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Analysis for Single nucleotide polymorphism related type 2 diabetes in insulin signaling pathway

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Short Abstract: Genetic factors contribute to human disease interacted with environmental factors. Environmental factors are confound variable finding genetic factors. We controled variables which has influence on disease phenotype to analyze SNPs. And we compared with insulin resistant group and insulin sensitive group using HOMA-IR value. This result found 2 SNPs of INSR and 1 SNP of CBL and 1 SNP of PRIKCZ.

Long Abstract:
Single nucleotide polymorphism in human genomes has generated a lot of interest from both the biomedical research community and industry. And single nucleotide polymorphisms were currently being developed for use in disequilibrium analysis. So we studied single nucleotide polymorphism related with complex disease marker. The research related with a chronic disease is administered investigation for disease marker detection. But, in complex disease, the factor for certain diagnosis was accompanied with equivocally of result. Because experimental block design of data was not made for unknown various factors. There have difference of diagnosis standard according to a factor out of consideration. For example sex (male and female), age level, and life style and so on.
Then selection for control variables or confound variables in general research is received wide publicity as a preliminary process of consequence. So, when we studied effect of disease related single nucleotide polymorphism, the control of covariates has influenced on interpretation of result. It will improve the quality.
On the one hand impaired insulin action is a key feature of type 2 diabetes and helps to find insulin resistances and metabolic disorders to understand the genetics of diabetes. Here we describe a difference of risk alleles between insulin resistant group and insulin sensitive group. Insulin resistance diminish effectiveness of insulin in lowered blood sugar levels. It is usually due to insulin binding by antibodies, but abnormalities in insulin receptors on cell surfaces also occur. Thus, by definition, insulin resistance is a defect in signal transduction. The signaling mechanisms involved in the various biologic responses on a few pathways that are critical for its regulation of glucose and lipid metabolism.

We analyzed a correlation between type 2 diabetes and 80 single nucleotide polymorphisms in 15 genes located in insulin pathway. Here we found effective factors using homeostasis model assessment related with insulin resistance for confound variable. Insulin resistance is the most important risk factor for the development of type 2 diabetes and is perhaps the greatest threat to our children's health. The homeostasis model assessment estimates steady state beta cell function and insulin sensitivity, as percentages of a normal reference population. First, we analyzed for insulin sensitivity.

The study population is comprised of 1,145 control subjects and 324 patients with type 2 diabetes mellitus. First of all, we carried out chi-square testing between type 2 diabetes and 80 single nucleotide polymorphism to select significant single nucleotide polymorphism. The result of chi-square test showed significant 2 single nucleotide polymorphism of INSR, 1 single nucleotide polymorphism of RAPGEF1, and 2 single nucleotide polymorphism of PTRN1. But, It is hard to say that these SNPs are related with insulin resistance of single nucleotide polymorphism in insulin signaling pathway.

Therefore we restricted analysis group as the 75 percent quartiles population of HOMA-IR value (HOMA-IR > 2.0571). HOMA-IR has the use as one of insulin resistance measurement method. HOMA-IR was calculated as [Glucose (mg/dL) X insulin (uU/mL) / 405]. After that, we performed statistical test to detection of single nucleotide polymorphism which was related by insulin resistance. The test result analyzed 2 single nucleotide polymorphism of INSR and 1 single nucleotide polymorphism of CBL (p-value < 0.05).

In the 25 percent quartiles population of HOMA-IR value (HOMA-IR < 0.9735), we found significant 1 single nucleotide polymorphism of PRIKCZ and 1 single nucleotide polymorphism of CBL (p-value < 0.05). We came to the conclusion that significant single nucleotide polymorphism in this group effected another factor but insulin resistance effects.

In summary, we found single nucleotide polymorphism leading to type 2 diabetes related insulin resistance of genes located in insulin pathway.