RESEARCH PAPER

Analysis Of Srnx1 Receptor Gene Polymorphism Among Completely Edentulous Diabetic Patient Case Control Study

Prathiyangara Lakshmanan[1], Karthikeyan Murthykumar[2], Vijayashree Priyadharshini[3], Dhanraj Ganapathy[4*]

[1]Undergraduate student, Saveetha Dental College and Hospital, Saveetha Institute of Medical and Technical Sciences, Saveetha University, Chennai-600077. Email: 152201002.sdc@saveetha.com

[2]Senior Lecturer, Department of Periodontics, Saveetha Dental College and Hospital, Saveetha Institute of Medical and Technical Sciences, Saveetha University, Chennai-600077. Email: karthikeyanmurthykumar@gmail.com

[3]Associate Professor, Department of Microbiology, Saveetha Dental College and Hospital, Saveetha Institute of Medical and Technical Sciences, Saveetha University, Chennai-600077. Email: vijayashreej.sdc@saveetha.com

[4*]Professor and Head, Department of Prosthodontics, Saveetha Dental College and Hospital, Saveetha Institute of Medical and Technical Sciences, Saveetha University, Chennai-600077. Email: dhanraj.sdc@saveetha.com

Corresponding Author: Dhanraj Ganapathy, Professor and Head, Department of Prosthodontics, Saveetha Dental College and Hospital, Saveetha Institute of Medical and Technical Sciences, Saveetha University, Chennai-600077. Email: dhanraj.sdc@saveetha.com

ABSTRACT

Introduction

Diabetes mellitus is a chronic metabolic disorder associated with increased oxidative stress, impaired wound healing, and accelerated periodontal destruction, often culminating in complete edentulism. Sulfiredoxin-1 (SRXN1), a critical antioxidant enzyme regulated by the NRF2 signaling pathway, plays a key role in restoring hyperoxidized peroxiredoxins and maintaining cellular redox homeostasis. Genetic polymorphisms in the SRXN1 gene may influence antioxidant defense capacity and thereby affect oral tissue susceptibility in diabetic individuals.

Aim

To evaluate the association between SRXN1 gene polymorphism and complete edentulism among diabetic patients.

Materials and Methods

This case–control study included 50 diabetic participants recruited from a dental institution following ethical approval and informed consent. The test group consisted of 25 completely edentulous diabetic patients, and the control group comprised 25 non-edentulous diabetic patients. Peripheral venous blood samples were collected, and genomic DNA was extracted using the Qiagen DNA extraction kit. The polymorphic region of the SRXN1 gene was amplified by polymerase chain reaction (PCR). Genotyping was performed using PCR-restriction fragment length polymorphism (PCR-RFLP) analysis, and selected samples were validated by sequencing. Genotype and allele frequencies were compared using the chi-square test with SPSS software. Statistical significance was set at $p < 0.05$.

Results

A statistically significant difference in genotype distribution was observed between the groups ($p = 0.0081$). The TT homozygous genotype was more frequently detected in the control group than in the edentulous group, suggesting a potential protective role against complete edentulism in diabetic patients.

Conclusion

SRXN1 gene polymorphism may influence susceptibility to complete edentulism in diabetic individuals. The TT genotype appears to confer a protective effect. These findings highlight the role of oxidative stress-related genetic factors in advanced oral disease progression and warrant further large-scale multicenter investigations.

Keywords

SRXN1 gene; polymorphism; diabetes mellitus; oxidative stress; complete edentulism; PCR-RFLP

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INTRODUCTION

Diabetes mellitus is a chronic metabolic disorder characterized by persistent hyperglycemia resulting from defects in insulin secretion, insulin action, or both. Chronic hyperglycemia induces oxidative stress and systemic inflammation, contributing to multiple microvascular and macrovascular complications [1,2]. Among the oral manifestations of diabetes, periodontal disease is one of the most prevalent and severe complications.

Oxidative stress plays a central role in the pathogenesis of diabetic complications. Sustained hyperglycemia enhances mitochondrial production of reactive oxygen species (ROS), leading to cellular damage and impaired tissue repair [3]. In periodontal tissues, excessive ROS promotes connective tissue breakdown, osteoclastic activation, and alveolar bone resorption [4].

Periodontal disease is a multifactorial inflammatory condition influenced by microbial, environmental, systemic, and genetic factors [5,6]. Genetic susceptibility plays a significant role in determining host inflammatory response and disease progression [7]. Polymorphisms in genes regulating oxidative stress pathways may alter antioxidant defense mechanisms and influence periodontal destruction severity [8].

Sulfiredoxin-1 (SRXN1) is an antioxidant enzyme involved in restoring hyperoxidized peroxiredoxins and maintaining intracellular redox balance through the NRF2 signaling pathway [9]. Alterations in SRXN1 gene expression or function may compromise antioxidant capacity, increasing susceptibility to inflammatory tissue damage.

Although oxidative stress has been implicated in both diabetes and periodontal disease, limited evidence exists regarding the association between SRXN1 gene polymorphism and complete edentulism in diabetic individuals. Therefore, the present study aimed to evaluate the association between SRXN1 gene polymorphism and susceptibility to complete edentulism among patients with type 2 diabetes mellitus.

MATERIALS AND METHODS

Study Design and Population

This cross-sectional case–control study was conducted among diabetic patients reporting to a dental institution after obtaining ethical clearance and informed consent. The study design followed standard epidemiological principles for genetic association studies [6].

A total of 50 participants were enrolled and divided into two groups:

Group A (Control): 25 non-edentulous diabetic patients

Group B (Test): 25 completely edentulous diabetic patients

Inclusion criteria included diagnosed type 2 diabetes mellitus and age above 35 years. Patients with systemic inflammatory diseases other than diabetes, smokers, immunocompromised individuals, and those with recent oral surgical procedures were excluded to reduce confounding variables [5].

Sample Collection and DNA Extraction

Five milliliters of peripheral venous blood were collected from the antecubital fossa using sterile EDTA-coated vacutainers. Genomic DNA was extracted using a standard salting-out method as described by Miller et al. [10]. DNA purity and concentration were assessed using spectrophotometry to ensure suitability for amplification.

Polymerase Chain Reaction and Genotyping

The polymorphic region of the SRXN1 gene was amplified using polymerase chain reaction (PCR) following established enzymatic amplification protocols [11]. Amplification was performed in a 20-µL reaction mixture containing genomic DNA, primers, and PCR master mix.

PCR products were confirmed by electrophoresis on 1% agarose gel. Genotyping was performed using polymerase chain reaction–restriction fragment length polymorphism (PCR-RFLP) analysis as described in classical genetic mapping studies [12]. The digested products were resolved on 2% agarose gel and visualized under UV illumination. Selected samples were subjected to sequencing to validate genotyping accuracy.

Statistical Analysis

Genotype and allele frequencies were compared between groups using the chi-square (χ^2) test. Hardy–Weinberg equilibrium was assessed using exact testing methods for genetic association studies [13]. Odds ratios (OR) with 95% confidence intervals were calculated to evaluate risk association. Statistical analysis was performed using SPSS version 23.0, and $p < 0.05$ was considered statistically significant.

Results

Genotype Frequency Analysis

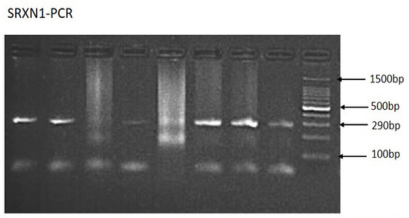

Figure 1: Agarose gel electrophoretogram showing amplification of SRXN1 gene spanning run along with standard DNA ladder [Lane M = 100 bp DNA marker]

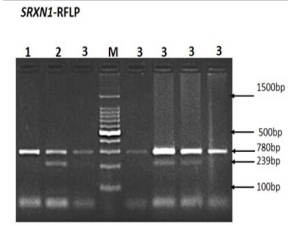

Figure : Agarose gel electrophoretogram showing Btg digested amplicon of SRXN1 gene at (Homozygous: TT – 290 bp; Heterozygous: TC – 290+209+81 bp; Homozygous: CC -209+81 bp) [Lane M = 100 bp DNA marker]

Gel Electrophoresis Findings

Distinct banding patterns were observed for different genotypes. Restriction digestion confirmed the presence of polymorphic variations in the SRXN1 gene across the study groups.

Group	TT (Homozygous reference)	TC (Heterozygous)	CC (Homomozygous variant)	T	C	HWE(p value)
CASE(25)	6	19	0	0.62	0.38	0.009
CONTROL(25)	15	10	0	0.80	0.20	0.458

The TT homozygous genotype was observed more frequently in the control group than in the case group. This difference in genotype distribution was statistically significant (p = 0.0081), suggesting a potential protective role of the TT genotype against edentulism in diabetic individuals.

DISCUSSION

Diabetes-induced oxidative stress significantly contributes to periodontal tissue destruction and impaired wound healing [3,4]. Persistent ROS production leads to connective tissue breakdown, collagen degradation, and increased osteoclastic activity, accelerating alveolar bone loss and tooth loss [4,14].

Genetic factors are increasingly recognized as important determinants of periodontal disease susceptibility [5,7]. Variations in antioxidant defense genes may influence host capacity to neutralize oxidative stress, thereby modulating disease severity [8].

SRXN1 plays a critical role in restoring oxidatively damaged peroxiredoxins and maintaining redox homeostasis [9]. Dysfunction or reduced activity of this enzyme may exacerbate oxidative tissue injury under hyperglycemic conditions.

Previous studies have demonstrated associations between oxidative stress gene polymorphisms and diabetic complications such as nephropathy and vascular dysfunction [15,16]. Similar associations have been reported in inflammatory oral diseases, supporting the hypothesis that antioxidant pathway genes influence periodontal susceptibility [17,18].

In the present study, a significant association was observed between SRXN1 gene polymorphism and complete edentulism among diabetic patients. The higher prevalence of the TT genotype in the non-edentulous group suggests a possible protective effect, potentially due to enhanced antioxidant regulation.

These findings align with emerging evidence that oxidative stress–related genetic variations influence susceptibility to chronic inflammatory diseases [19,20]. However, the relatively small sample size represents a limitation of the study. Larger multicentric studies incorporating functional assays are recommended to validate these findings and establish the clinical utility of SRXN1 as a predictive biomarker.

CONCLUSION

The present study demonstrates a significant association between SRXN1 gene polymorphism and complete edentulism in diabetic patients. The TT genotype appears to confer a protective effect against tooth loss. These findings underscore the importance of oxidative stress-related genetic factors in oral disease progression and highlight the potential for precision-based preventive strategies in diabetic populations.

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