

Relationship between *SLC22A1* and *SLC22A4* gene polymorphisms and risks of type 2 diabetes in Chinese Han population.

Guanghui Long¹, Guangtao Zhang¹, Fangting Zhang², Dongshuo Ye³, Dengke Yang³, Yinke Yang^{3*}

¹Department of Hepatobiliary Surgery, Peking University Shenzhen Hospital, Shenzhen, Guangdong, PR China

²Center Laboratory, Peking University Shenzhen Hospital, Shenzhen, Guangdong, PR China

³Shenzhen Overseas Venture Park (Longgang), Shenzhen BioScien Pharmaceuticals. Co. Ltd., Shenzhen, Guangdong, PR China

Abstract

Objective: This study was conducted to investigate the relationship between *SLC22A1* and *SLC22A4* gene polymorphisms and genetic susceptibility to type 2 diabetes in Chinese Han population.

Methods: The research group comprised 110 patients with type 2 diabetes in Chinese Han population, while and the control group consisted of 110 healthy volunteers. The polymorphisms of *SLC22A1* gene rs628031 and rs2282143 loci and *SLC22A4* gene rs2073838 and rs272893 loci were detected in the subjects in the two groups. Genotype distributions and allele frequencies of the two genes were compared between the research and control groups.

Results: Statistically significant differences were identified in the genotype distributions of *SLC22A1* gene rs628031 and rs2282143 loci between the research and control groups ($P < 0.05$). The A allele frequency of *SLC22A1* gene rs628031 locus and the T allele frequency of rs2282143 locus were higher in the research group than in the control group; these differences were statistically significant ($P < 0.05$). The genotype distributions and allele frequencies of *SLC22A4* gene rs2073838 locus exhibited no significant difference between the research and control groups ($P > 0.05$). However, the genotype distributions of rs272893 locus showed a significant difference between the research and control groups ($P < 0.05$).

Conclusion: The polymorphisms of *SLC22A1* gene rs628031 and rs2282143 loci and *SLC22A4* gene rs272893 locus of patients with type 2 diabetes indicated a significant difference between the research and control groups, thereby suggesting that these genetic locus mutations increase the risk in patients with type 2 diabetes in Chinese Han population.

Keywords: Chinese Han population, Gene polymorphism, Type 2 diabetes, Genetic susceptibility.

Accepted on November 29, 2017

Introduction

Diabetes has become a worldwide public health concern given the increase in the occurrence of this disease [1]. This study showed that *SLC22A1* and *SLC22A4* genes influence the curative effect on patients with type 2 diabetes who took metformin [2]. The polymorphisms of *SLC22A1* gene rs628031 and rs2282143 loci and *SLC22A4* gene rs2073838 and rs272893 loci were closely related to the effectiveness of metformin. However, the correlation between the abovementioned loci polymorphisms of the two genes and the risks in patients with type 2 diabetes mellitus remain to be investigated [3]. The polymorphisms of the above gene loci in 110 cases of healthy volunteers and 110 patients with type 2 diabetes were used in this study considering their conditions. Moreover, the relationship between the gene polymorphisms

and genetic susceptibility to type 2 diabetes mellitus was detected in this study. The results were presented as follows.

Materials and Methods

Clinical data

The research group comprised 110 patients with type 2 diabetes who were admitted to our hospital from February 2015 to July 2016. According to the matching principle, the control group consisted of 110 healthy volunteers from the physical examination center. A total of 122 males and 98 females, aged 20-80 y, with an average of 42.8 ± 5.0 y were selected.

Inclusion criteria [4]: the patients in the research group were selected in accordance with the relevant standards in the "prevention and treatment guidelines for diabetes mellitus in