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Common Variants in CDKAL1, CDKN2A/B, IGF2BP2, SLC30A8, and HHEX/IDE Genes Are Associated With Type 2 Diabetes and Impaired Fasting Glucose in a Chinese Han Population

Ying Wu,1 Huaxing Li,1 Ruth J.F. Loos,2 Zhijie Yu,1 Xingwang Ye,1 Lihua Chen,1 An Pan,1 Frank B. Hu,3 and Xu Lin1

OBJECTIVE—Genome-wide association studies have identified common variants in CDKAL1, CDKN2A/B, IGF2BP2, SLC30A8, HHEX/IDE, EXT2, and LOC387761 loci that significantly increase the risk of type 2 diabetes. We aimed to replicate these observations in a population-based cohort of Chinese Hans and examine the associations of these variants with type 2 diabetes and diabetes-related phenotypes.

RESEARCH DESIGN AND METHODS—We genotyped 17 single nucleotide polymorphisms (SNPs) in 3,210 unrelated Chinese Hans, including 424 participants with type 2 diabetes, 878 with impaired fasting glucose (IFG), and 1,908 with normal fasting glucose.

RESULTS—We confirmed the associations between type 2 diabetes and variants near CDKAL1 (odds ratio 1.49 [95% CI 1.27–1.75]; \( P = 8.91 \times 10^{-7} \)) and CDKN2A/B (1.31 [1.12–1.54]; \( P = 1.0 \times 10^{-7} \)). We observed significant association of SNPs in IGF2BP2 (1.17 [1.03–1.32]; \( P = 0.014 \)) and SLC30A8 (1.12 [1.01–1.25]; \( P = 0.033 \)) with combined IFG/type 2 diabetes. The SNPs in CDKAL1, IGF2BP2, and SLC30A8 were also associated with impaired \( \beta \)-cell function estimated by homeostasis model assessment of \( \beta \)-cell function. When combined, each additional risk allele from CDKAL1-rs9465871, CDKN2A/B-rs10811661, IGF2BP2-rs4402960, and SLC30A8-rs13266634 increased the risk for type 2 diabetes by 1.24-fold (\( P = 2.85 \times 10^{-7} \)) or for combined IFG/type 2 diabetes by 1.21-fold (\( P = 6.31 \times 10^{-11} \)). None of the SNPs in EXT2 or LOC387761 exhibited significant association with type 2 diabetes or IFG. Significant association was observed between the HHEX/IDE SNPs and type 2 diabetes in individuals from Shanghai only (\( P < 0.013 \)) but not in those from Beijing (\( P > 0.33 \)).

CONCLUSIONS—Our results indicate that in Chinese Hans, common variants in CDKAL1, CDKN2A/B, IGF2BP2, and SLC30A8 loci independently or additively contribute to type 2 diabetes risk, likely mediated through \( \beta \)-cell dysfunction.

Diabetes 57:2834–2842, 2008

The rapid increase in prevalence of type 2 diabetes has been a major public health challenge worldwide, including China. The total number of people with diabetes in China is estimated to increase from 20.8 million in 2000 to 42.3 million in 2030 (1). Besides the important contribution of environmental factors, including changes in dietary patterns and lifestyle, genetic determinants also play a major role in type 2 diabetes susceptibility. Over the past decade, serious efforts have been put into the search for type 2 diabetes susceptibility genes, but progress has been slower than anticipated (2,3). Although common variants in a few genes including PPARG, KCNJ11, and TCF7L2 have been convincingly replicated in individuals with European ancestry, relatively few studies have been conducted in Chinese, and, so far, no variants have been unambiguously confirmed as diabetes susceptibility loci in Chinese. However, recent advances in genome-wide association studies (GWASs) have revived the initial optimism and accelerated the discovery of diabetes susceptibility genes (4–6).

The first GWAS, conducted in a French case-control cohort, confirmed TCF7L2 as a major type 2 diabetes susceptibility gene and identified four novel loci consistently associated with type 2 diabetes (7). These loci are located in chromosomal regions that harbor several genes involved in \( \beta \)-cell function or development, including a variant in the SLC30A8 (zinc transporter solute carrier family 30 member 8) gene, variants located in a linkage disequilibrium (LD) block that contains the IDE (insulin-degrading enzyme), KIF11 (kinesin family member 11), and the HHEX (hematopoietically expressed homeobox) genes, as well as variants in another LD block that contains genes encoding EXT2 (exostin 2). A fourth locus mapped to a hypothetical gene LOC387761 on chromosome 11. Four subsequent GWASs (8–12), performed in European case-control studies, confirmed the SLC30A8 and HHEX/IDE genes as type 2 diabetes susceptibility loci. Furthermore, additional variants in several new gene regions were also identified, including single nucleotide polymorphisms (SNPs) in the CDKAL1 gene, which encodes the CDK5 regulatory subunit associated protein 1-like 1; in the CDKN2A/B genes, which encode the cyclin-dependent kinase inhibitor p15INK4b and p16INK4a; in the IGF2BP2 gene, which encodes the IGF-2 mRNA binding protein 2; and a variant in a region of chromosome 11, not known to contain any genes. Most of these newly identified loci are suggested to play a role in the regulation

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Y.W. and H.L. contributed equally to this article.
of insulin production and β-cell function (5,7,9,12–15). It is unclear whether these variants have the same effect in Chinese populations, which have a different genetic background and lower diabetes prevalence compared with European populations (16–18).

Although case-control studies provide a useful design for the discovery of susceptibility loci, they are limited in providing insight into the mechanisms through which genetic variants exert their effect on the risk of type 2 diabetes. Population-based cohort studies with detailed measures of diabetes-related traits, however, might unravel the physiopathology that underlies the association between the newly discovered genetic variants and diabetes. The purpose of this study is to examine whether these novel variants are individually or collectively associated with type 2 diabetes and related traits in a population-based Chinese Han cohort including 3,210 unrelated individuals from Beijing and Shanghai.

RESEARCH DESIGN AND METHODS

The study sample consisted of 3,210 individuals (1,423 men and 1,787 women) from the Study on Nutrition and Health of Aging Population in China. The study population, design, and protocols of this population-based cohort study have been previously described (19). Briefly, all participants were unrelated Chinese Hans, aged 50–70 years, with at least 20 years residence in Beijing or Shanghai. Among them, 424 participants had type 2 diabetes (267 had previously diagnosed type 2 diabetes and 157 had screen-detected and treatment-naive type 2 diabetes), 578 participants had impaired fasting glucose (IFG) (all 578 were screen detected and treatment naive), and 1,908 participants had normal fasting glucose (NFG). Type 2 diabetes was defined by either 1999 World Health Organization criteria (20) or previously diagnosed type 2 diabetes. NFG and IFG were defined as fasting glucose <5.6 mmol/l (100 mg/dl) and 5.6 mmol/l (100 mg/dl) less than or equal to fasting glucose <7.0 mmol/l (126 mg/dl), respectively. The study was conducted simultaneously in both Beijing and Shanghai from March to June 2005. The participants were recruited from two urban districts (400 participants for each district) and one rural district (800 participants), representing people with high to low socioeconomic status, using a multistage sampling method in each city. All participants were selected randomly from the eligible candidates listed in the residential registration record. One person from each household was allowed to participate, and at least 40% of the total participants were men in each district. Individuals with the following conditions were excluded from the study: 1) severe psychological disorders, physical disabilities, cancer, cardiovascular disease, Alzheimer’s disease, or dementia, within 6 months; or 2) currently diagnosed with tuberculosis, AIDS, and other communicable diseases. All participants attended a physical examination, during which standard anthropometric measurements and overnight fasting blood samples were collected. Glucose was measured enzymatically on an automatic analyzer (Hitachi 7080; Hitachi, Tokyo, Japan) with reagents purchased from Wako Pure Chemical Industries (Osaka, Japan). Fasting insulin was determined by radioimmunoassay (Linco Research, St. Charles, MO). AIC concentrations were measured by turbidometric immunoassay in red blood cells on the Hitachi 7080 Analyzer using reagents from Roche Diagnostics (Indianapolis, IN). Homeostasis model assessment (HOMA) of insulin sensitivity (HOMA-S) and β-cell function (HOMA-B) were estimated using Levy’s computer model (21). Written informed consent was obtained from all participants, and study protocols were approved by the institutional review board of the Institute for Nutritional Sciences. The phenotypic characteristics of the population are shown in Table 1.

**TABLE 1**

<table>
<thead>
<tr>
<th>Characteristic</th>
<th>Beijing</th>
<th>Shanghai</th>
<th>P</th>
</tr>
</thead>
<tbody>
<tr>
<td>All samples</td>
<td>3,210 (44.3)</td>
<td>3,210 (44.3)</td>
<td></td>
</tr>
<tr>
<td>n (% male)</td>
<td>1,574 (45.2)</td>
<td>1,636 (45.3)</td>
<td>0.0005</td>
</tr>
<tr>
<td>Age (years)</td>
<td>58.6 ± 6.0</td>
<td>58.3 ± 5.9</td>
<td></td>
</tr>
<tr>
<td>BMI (kg/m²)</td>
<td>24.2 (22.0–26.6)</td>
<td>25.1 (22.8–27.4)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Fasting glucose (mmol/l)</td>
<td>5.84 ± 1.74</td>
<td>6.16 ± 1.96</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>AIC (%)</td>
<td>5.99 ± 1.10</td>
<td>5.90 ± 0.96</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Fasting insulin (pmol/l)</td>
<td>82.2 (59.4–110.2)</td>
<td>81.0 (57.6–110.7)</td>
<td>0.777</td>
</tr>
<tr>
<td>HOMA-B (%)</td>
<td>110.3 ± 47.0</td>
<td>100.1 ± 44.9</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>HOMA-S (%)</td>
<td>63.7 (47.1–86.9)</td>
<td>64.0 (47.3–89.5)</td>
<td>0.0454</td>
</tr>
<tr>
<td>IFG (%)</td>
<td>578 (27.4)</td>
<td>272 (13.3)</td>
<td>&lt;0.0001</td>
</tr>
<tr>
<td>Type 2 diabetes (%)</td>
<td>424 (13.2)</td>
<td>152 (9.3)</td>
<td></td>
</tr>
</tbody>
</table>

Data are means ± SD, median (interquartile range), or n (%), unless otherwise indicated. P represents significance of the differences between individuals from Beijing and from Shanghai.
### RESULTS

We first examined the association with the risk of type 2 diabetes and IFG (Table 2). The four CDKAL1 SNPs spanned two LD blocks ($r^2 = 1.0$ for rs7754840 and rs10946398 and 0.96 for rs7756992 and rs9465871) and were each significantly associated with type 2 diabetes (odds ratios ranged between 1.38 and 1.75; $P < 1.9 	imes 10^{-7}$) and with combined IFG/type 2 diabetes (between 1.20 and 1.22; $P < 0.0013$). The CDKAL1A/rs10811661 variant was also associated with type 2 diabetes (odds ratio 1.31 [95% CI 1.12–1.54]; $P = 0.001$) and combined IFG/type 2 diabetes (1.26 [1.13–1.41]; $P = 2.76 	imes 10^{-5}$). The second CDKAL1A/rs10811661 variant was also associated with type 2 diabetes (odds ratio 1.31 [95% CI 1.12–1.54]; $P = 0.001$) and combined IFG/type 2 diabetes (1.26 [1.13–1.41]; $P = 2.76 	imes 10^{-5}$). The second CDKAL1A/rs10811661 variant was also associated with type 2 diabetes (odds ratio 1.31 [95% CI 1.12–1.54]; $P = 0.001$) and combined IFG/type 2 diabetes (1.26 [1.13–1.41]; $P = 2.76 	imes 10^{-5}$). The second CDKAL1A/rs10811661 variant was also associated with type 2 diabetes (odds ratio 1.31 [95% CI 1.12–1.54]; $P = 0.001$) and combined IFG/type 2 diabetes (1.26 [1.13–1.41]; $P = 2.76 	imes 10^{-5}$).
To examine whether the associations for the CDKAL1 variants were independent, we performed additional multiple regression analyses that included all four CDKAL1 SNPs in one model. Results showed that none of the four SNPs remained significant \((P = 0.17)\). Next, we tested whether the two CDKAL1 “pairs” (rs7754840 and rs7756992 were chosen to represent each of the pairs) were independent from each other for the associations with type 2 diabetes or related quantitative traits in multiple regression models with both rs7754840 and rs7756992 genotypes in the model, with age, sex, region, and BMI (where appropriate) as covariates. The results revealed that the association seems to be driven by rs7754840, for the associations with type 2 diabetes, BMI, and HOMA-B, or by rs7756992, for the association with A1C, but interestingly, rs7754840 and rs7756992 seem to have independent effects on the associations with HOMA-S or insulin (online appendix Table 2).

We also performed a meta-analysis with the data from the previously published studies (10–12), including those from Japanese, Korean, and Hong Kong Chinese populations (22–25), to assess the heterogeneity between Caucasians and Asians for the CDKAL1 and CDKN2A/B loci (rs7754840 and rs10811661 were chosen to represent each of them, respectively). The results showed that for the CDKN2A/B loci (rs10811661), the heterogeneity between Caucasians and Asians did not reach significance \((P = 0.059)\), while a significant heterogeneity was observed between Caucasians and Asians \((P = 8.872 \times 10^{-8})\) for the CDKAL1 loci (rs7754840) (online appendix Fig. 1), and this is consistent with the recent finding reported by Ng et al. (25).

Although we did not observe the association among the LOC3877671 SNP rs74800010 and type 2 diabetes or IFG, we found that the allele that increased the diabetes risk in European populations was modestly associated \((P < 0.03)\) with increased insulin sensitivity (HOMA-S) and lower fasting insulin levels. Furthermore, despite a strong association between the CDKN2A/B SNP rs10811661 and type 2 diabetes, no association was observed with any of the diabetes-related quantitative traits. The intergenic SNP rs9300039 and the three EXT2 SNPs (rs7340878, rs11037990, and rs1113132) were not associated with any of the diabetes-related quantitative traits.

We found no evidence of multiplicative gene-gene interactions among the main SNPs (rs9465871, rs10811661, rs4402900, and rs13266634) in each of the CDKAL1, CDKN2A/B, IGF2BP2, and SLC30A8 genes. A significantly higher proportion of participants with type 2 diabetes carry increasing numbers of risk alleles, compared with participants with NFG (Fig. 1A). In combined analysis, each additional risk allele increased the risk of type 2 diabetes by 1.24-fold \((P = 2.85 \times 10^{-5})\) (Fig. 1B) and combined IFG/type 2 diabetes by 1.21-fold \((P = 6.31 \times 10^{-11})\) (Fig. 1C). Participants harboring seven or all eight risk alleles had a 4.44-fold increased risk for type 2 diabetes \((P = 5 \times 10^{-4})\) compared with those with one or no risk alleles (Fig. 1B). Consistently, participants with increasing numbers of risk alleles tended to have increased fasting levels of plasma glucose \((P = 0.013)\) (Fig. 1D) and A1C \((P = 0.07)\) (Fig. 1E), as well as decreased HOMA-B values \((P = 3.34 \times 10^{-7})\) (Fig. 1F). Of note, participants with increasing numbers of risk alleles tended to have significantly lower BMI \((P = 5.3 \times 10^{-5})\) (Fig. 1F), which is consistent with previous results found for the CDKAL1 and SLC30A8 polymorphisms (Table 3).

DISCUSSION

In this study of Chinese Hans, we replicated associations with several diabetes susceptibility variants recently identified through GWASs in white Europeans (7–12). Variants in CDKAL1, CDKN2A/B, IGF2BP2, SLC30A8, and HHEX loci were significantly associated with the risk of type 2 diabetes or combined IFG/type 2 diabetes. Furthermore, variants in CDKAL1 and IGF2BP2 were strongly associated with β-cell function estimated by HOMA-B.

The risk alleles of the CDKAL1 variants increased diabetes risk by \(\sim 1.4\)-fold. These associations were stronger than those observed in individuals of European Ancestry (8–10,12) (online appendix Table 1), and CDKAL1 risk allele frequencies are also substantially higher in Chinese (43–55%) than Europeans (15–31%). Moreover, significant heterogeneity between Caucasians and Asians was found for the CDKAL1 loci (rs7754840) in the meta-analysis that combined the data from the previous studies in white Europeans, Japanese, Korean, Hong Kong Chinese, and our study \((P = 8.872 \times 10^{-8})\) (online appendix Fig. 1), while no significant heterogeneity was observed among the Asians \((P = 0.369)\). These observations suggest that these CDKAL1 variants might play an even more important role in diabetes susceptibility in Chinese. The risk allele of the first pair of CDKAL1 variants was strongly associated with reduced β-cell function (HOMA-B) and increased A1C levels, while the second pair of CDKAL1 variants showed an association with impaired β-cell function (HOMA-B) and higher glucose levels, as well as with increased A1C. The results from additional multiple regression analyses suggest that the four SNPs most likely represent the effects of a single CDKAL1 locus. However, none of these four SNPs stands out as being the variant driving the association. Therefore, we assume that none of them is likely to be the causal variant, but presumably they are in moderate to high LD with the causal SNP and are therefore less consistently associated with the traits of interest. This region would benefit from a detailed fine mapping to identify possible causal variants in future studies. These results support previous findings (9,13,26) that the four CDKAL1 SNPs confer the risk of type 2 diabetes through reduced insulin secretion, although the causal SNP is yet to be identified.

We also observed significant association between CDKN2A/B rs10811661 and type 2 diabetes and IFG with a slightly higher odds ratio \((\sim 1.3)\) than that observed in Europeans \((\sim 1.20)\) (10–12). The risk allele is twice as prevalent in Chinese Hans (46%) as in Europeans (21%). However, we did not observe significant heterogeneity between Caucasians and Asians in the meta-analysis with data from the previously published studies \((P = 0.059)\). Interestingly, none of the diabetes-related traits showed an association with CDKN2A/B rs10811661. The second CDKN2A/B variant, rs564398, which is less frequent in Chinese Hans (13%) than in Europeans (38%), was not associated with type 2 diabetes or any related traits.

The association between variants in IGF2BP2 and type 2 diabetes was not significant, although the odds ratios were similar to those observed in European populations \((\sim 1.15)\), suggesting that our study may not have been sufficiently powered. Indeed, assuming an additive model and a minor allele frequency of 25%, we had <50% power
<table>
<thead>
<tr>
<th>SNP identification (major/minor allele)</th>
<th>Glucose (mmol/L)*</th>
<th>A1C (%)*</th>
<th>Insulin (pmol/L)*</th>
<th>HOMA-B (%)*</th>
<th>HOMA-S (%)*</th>
<th>BMI (kg/m²)*</th>
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<tr>
<td></td>
<td>n</td>
<td>Means ± SE</td>
<td>P&lt;sub&gt;‡&lt;/sub&gt;</td>
<td>Means ± SE</td>
<td>P&lt;sub&gt;‡&lt;/sub&gt;</td>
<td>Means ± SE</td>
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<td>rs10946398 (A/C)</td>
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<td>Genotype AA</td>
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<td>5.78 ± 0.03</td>
<td>80.4 ± 1.3</td>
<td>115.9 ± 1.4</td>
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<td>Genotype AC</td>
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<td>78.7 ± 1.0</td>
<td>112.8 ± 1.1</td>
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<td>516</td>
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<td>5.85 ± 0.04</td>
<td>77.1 ± 1.7</td>
<td>99.4 ± 1.8</td>
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<td>Genotype GG</td>
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<td>Genotype GG</td>
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<td>Genotype TT</td>
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<td>5.60 ± 0.04</td>
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<td>5.81 ± 0.03</td>
<td>78.3 ± 1.3</td>
<td>110.7 ± 1.5</td>
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<td>0.04</td>
<td>5.84 ± 0.02</td>
<td>80.3 ± 1.0</td>
<td>113.9 ± 1.1</td>
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<td>114.4 ± 1.7</td>
<td>67.8 ± 1.3</td>
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<tr>
<td>Genotype AA</td>
<td>1,597</td>
<td>5.54 ± 0.03</td>
<td>0.10</td>
<td>5.80 ± 0.02</td>
<td>80.0 ± 1.0</td>
<td>115.3 ± 1.1</td>
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<tr>
<td>Genotype AC</td>
<td>1,443</td>
<td>5.64 ± 0.04</td>
<td>0.029</td>
<td>5.85 ± 0.02</td>
<td>78.2 ± 1.1</td>
<td>111.0 ± 1.3</td>
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<tr>
<td>Genotype CC</td>
<td>167</td>
<td>5.66 ± 0.10</td>
<td>0.11</td>
<td>77.1 ± 2.9</td>
<td>108.2 ± 3.3</td>
<td>68.1 ± 2.5</td>
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### TABLE 3

Continued

<table>
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<tr>
<th>SNP identification (major/minor allele)</th>
<th>n</th>
<th>Glucose (mmol/l)*</th>
<th>AIC (%)†</th>
<th>Insulin (pmol/l)‡</th>
<th>HOMA-B (%)‡</th>
<th>HOMA-S (%)‡</th>
<th>BMI (kg/m²)§</th>
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</thead>
<tbody>
<tr>
<td></td>
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<td>Means ± SE</td>
<td>Mean ± SE</td>
<td>Means ± SE</td>
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<td>P‡</td>
<td>P§</td>
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</tbody>
</table>

**SLC30A8**
- rs1326634 (C/T)
  - Genotype
    - CC: 969
    - CT: 1,411
    - TT: 531

- rs1113132 (C/G)
  - Genotype
    - CC: 989
    - CG: 1,422
    - GG: 506

- rs1103909 (T/C)
  - Genotype
    - TT: 996
    - TC: 1,390
    - CC: 509

- rs3740878 (A/G)
  - Genotype
    - TT: 931
    - TC: 1,396
    - CC: 509

**LOC387761**
- rs7480010 (A/G)
  - Genotype
    - AA: 1,718
    - AG: 1,004
    - GG: 145

**Intergenic**
- rs3900089 (C/A)
  - Genotype
    - CC: 1,550
    - CA: 1,130
    - AA: 212

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Data are *means ± SE* or †geometric means ± SE, unless otherwise indicated. Alleles in bold are the risk alleles for type 2 diabetes identified by previous studies while alleles underlined are the risk alleles for type 2 diabetes or IFG observed in this study. ‡Adjusted for age, sex, region, and BMI. §Adjusted for age, sex, and region. ¶The associations remained significant after Bonferroni correction for multiple tests, and the Bonferroni corrected cutoff P value is 0.0014 (0.05/36 tests).
FIG. 1. Combined effects of increasing numbers of the risk alleles from CDKAL1-rs9465871, CDKN2A/B-rs10811661, IGF2BP2-rs4402960, and SLC30A8-rs13266634. A: The risk allele distribution in the participants with NFG and participants with type 2 diabetes. □, control; ■, type 2 diabetes. Each additional risk allele increased the risk of type 2 diabetes by 1.24-fold ($P = 6.31 \times 10^{-11}$) (B) and of IFG and diabetes combined by 1.21-fold ($P = 2.85 \times 10^{-7}$) (C). B: Participants harboring seven or all eight risk alleles had a 4.44-fold increased risk for type 2 diabetes ($P = 5 \times 10^{-4}$) compared with the reference group. Consistently, participants with increasing numbers of risk alleles tended to have increased fasting levels of plasma glucose ($P = 0.013$) (D) and A1C ($P = 0.07$) (E), as well as decreased HOMA-B values ($P = 3.34 \times 10^{-7}$) (F) and lower BMI ($P = 5.3 \times 10^{-3}$) (H), but showed no association with plasma insulin ($P = 0.13$) (G).
to detect previously reported odds ratios at \( P < 0.05 \). We did, however, find a significant association with combined IFG/type 2 diabetes. The associations with HOMA-B suggest that IGF2BP2 confer type 2 diabetes risk through a reduced β-cell function. Similarly, we found no association between the SLC30A8 rs13266634 variant and type 2 diabetes, while an association with combined IFG/type 2 diabetes reached borderline significance. Interestingly, the risk allele that increased diabetes risk in Europeans was also associated with a lower BMI in this population.

We also failed to find any evidence for association between type 2 diabetes and the SNPs in EXT2 (rs3740878, rs11037909, and rs1113132) and the intergenic SNP rs9300039, despite ~80% power to detect previously reported effect estimates (7). Although these SNPs exhibited marginal associations with type 2 diabetes in the original study (7), they were largely negative in the subsequent four GWASs and other replication studies in samples from U.K. (8,12), Finnish (10,11), Swedish (10), Icelandic (9), German (27), and Japanese (23) populations. Therefore, the original associations for these SNPs were either population specific or overestimated due to the “winner’s curse” (28,29), but the consistent lack of replication suggests that these findings were more likely false-positives. Meta-analyses or studies with larger sample sizes will be required to draw definitive conclusions. Although there was no association between rs7480010 (LOC387761) and type 2 diabetes or IFG, the allele conferring risk of diabetes in Europeans was associated with increased insulin sensitivity and showed a tendency toward a reduced β-cell function as well. For the three SNPs in HHEX/IDE gene region, the associations with type 2 diabetes or IFG were observed only in Shanghai individuals in whom each risk allele resulted in 1.45- to 1.79-fold increased diabetes risk, suggesting that geographical stratification may exist in our population for these SNPs and their roles in type 2 diabetes susceptibility. However, given the relatively small sample size, we cannot rule out sampling bias. This observation needs to be confirmed in larger studies.

We found no evidence of pairwise synergistic gene-gene interactions on type 2 diabetes and the related phenotypes among CDKAL1-rs9465871, CDKN2A/B-rs10811661, IGF2BP2-rs4402960, and SLC30A8-rs13266634. In joint analyses, the risk of type 2 diabetes was increased by 1.24-fold for each additional risk allele, and participants with seven or all eight risk alleles (3.8%) had a 4.44-fold increased risk of type 2 diabetes (\( P = 5 \times 10^{-4} \)) compared with those with one or no risk allele. These results are consistent with those reported by Scott et al. (11), who examined combined effects of 10 risk variants in a GWAS of European populations. Compared with Scott’s study, the advantage of our study is that our data are based on the general population. However, a replication in larger population is required to examine whether combinations of risk alleles from these variants have good predictive and diagnostic potential in Chinese Hans.

In conclusion, we replicated the association of type 2 diabetes with the SNPs in CDKAL1 and CDKN2A/B genes and confirmed that the SNPs in SLC30A8 and IGF2BP2 were associated with the risk of combined IFG/type 2 diabetes. Most of these SNPs were also associated with the impaired β-cell function. Importantly, the risk variants in CDKAL1, CDKN2A/B, IGF2BP2, and SLC30A8 appear to act in an additive manner to increase the risk of type 2 diabetes and related phenotypes. These results provide solid evidence for the notion that these variants individually or collectively contribute to the risk of type 2 diabetes in the Chinese Han population, possibly by impairing β-cell function or reducing insulin secretion.

ACKNOWLEDGMENTS
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