwise) tests. The list of the 39 successful tag SNPs used in this analysis, with chromosomal position, major allele, and MAF in both the HapMap and Framingham population, is presented in Table 2. The list of 95 captured SNPs with their tags is listed in the online appendix (Supplemental Table 1).

We examined whether individual SNPs in ENPP1 were associated with hyperglycemia and insulin resistance traits in the FHS population. We first focused our attention on our principal polymorphism of interest, rs1044498.
(K121Q), using three different genetic models: additive, dominant, and recessive. Table 3 presents mean trait levels for each genotypic group, with \( P \) values for association with K121Q before and after adjustment for BMI. Several associations with insulin resistance traits reached nominal levels of significance: specifically, under the additive model, the Q allele was associated with higher FPG (\( P < 0.01 \)), A1C (\( P < 0.006 \)), fasting insulin (\( P < 0.006 \)), and HOMA-IR (\( P < 0.006 \)); all of these associations remained significant after adjusting for BMI. Similar \( P \) values were obtained under the dominant genetic model. In this population sample, there were no differences in mean trait value across genotypic groups at ENPP1 K121Q for BMI (\( P > 0.32 \)) or waist circumference (\( P > 0.64 \)), both tested as continuous traits. When we compared the distribution of genotypes at this locus across individuals who were of normal weight (BMI <25 kg/m\(^2\)), overweight (BMI 25–30 kg/m\(^2\)), or obese (BMI >30 kg/m\(^2\)), we found no association of K121Q with obesity as a categorical trait (\( P = 0.66 \)). We also found no significant deviation from the null hypothesis of no association when our cohort was divided by BMI cutoffs at 25, 30, and 35 kg/m\(^2\) (data not shown).

We then explored whether these consistent associations might be driven by other polymorphisms in the region. Table 4 displays the ENPP1 SNPs for which we detected nominally significant associations with any of the glycemic traits under study. Figure 1A (glucose-related traits) and 1B (insulin-related traits) display the \( P \) values for rs1044498 (K121Q) in comparison with those obtained for other SNPs across the genomic segment. Although K121Q was the SNP that showed the strongest association with fasting insulin and HOMA-IR (Fig. 1B), two other SNPs (rs7775386 and rs7773477, located in intron 1 and at the exon 2-intron 2 junction, respectively) achieved similar \( P \) values for associations with FPG and A1C; these two SNPs were also nominally associated with HOMA-IR (Table 4). To determine whether the effects of rs7775386 and rs7773477 were independent from K121Q or produced an association signal simply because they are in tight linkage disequilibrium with K121Q, we calculated the \( r^2 \) among these SNPs.
ENPP1 POLYMORPHISMS AND GLYCEMIC TRAITS

TABLE 3
Association between rs1044498 (K121Q) and diabetes-related quantitative traits

<table>
<thead>
<tr>
<th>Trait</th>
<th>KK</th>
<th>KQ</th>
<th>QQ</th>
<th>Percent variance explained</th>
<th>Additive</th>
<th>Recessive</th>
<th>Dominant</th>
</tr>
</thead>
<tbody>
<tr>
<td>n</td>
<td>1,982</td>
<td>695</td>
<td>74</td>
<td></td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td>FPG (mg/dl)</td>
<td>99 ± 23.9</td>
<td>101 ± 29.6</td>
<td>107 ± 43.0</td>
<td>0.17 (0.11)</td>
<td>0.01 (0.02)</td>
<td>0.07 (0.16)</td>
<td>0.02 (0.03)</td>
</tr>
<tr>
<td>A1C (%)</td>
<td>5.39 ± 0.93</td>
<td>5.48 ± 1.02</td>
<td>5.72 ± 1.24</td>
<td>0.40 (0.30)</td>
<td>0.006 (0.01)</td>
<td>0.03 (0.03)</td>
<td>0.02 (0.03)</td>
</tr>
<tr>
<td>Mean FPG (mg/dl)</td>
<td>99.1 ± 19.92</td>
<td>99.6 ± 21.23</td>
<td>101 ± 21.5</td>
<td>0.005*</td>
<td>0.21 (0.26)</td>
<td>0.42 (0.63)</td>
<td>0.25 (0.27)</td>
</tr>
<tr>
<td>Fasting insulin (µU/ml)</td>
<td>29.5 ± 11.57</td>
<td>31.3 ± 13.87</td>
<td>31.2 ± 12.09</td>
<td>0.32 (0.22)</td>
<td>0.006 (0.01)</td>
<td>0.58 (0.96)</td>
<td>0.003 (0.006)</td>
</tr>
<tr>
<td>HOMA-IR</td>
<td>7.5 ± 4.71</td>
<td>8.06 ± 5.43</td>
<td>8.05 ± 4.37</td>
<td>0.29 (0.19)</td>
<td>0.006 (0.01)</td>
<td>0.56 (0.95)</td>
<td>0.004 (0.005)</td>
</tr>
<tr>
<td>HOMA-B</td>
<td>345.8 ± 179.4</td>
<td>329.1 ± 444.7</td>
<td>336.8 ± 136.6</td>
<td>0.04 (0.03)</td>
<td>—</td>
<td>—</td>
<td>—</td>
</tr>
<tr>
<td>Fasting insulin (% BMI)</td>
<td>25.8 ± 7.36</td>
<td>25.4 ± 7.76</td>
<td>26.3 ± 7.42</td>
<td>0.03 (0.01)</td>
<td>0.31 (0.42)</td>
<td>0.29 (0.15)</td>
<td>0.12 (0.15)</td>
</tr>
<tr>
<td>Waist circumference (inches)</td>
<td>36.5 ± 5.55 °</td>
<td>36.4 ± 5.93</td>
<td>37.6 ± 6.01</td>
<td>0.02 (0.04)</td>
<td>0.64 (0.35)</td>
<td>0.43 (0.93)</td>
<td>0.80 (0.30)</td>
</tr>
<tr>
<td>BMI (kg/m²)</td>
<td>27.4 ± 4.83</td>
<td>27.5 ± 5.19</td>
<td>28.4 ± 6.26</td>
<td>0.06</td>
<td>0.32</td>
<td>0.42</td>
<td>0.40</td>
</tr>
</tbody>
</table>

All quantitative trait values are unadjusted means ± SD, with P values without parentheses adjusted for sex and age and P values in parentheses additionally adjusted for BMI. Associations between rs1044498 (K121Q) and selected quantitative metabolic traits in the FHS, with P values for the additive, recessive, and dominant genetic models are shown. The major (A) and minor (C) alleles code for the amino acids lysine (K) and glutamine (Q), respectively. The MAF is 15% in Framingham. Mean FPG, FPG averaged over exams 3–7 comprising 16 years; Fasting insulin, FPG averaged over exams 3–7 comprising 16 years.

TABLE 4
Nominally significant associations (P < 0.05) of selected ENPP1 SNPs with diabetes-related quantitative traits

<table>
<thead>
<tr>
<th>SNP (MM/Mm/mm)</th>
<th>Alleles (M/m)</th>
<th>MAF</th>
<th>r²</th>
<th>Trait</th>
<th>MM</th>
<th>Mm</th>
<th>mm</th>
<th>P value</th>
</tr>
</thead>
<tbody>
<tr>
<td>rs7752279 (926/1,343/528)</td>
<td>G/A</td>
<td>0.43</td>
<td>0.106</td>
<td>A1C</td>
<td>5.38 ± 0.89</td>
<td>5.42 ± 0.95</td>
<td>5.53 ± 1.14</td>
<td>0.01 (0.02)</td>
</tr>
<tr>
<td>rs9493989 (1,375/1,164/225)</td>
<td>T/C</td>
<td>0.29</td>
<td>0.026</td>
<td>A1C</td>
<td>5.4 ± 0.94</td>
<td>5.43 ± 0.98</td>
<td>5.55 ± 1.09</td>
<td>0.046</td>
</tr>
<tr>
<td>rs13211931 (2,540/224/6)</td>
<td>G/T</td>
<td>0.04</td>
<td>0.063</td>
<td>Fasting insulin</td>
<td>30.3 ± 12.15</td>
<td>29.9 ± 12.46</td>
<td>29.4 ± 12.37</td>
<td>(0.046)</td>
</tr>
<tr>
<td>rs7775386 (2,031/642/55)</td>
<td>C/T</td>
<td>0.14</td>
<td>0.664</td>
<td>FPG</td>
<td>99 ± 23.4</td>
<td>102 ± 33.1</td>
<td>103 ± 35.5</td>
<td>0.005 (0.004)</td>
</tr>
<tr>
<td>rs7773477 (2,239/489/34)</td>
<td>A/G</td>
<td>0.10</td>
<td>0.591</td>
<td>Mean FPG</td>
<td>5.39 ± 0.9</td>
<td>5.53 ± 1.16</td>
<td>5.64 ± 1.05</td>
<td>0.004 (0.005)</td>
</tr>
<tr>
<td>rs7773477 (2,509/235/7)</td>
<td>G/T</td>
<td>0.05</td>
<td>0.285</td>
<td>Mean FPG</td>
<td>7.5 ± 4.78</td>
<td>8 ± 5.4</td>
<td>7.8 ± 4.12</td>
<td>0.04 (0.03)</td>
</tr>
<tr>
<td>rs9493116 (2,377/343/20)</td>
<td>A/G</td>
<td>0.07</td>
<td>0.410</td>
<td>Mean FPG</td>
<td>5.41 ± 0.95</td>
<td>5.56 ± 1.15</td>
<td>5.58 ± 0.54</td>
<td>0.03 (0.04)</td>
</tr>
<tr>
<td>rs1510 (2,105/608/30)</td>
<td>G/C</td>
<td>0.12</td>
<td>0.026</td>
<td>Mean FPG</td>
<td>5.45 ± 1</td>
<td>5.33 ± 0.85</td>
<td>5.75 ± 1.16</td>
<td>(0.048)</td>
</tr>
</tbody>
</table>

All quantitative trait values are crude means ± SD, with P values without parentheses adjusted for sex and age and P values in parentheses additionally adjusted for BMI. Associations between SNPs (listed in order of increasing chromosomal position, with genotype counts in parentheses following the rs number) and phenotypic traits that had nominal P values < 0.05 using an additive genetic model are shown. The MAFs are based on data from FHS unrelated participants. The extent of linkage disequilibrium of each SNP in relation to rs104498 (K121Q) is shown by presenting r² values obtained from the unrelated subset of our FHS sample. M, major allele; m, minor allele; mean FPG, FPG averaged over exams 3–7 comprising 16 years.
action $P$ value $= 0.014$, $\beta$ estimate $= 0.016$). This indicates a stronger genetic association of the Q allele with insulin resistance traits among people who have a higher BMI.

**DISCUSSION**

The association of the K121Q polymorphism in ENPP1 with insulin resistance and type 2 diabetes has been controversial. Regarding insulin resistance, Pizzuti et al. (2) found that nonobese, nondiabetic Q allele carriers were more insulin resistant than KK homozygotes, as defined both by OGTT and the euglycemic clamp. Subsequent studies reported both positive (20) and negative evidence (10) of association with insulin resistance. For type 2 diabetes, an initial positive result of association by members of our group (13) documented a locus (22–26). Nevertheless, a recent comprehensive meta-analyses (10, 12, 21); however, three very large association studies (including one by members of our group) gone extensive phenotypic characterization in a longitudinal fashion; and 4) its family component reduces the risk of population stratification.

In this study, we captured most of the common genetic variation in ENPP1 and studied its putative association with glycemic traits in a comprehensive manner. Using the FHS population to characterize the common variation around a quantitative glycemic or obesity trait; and 3) it has undergone extensive phenotypic characterization in a longitudinal fashion. Given the new evidence suggesting a real association of this polymorphism with type 2 diabetes and functional reports implicating ENPP1 and its polymorphism K121Q in mechanisms of insulin resistance (1, 8, 27–29), we decided to examine its association with insulin resistance traits in a homogeneous population cohort previously unexamined for this variant. In addition, we aimed to determine whether any association, if present, stemmed from ENPP1 K121Q or another polymorphism in the region, and we aimed to characterize the putative modifying effect of BMI. The Framingham offspring cohort is particularly advantageous for such a study: 1) As a population cohort, it is free of ascertainment biases, which may restrict the range of variation around a quantitative glycemic or obesity trait; 2) it is an ethnically homogeneous sample; 3) it has undergone extensive phenotypic characterization in a longitudinal fashion; and 4) its family component reduces the risk of population stratification.

In this study, we captured most of the common genetic variation in ENPP1 and studied its putative association with glycemic traits in a comprehensive manner. Using the FHS population to characterize the common variation across the ENPP1 locus, we confirmed the association of the Q allele in ENPP1 K121Q with hyperglycemia, as demonstrated by elevated FPG and A1C, under both the
additive and dominant models. This supports the hypothesis that only one copy of the Q allele is necessary to cause an effect on quantitative phenotypes. We also demonstrated that the effect of K121Q on hyperglycemia is likely mediated via insulin resistance, because the Q allele is also associated with elevated fasting insulin and HOMA-IR. The lack of an association with the Gutt insulin sensitivity index may reflect differences in insulin resistance at the tissue level (basal hepatic insulin resistance vs. peripheral glucose disposal after an oral load) or indicate an imperfect correlation of these surrogate measures with true insulin resistance. Although other polymorphisms in the region showed similar associations with glycemic traits, our regression analysis demonstrated that the effect of two other significant SNPs was removed when incorporating K121Q in the models, suggesting that K121Q is the variant with the actual effect on glycemic and insulin resistance traits, as might be predicted by its impact on amino acid sequence. Because these associations represent confirmation of previous findings and other variants in the region were genotyped as a fine-mapping exercise, we do not believe statistical correction for the multiple variants analyzed is warranted.

Having established the association between ENPP1 K121Q and hyperglycemia, we explored the interaction between K121Q and BMI because of preliminary evidence that the effect of the Q allele on glycemic traits is mediated by an increase in adiposity (3,5,7,13,30) and suggestions that this variant may also contribute to obesity traits (5,6,31–33). Although we observed no association of ENPP1 K121Q with BMI or waist circumference, our interaction analysis supports the observation that a higher BMI strengthens the association of this particular polymorphism with elevated insulin resistance and glucose levels. This finding is consistent with the hypothesis that the net effect of the ENPP1 Q121 variant in modulating the risk of insulin resistance and related clinical outcomes is barely detectable in lean individuals while becoming more evident in the context of an “obesogenic” background, where the deleterious effect of the Q121 variant on the glucose disposal of skeletal muscle may be superimposed on that exerted by high BMI itself (30). This model is consistent with our previous meta-analysis in which we noted that the Q121 variant confers a modest risk of type 2 diabetes in whites with a greater effect as BMI increases. Such BMI × genotype interactions may be particularly evident with regard to genes that cause hyperglycemia by augmenting insulin resistance rather than in those that contribute to diabetes risk by diminishing insulin secretion. Because of the relationship between obesity and insulin resistance, there is more likely to be a correlation between increased adiposity and the effects of genes that modify insulin action.

In summary, our study adds further evidence in support of a potential causative role of the ENPP1 gene in the inheritance and pathophysiology of type 2 diabetes. We found that the Q allele of K121Q in ENPP1 appears to be the common variant most strongly associated with diabetes-related traits in whites, confirmed that K121Q is associated with hyperglycemia and a greater degree of insulin resistance, and found an adiposity-SNP interaction, with a greater strength of association of K121Q with diabetes-related quantitative traits in people with obesity.

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