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Prediction of fasting blood glucose level within a Korean population

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Abstract

Fasting Blood Glucose (FBG) level is prevalent trait to predict several diseases. In the present study, we identified markers for prediction of blood glucose level. The genotype data of a total of 5,013 samples (2,373 men and 2,640 women) were obtained from the Korea Association Resource (KARE) project. We collected markers from a genome-wide association study (GWAS) catalog which included additional markers from nearby regions of GWAS catalog markers. In order to establish a FBG prediction model, we selected significant single nucleotide polymorphisms (SNPs) using a 10-fold cross-validation. In addition, we validated our prediction model using the final validation set. We selected a total of 7 SNP comprised of 2 SNPs (*rs7754840* and *rs12699673*) for the men and 5 SNPs (*rs102275, rs1574285, rs2908289, rs6494307*, and *rs917793*) for the women from the 10-fold cross-validation process. The results of the 10-fold across-validation process in the men and the women indicated upward trends of FBG levels. Also, we validated our prediction model using the final validation set. In the final validation set, increased trends were observed across all of the sets. Our prediction model for FBG may be helpful to further FBG related studies.

Keywords

Genome-wide association study; SNP; Fasting blood glucose; weighted genetic risk score; SNP marker.

Introduction

Diabetes Mellitus (DM) is one of the most serious health problems in the world [1,2]. Of the various diagnosis factors for DM, Fasting Blood Glucose (FBG) level is an important factor for diagnosis of prediabetes as it has a high association with the development rate of diabetes [3]. In addition, more recent studies have observed that prediabetes status is associated with risk of coronary heart disease in both diabetic and nondiabetic subjects [4,5]. The comparison between subjects with prediabetes and normal subjects has also found that prediabetic status increases the risk of cardiovascular disease and other related symptoms such as stroke and coronary heart disease [6].

Due to the importance of FBG, large-scale genome-wide association studies have been conducted and have found numerous markers significantly associated with FBG level, such as *G6PC2, FOXA2, MTNR1B*, and *LEPR* [7-10]. Following replication studies also have identified the associations between these genes and FBG level. For example, one previous study reported significant association between the *rs10830963* in *MTNR1B* and FBG level in Bosnian and Herzegovinian population [11]. The *rs560887* in *G6PC2* also showed significant associations with reduced FBG levels in normal subject of Hispanic populations [12].

Several function studies have also provided evidences of a relationship between the significant SNPs and FBG level. The previous study demonstrated that two SNPs (*rs560887* and *rs2232316*) in G6PC2 are responsible for increasing of FBG level by enhancing G6PC2 pre-mRNA splicing and regulating transcription factor binding affinity [13]. Another study showed that rs1137100 in the LEPR gene is associated with glucose homeostasis [14].

Based on these previous observations, it is clear that there is a significant association between FBG levels and SNPs. And also, according to the relation of FBG with disease occurrence, we anticipate that the prediction of FBG level using SNP may suggest possible role in public health.

In the present study, we aimed to establish a prediction model of FBG for Korean men and women using the weighted genetic risk score (wGRS) method. We used the genotype data obtained from the Korea Association Resource (KARE) project. Only the SNPs which were reported in previous studies were used to construct prediction model. Also, we applied 10-fold cross-validation to our analysis procedure to improve the validity of our analysis.

Materials and Methods

Study subjects

A total 8,840 subjects (4,182 men and 4,658 women) initially used for this study. The genotype data was derived from KARE project [15] that approved by Public Institutional Bioethics Committee designated by the Ministry of Health and Ware (P01-201502-31-002). For quality of data, we removed inadequate samples and SNPs that have the data of call rate with under 0.98. The data of SNPs were also deleted with minor allele frequency (MAF) under 0.05. Finally, the 5,013 subjects (2,373 men and 2,640 women) were selected for further analyses. Among the 5,013 samples, we used 90% (2,135 men and 2,376 women) of samples as a SNP selection set for 10-fold cross validation process. The rest of samples (238 men and 264 women) were used as a final validation set.

Statistical analysis

The SNP were collected from GWAS catalog markers which were associated with blood glucose studies. In order to obtain genotype data, we used data of the collected markers of GWAS and other data derived from KARE data (2,581 SNPs) of nearby regions which are ±50 kb from the GWAS markers. Among the SNPs, we performed calculating the coefficients of Linkage Disequilibrium (LD) to avoid high LD values using the Haploview software [16]. Consequently, we obtained 207 SNP markers, which have shown related blood glucose studies previously. The regression analysis was conducted for the p-value that was used for identification SNPs in the training sets. We conducted the regression analysis using the GoldenHelix-SVS8 software (Bozeman, MT, USA).

SNP selection for fasting blood glucose

In order to prediction model, men subjects (2,135 samples) and women subjects (2,376 samples) were used for testing SNP selection sets separately. Using the training sets (1,921 men and 2,138 women) and the test sets (214 men and 238 women) of genotype data, 10-fold cross validation was conducted for identify SNPs. The SNP markers were selected for less than 0.05 of p-value across all sets from the top of 20 SNPs that were identified LD. Each p-value of 20 SNP markers is shown in Table 2 and Table 3. These SNPs were used for the wGRS. The wGRS was calculated by using the following formula: Weighted genetic risk score (wGRS) = $\sum_{i=1}^{n} w_i \times SNP_i$ where w_i is weight that means the regression slope of selected SNPs, is the number of allele of FBG [17]. We conducted analysis separately by gender, using these scores to divide into 4 blocks after ascending sort of score. Then we calculated average of FBG values of each blocks and obtained the graphs. For validation these SNPs, the final validation sets (238 in men subjects and 264 in women subjects) were performed statistical analysis as same manner, resulting in trend line.

Results

Clinical profile of the study subjects

In the present study, we used the genotype data obtained from a total of 5,013 individuals comprised of 2,373 men and 2,640 women subjects. Of the total samples, 90% (n=4,511) were used in the SNP selection set to obtain the significant SNPs for constructing the prediction model. The remaining 10% (n=502) were used in the Final validation set. The average age of men population was slightly lower than that of the women population in all analysis groups (51.57 vs. 52.62; 51.61 vs. 52.57; and 51.26 vs. 53.06 in the total subjects, SNP selection set, and final validation set, respectively). The FBG level was generally higher in men than women (90.46 vs. 85.74; 90.32 vs. 85.53; 91.70 vs. 86.44 in total subjects, SNP selection set, and final validation set). Detailed clinical profile of the samples is described in Table 1.

SNP selection to construct prediction model

To select SNPs for FBG prediction model, we performed 10-fold cross validation based on regression analyses using a total of 207 SNPs which collected from a GWAS catalog and nearby SNPs. After performing the 10-fold cross-validation process, we found that two SNPs (*rs7754840* in *CDKAL1* and *rs12699673* located near *DGKB*) had constantly significant association with FBG level for men subject in all 10 training sets (Table 2). Similarly, we selected five SNPs (*rs102275* in *TMEM258*, *rs1574285* in *GLIS3, rs2908289* in *GCK,*

rs6494307 located near *C2CD4B* and *rs917793* in *YKT6*) which had consistent significant association with FBG level for women subject (Table 3). Detailed information of selected SNPs was listed in Table 4 with their allele information, location, and genotype counts.

Results of prediction model for Fasting blood glucose level

Using the selected SNPs, we constructed a prediction model for FBG using wGRS method. We observed upward trends of blood glucose levels with increasing of wGRS in both men and women population (Figure 1). Finally, we applied wGRS of both men and women population in the final validation set. As we expected, fasting blood glucose levels increased with wGRS (Figure 2).

Discussion

As diabetes mellitus type 2 (T2DM) is important to public health problem, numerous studies have been focused on identifying significant markers for T2DM. However, several previous reports have indicated that FBG might play a role in the prevention and treatment for various glucose-related diseases. One previous study showed that an increase in FBG level was significantly associated with upward diagnosis factors such as BMI and HDL-c [18]. Another recent study supported the correlation between FBG level and various clinical factors such as HbA1c, insulin, C-peptide and triglycerides [19]. These observations indicated that a prediction model for FBG level might contribute to public health not only with respect to diseases related to blood glucose but various factors of diseases.

In the present study, We used a total of 5,013 individuals to establish a prediction model for FBG level. Due to the low average FBG level of women compared to men, we decided to construct gender-specific FBG models rather than a single comprehensive model using total subjects. Based on our results, we selected two SNPs (*rs7754840* and *rs12699673*) for men and five SNPs (*rs6494307, rs1574285, rs102275, rs2908289, and rs917793*) for women population. Numerous previous studies have demonstrated the relationship between the SNPs and glucose-related phenotypes.

Of the two polymorphisms for men population, rs7754840 (linked to *rs9356744*, r2 = 0.902) which is located in CDKAL1 was significantly associated with the Gestational Diabetes Mellitus (GDM). And it was used in the prediction model for T2DM in a Japanese population [20,21]. This significance was also found in other populations such as Iranian population and in large-scale meta-analysis using various populations [22,23]. Another study suggested an association between DPP-4 inhibitors which was used for T2DM treatment with *rs7754840* [24]. The other selected SNP, *rs2191349* (linked to *rs12699673*, r2 = 0.893) located near DGKB was responsible for various phenotypes of glucose metabolism. One previous study using Korean population proved an effect of *rs2191349* in beta-cell function [25]. Other several studies have also support the association between the reduction of insulin and fasting glucose concentration [26,27].

As with the men population, numerous evidences has been found for the polymorphisms in the women subjects, with the exception two SNPs (*rs6494307* located near *C2CD4B* and *rs1574285* in *GLIS3*). The two SNPs, *rs174550* (correlated with *rs102275* in *TMEM258*, r^2 = 1.000) and *rs4607517* (correlated with *rs917793* in *YKT6*, r^2 = 0.886), have been found to affect beta-cell function, and were associated with GDM or prediabetes [25,28,29]. In addition, *rs730497* (absolute LD with *rs2908289* in *GCK*, r^2=1.000) showed an effect to HbA1c level which was an important diagnosis factor for chronic glycemic and hyperglycemia

[30,31]. However, there were no evidences of *rs6494307* and *rs1574285* impact on fasting glucose level or glucose related diseases. Further studies may be needed to identify the role of the SNPs in glucose metabolism.

The lack of confirmation using other independent cohorts was also one of limitation of the present study. Due to the problem, we selected only significant SNPs which had been reported on in previously studies. In this study, we set aside 10% of the total samples as a final validation set to overcome this limitation. Future studies might consider our limitation to build a more precise prediction model for FBG level using population-specific markers.

Conclusion

In summary, we constructed gender-specific FBG prediction models using genotype data from a Korean population. For the models, we selected two SNPs for men and five SNPs for women. Both of our models showed constantly upward trends of FBG level with increasing of wGRS. Prediction models of the present study might be useful for further glucose concentration studies and glucose-related diseases.

References

1. Collaboration NCDRF: Effects of diabetes definition on global surveillance of diabetes prevalence and diagnosis: a pooled analysis of 96 population-based studies with 331,288 participants. Lancet Diabetes Endocrinol. 2015; 3: 624-637.

2. Global Burden of Metabolic Risk Factors for Chronic Diseases C: Cardiovascular disease, chronic kidney disease, and diabetes mortality burden of cardiometabolic risk factors from 1980 to 2010: a comparative risk assessment. Lancet Diabetes Endocrinol. 2014; 2: 634-647.

3. Tabak AG, Herder C, Rathmann W, Brunner EJ, Kivimaki M. Prediabetes: a high-risk state for diabetes development. Lancet. 2012; 379: 2279-2290.

4. Decode Study Group EDEG: Is the current definition for diabetes relevant to mortality risk from all causes and cardiovascular and noncardiovascular diseases? Diabetes Care. 2003; 26: 688-696.

5. Mit LU, Saxena R, Voight BF, Lyssenko V, Burtt NP, et al. Genome-wide association analysis identifies loci for type 2 diabetes and triglyceride levels. Science. 2007; 316: 1331-1336.

6. Huang Y, Cai X, Mai W, Li M, Hu Y. Association between prediabetes and risk of cardiovascular disease and all cause mortality: systematic review and meta-analysis. BMJ. 2016; 355: 5953.

7. Bouatia-Naji N, Rocheleau G, Van Lommel L, Lemaire K, Schuit F, et al. A polymorphism within the G6PC2 gene is associated with fasting plasma glucose levels. Science 2008, 320:1085-1088.

8. Xing C, Cohen JC, Boerwinkle E. A weighted false discovery rate control procedure reveals alleles at FOXA2 that influence fasting glucose levels. Am J Hum Genet. 2010; 86: 440-446.

9. Prokopenko I, Langenberg C, Florez JC, Saxena R, Soranzo N, et al. Variants in MTNR1B influence fasting glucose levels. Nat Genet. 2009; 41: 77-81.

10. Go MJ, Hwang JY, Jang HB, Heo L, Park TJ, et al. A genome-wide association study identifies a LEPR gene as a novel predisposing factor for childhood fasting plasma glucose. Genomics. 2014; 104: 594-598.

11. Semiz S, Dujic T, Velija-Asimi Z, Prnjavorac B, Bego T, et al. Effects of melatonin receptor 1B gene variation on glucose control in population from Bosnia and Herzegovina. Exp Clin Endocrinol Diabetes. 2014; 122: 350-355.

12. Demirci FY, Dressen AS, Hamman RF, Bunker CH, Kammerer CM, et al. Association of a common G6PC2 variant with fasting plasma glucose levels in non-diabetic individuals. Ann Nutr Metab. 2010; 56: 59-64.

13. Baerenwald DA, Bonnefond A, Bouatia-Naji N, Flemming BP, Umunakwe OC, et al. Multiple functional polymorphisms in the G6PC2 gene contribute to the association with higher fasting plasma glucose levels. Diabetologia. 2013; 56: 1306-1316.

14. Lakka TA, Rankinen T, Weisnagel SJ, Chagnon YC, Lakka HM, et al. Leptin and leptin receptor gene polymorphisms and changes in glucose homeostasis in response to regular exercise in nondiabetic individuals: the HERITAGE family study. Diabetes. 2004; 53: 1603-1608.

15. Cho YS, Go MJ, Kim YJ, Heo JY, Oh JH, et al. A large-scale genome-wide association study of Asian populations uncovers genetic factors influencing eight quantitative traits. Nat Genet. 2009; 41: 527-534.

16. Barrett JC, Fry B, Maller J, Daly MJ. Haploview: analysis and visualization of LD and haplotype maps. Bioinformatics. 2005; 21: 263-265.

17. Hung CF, Breen G, Czamara D, Corre T, Wolf C, et al. A genetic risk score combining 32 SNPs is associated with body mass index and improves obesity prediction in people with major depressive disorder. BMC Med. 2015; 13: 86.

18. Sarwar N, Gao P, Seshasai SR, Gobin R, Kaptoge S, et al. Diabetes mellitus, fasting blood glucose concentration, and risk of vascular disease: a collaborative meta-analysis of 102 prospective studies. Lancet. 2010; 375: 2215-2222.

19. Kloppenborg JT, Fonvig CE, Nielsen TRH, Mollerup PM, Bojsoe C, et al. Impaired fasting glucose and the metabolic profile in Danish children and adolescents with normal weight, overweight, or obesity. Pediatr Diabetes. 2017.

20. Rosta K, Al-Aissa Z, Hadarits O, Harreiter J, Nadasdi A, et al. Association Study with 77 SNPs Confirms the Robust Role for the rs10830963/G of MTNR1B Variant and Identifies Two Novel Associations in Gestational Diabetes Mellitus Development. PLoS One. 2017; 12: e0169781.

21. Imamura M, Shigemizu D, Tsunoda T, Iwata M, Maegawa H, et al. Assessing the clinical utility of a genetic risk score constructed using 49 susceptibility alleles for type 2 diabetes in a Japanese population. J Clin Endocrinol Metab. 2013; 98: E1667-1673.

22. Mansoori Y, Daraei A, Naghizadeh MM, Salehi R. Significance of a common variant in the CDKAL1 gene with susceptibility to type 2 diabetes mellitus in Iranian population. Adv Biomed Res. 2015; 4: 45.

23. Tuerxunyiming M, Mohemaiti P, Wufuer H, Tuheti A. Association of rs7754840 G/C polymorphisms in CDKAL1 with type 2 diabetes: a meta-analysis of 70141 subjects. Int J Clin Exp Med. 2015; 8: 17392-17405.

24. Osada UN, Sunagawa H, Terauchi Y, Ueda S. A Common Susceptibility Gene for Type 2 Diabetes Is Associated with Drug Response to a DPP-4 Inhibitor: Pharmacogenomic Cohort in Okinawa Japan. PLoS One. 2016; 11: e0154821.

25. Hong KW, Chung M, Cho SB. Meta-analysis of genome-wide association study of homeostasis model assessment beta cell function and insulin resistance in an East Asian population and the European results. Mol Genet Genomics. 2014; 289: 1247-1255.

26. Wagner R, Dudziak K, Herzberg-Schafer SA, Machicao F, Stefan N, et al. Glucose-raising genetic variants in MADD and ADCY5 impair conversion of proinsulin to insulin. PLoS One. 2011; 6: e23639.

27. Renstrom F, Shungin D, Johansson I, Investigators M, Florez JC, et al. Genetic predisposition to long-term nondiabetic deteriorations in glucose homeostasis: Ten-year follow-up of the GLACIER study. Diabetes. 2011; 60: 345-354.

28. Tarnowski M, Malinowski D, Pawlak K, Dziedziejko V, Safranow K, et al. GCK, GCKR, FADS1, DGKB/TMEM195 and CDKAL1 Gene Polymorphisms in Women with Gestational Diabetes. Can J Diabetes. 2017; 41: 372-379.

29. Ohn JH, Kwak SH, Cho YM, Lim S, Jang HC, et al. 10-year trajectory of beta-cell function and insulin sensitivity in the development of type 2 diabetes: a community-based prospective cohort study. Lancet Diabetes Endocrinol. 2016; 4: 27-34.

30. An P, Miljkovic I, Thyagarajan B, Kraja AT, Daw EW, Pankow JS, et al. Genome-wide association study identifies common loci influencing circulating glycated hemoglobin (HbA1c) levels in non-diabetic subjects: the Long Life Family Study (LLFS). Metabolism. 2014; 63: 461-468.

31. Pare G, Chasman DI, Parker AN, Nathan DM, Miletich JP, et al. Novel association of HK1 with glycated hemoglobin in a non-diabetic population: a genome-wide evaluation of 14,618 participants in the Women's Genome Health Study. PLoS Genet. 2008; 4: e1000312.

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