

Single nucleotide polymorphisms in renalase gene-analysis for potential association with type 2 diabetic population in an indian population

Aishwarya Murali,^{1,2} Amrita A Iyer,¹ Lakshmi Subramanian,¹ Radha Venkatesan,³ V Mohan,³ Nitish R Mahapatra¹

¹Department of Biotechnology, Bhupat and Jyoti Mehta School of Biosciences, Indian Institute of Technology Madras, Chennai, India

²Department of Genetic Engineering, School of Biosciences, SRM University, Kattankulathur, Chennai, India

³Madras Diabetic Research Foundation, Chennai, India

Correspondence: Aishwarya Murali, Department of Biotechnology, Bhupat and Jyoti Mehta School of Biosciences, Indian Institute of Technology Madras, Chennai 600036, India, Email aishwarya.I126@gmail.com

Received: November 10, 2017 | **Published:** November 14, 2017

Copyright© 2017 Murali et al. This is an open access article distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited.

Diabetes is a common metabolic disorder in the Indian population. Individuals with diabetes are at higher risk of cardiovascular disease. Recent studies show that Renalase, a novel enzyme, plays a significant role in hypertension and coronary artery disease. The aim of the study is to investigate whether there is an association between the Renalase gene single nucleotide polymorphisms (SNPs) and type 2 diabetes in South Indian population. About 400 diabetic individuals with or without hypertension and 420 healthy individuals of South Indian origin were enrolled in the study. Among the 400 diabetic individuals, 216 individuals were hypertensive and 184 individuals were normotensive. SNPs rs2576178 in the promoter and rs10887800 in the intron of Renalase gene were genotyped using polymerase chain reaction and restriction fragment length polymorphism. The diabetic individuals were also subgrouped to hypertensive and normotensive individuals. The genotypic and allele frequency was determined. Logistic regression analysis was done to find the association between the genotypes and the disease condition. Analysis of variance test was done to check the association between the biochemical parameters and the genotypes. For the SNP rs2576178, there was a slightly higher

prevalence of A allele in diabetic group however the difference was not significant (OR = 1.017, 95% CI = 0.627 to 1.650). There was slightly higher prevalence of G allele in diabetic individuals with hypertension compared to normotensive individuals however the difference was not significant (OR = 1.034, 95% CI = 0.531 to 2.015). Biochemical parameters like urea and HbA1c were found to be associated with the genotypes. For the SNP rs10887800, the allele and genotypic frequencies were similar for diabetic and non diabetic individuals. However biochemical parameters like high density lipoprotein (HDL), low density lipoprotein (LDL), systolic blood pressure and HbA1c were associated with the genotypes. Our findings show that there is no significant association with the underlined genotypes and the disease condition in South Indian population. However the prevalence of the alleles for rs2576178 were different for diabetic individuals with hypertension compared to diabetic individuals without hypertension and diabetic individuals compared to healthy individuals. Both the SNPs are found to be associated with the varying levels of the biochemical parameters.