

Increased prevalence of type 2 diabetes in south asian population – a genetic perspective

Abstract

Type 2 diabetes is complex disorder which results from interaction between the genes and environment. The sudden increase in the incidence of diabetes across the world is attributed to multiple factors like rapid urbanisation, diet and lack of physical activity. Nevertheless, there are ample evidences that suggests diabetes to have a strong genetic basis. The incidence of diabetes is disproportionately higher in certain ethnic population, type 2 diabetes in special, is highly prevalent amongst South Asians and are six times more prone to type 2 diabetes when compared to the Caucasians.

Keywords: diabetes, south asians, genetic factors

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Introduction

Around 415million individuals around the world have type 2 diabetes, of which 78million are from South East Asia.¹ Many theories have been put forth to explain the increased genetic predisposition of type 2 diabetes in South Asian population. The two most well renowned hypothesis are – the ‘Thrifty gene’ hypothesis and ‘Genetic trash can’ hypothesis. The thrifty gene hypothesis postulates that genes of our earlier ancestors are genetically modified to cope up with the insecurities like lack of continuous supply of food and natural disasters like fire, flood and famine. People with metabolically efficient or ‘thrifty’ genes managed to efficiently store energy as fat when food is available and managed to survive later during periods of famine or non-availability of food. The hypothesis holds much more significance in the context that nearly 90 famines being reported in the South Asia over the past 2,500years.²

‘Genetic trash can’ hypothesis states that multiple neutral gene mutations increases risk of type 2 diabetes when accumulated and concentrated in a population. This hypothesis is equally consistent, considering that diabetogenes are generally recessive and increased prevalence of type 2 diabetes in South Asians might be attributed to the fact that they are less exogamous when compared to other ethnic population.³ Genetic susceptibility is observed in various factors like Body Mass Index (BMI) or waist circumference. For any given BMI or waist circumference, South Asians have approximately 6% higher total body fat when compared to Caucasians.⁴ South Asians also present with increased insulin resistance and early loss of beta cell function than Caucasians for any given age.

Genetics

Advancements in genetic technology over the past two decades has facilitated in better understanding of the intricate details regarding genes and genetic variations and also large scale genetic studies. The Text-mined Hypertension, Obesity, and Diabetes candidate Gene (T-HOD) database reports 563 identified genes which are associated with type 2 diabetes till date. Though only very few Genome-wide Associated Studies (GWAS) have been conducted so far on South Asian population, it provides valuable information on the observed genetic variations. One such GWAS conducted on south Asian population found six novel signals by single nucleotide polymorphisms (SNPs) near GRB14, ST6GAL1, VPS26A, HMG20A, AP3S2 and HNF4A.⁵

In a multistage meta-analysis, a novel locus at 13q12 in the SGCG gene which is associated with type 2 diabetes susceptibility was identified in the Punjabi Sikhs from India. An increased incidence of the autosomal recessive LGMD2C was also reported in this same population, which was attributed to the endogamy practised within the community,⁶ which is in line with the ‘genetic trash can’ hypothesis.

Epigenetics

Epigenetics is an inheritable phenomenon that affects gene expression without base pair changes and are characterised by DNA methylation and histone modifications.⁷ The epigenetic changes observed in type 2 diabetes are often attributed to the *milieu interior* of the foetus before birth (as in gestational diabetes) or due to early exposure to nutritional stressors during early life.⁸ Few authors claim that epigenetic changes play a central role in the pathogenesis of type 2 diabetes.^{8,9} Folic acid intake has been extensively studied for its effect on DNA methylation, as folate carries a methyl group which acts as a methyl donor for the DNA methylation. Apart from folate, dietary components like methionine, choline, betaine and vitamin B12 also act as methyl donors and influences the DNA methylation process. Similarly, sulforafane in broccoli and diallyl sulfide in garlic plays a significant role in histone modification¹⁰ exhibiting the protective effects of diet and nutrition in overcoming epigenetic changes.

Conclusion

In conclusion, type 2 diabetes is due to the complex interplay of genetics, epigenetics and environmental factors. This mini review considered the role of genetic and epigenetic factors in the development of type 2 diabetes in south Asians and also the possible role of environment in overcoming these modifications. The review highlights that most of the risk factors attributed to the Non-communicable diseases (NCDs) could be brought down considerably through appropriate control over environment and lifestyle.

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Conflict of interest

Author declares that there is no conflict of interest.

References

1. International Diabetes Federation. IDF Diabetes Atlas. 7th ed. *International Diabetes Federation*. Brussels, Belgium; 2015.
2. Murton B. Famine. *The Cambridge world history of food*. 2000;2:1411–1427.
3. Lev-Ran A. Thrifty genotype: how applicable is it to obesity and type 2 diabetes? *Diabetes Rev*. 1999;7:1–22.
4. Chandalia M, Lin P, Seenivasan T, et al. Insulin resistance and body fat distribution in South Asian men compared to Caucasian men. *PLoS one*. 2007;2(8):e812.
5. Kooner JS, Saleheen D, Sim X, et al. Genome-wide association study in individuals of South Asian ancestry identifies six new type 2 diabetes susceptibility loci. *Nat Genet*. 2011;43(10):984–989.
6. Saxena R, Saleheen D, Been LF, et al. Genome-wide association study identifies a novel locus contributing to type 2 diabetes susceptibility in Sikhs of Punjabi origin from India. *Diabetes*. 2013;62(5):1746–1755.
7. Handel AE, Ebers GC, Ramagopalan SV. Epigenetics: molecular mechanisms and implications for disease. *Trends Mol Med*. 2010;16(1):7–16.
8. Drong AW, Lindgren CM, McCarthy MI. The genetic and epigenetic basis of type 2 diabetes and obesity. *Clinical Pharmacology & Therapeutics*. 2012;92(6):707–715.
9. Wren JD, Garner HR. Data-mining analysis suggests an epigenetic pathogenesis for type 2 diabetes. *J Biomed Biotechnol*. 2005;2005(2):104–112.
10. Sang-Woon Choi, Simonetta Friso. Epigenetics: A New Bridge between Nutrition and Health. *Adv Nutr*. 2010;1:8–16.