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INPLASY

Clinicogenetic Characterization of SLC29A3-related Syndromes: A Case Series, Tracing Ancestral Variants, and Molecular Dynamics Simulation

INPLASY202510082

doi: 10.37766/inplasy2025.1.0082

Received: 20 January 2025

Published: 20 January 2025

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ADMINISTRATIVE INFORMATION

Support - Leo Foundation and NIH R01 grant.

Review Stage at time of this submission - Preliminary searches.

Conflicts of interest - None declared.

INPLASY registration number: INPLASY202510082

Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 20 January 2025 and was last updated on 20 January 2025.

INTRODUCTION

Review question / Objective What are the clinicogenetic characteristics of patients with SLC29A3-related syndromes, how do ancestral genetic variants contribute to disease pathology, and what are the structural-functional implications of these variants as analyzed through molecular dynamics simulation?

Condition being studied The study focuses on SLC29A3-related syndromes, a group of rare autosomal recessive disorders caused by mutations in the SLC29A3 gene, which encodes the equilibrative nucleoside transporter 3 (ENT3). These syndromes are characterized by a broad spectrum of clinical, genetic, and immunological abnormalities, often involving multisystemic histiocytosis, autoimmunity, and skeletal or developmental abnormalities.

METHODS

Participant or population In this study, the participants include patients with SLC29A3-related syndromes who have been diagnosed based on clinical symptoms, genetic testing, and/or family history. The review will focus on individuals with confirmed or suspected pathogenic variants in the SLC29A3 gene, which cause a spectrum of multisystemic disorders.

Intervention Not applicable.

Comparator Not applicable.

Study designs to be included We will include randomised trials, cohort, Case report, Case series, Cross-sectional, letter to the editor andcase– control studies.

Eligibility criteria In the future systematic screening process, when a single-gene SLC29A3-RS diagnosis is suspected, research papers, including clinical trials, case reports, letters, case-control studies, cross-sectional studies, and case series, will be included. Publications that fail to specify a causative gene, those that demonstrate non-monogenic causality for SLC29A3-RS (such as gross duplications, deletions, and aneuploidies), those involving acquired SLC29A3-RS patients, and those lacking sufficient clinical or patient phenotypic details will all be disqualified from the investigation. Only sequence variants that meet the American College of Medical Genetics and Genomics (ACMG) variant categorization criteria will be included. To avoid duplicate patient registration, factors such as authors, country, hospital, and patient characteristics will be carefully considered in the search.

Information sources Scopus, MEDLINE, Web of Science, EMBASE, and Google Scholar.

Main outcome(s) Identifying genes involved in genetic defects associated with warts and providing suggested methods for the diagnosis of SLC29A3-RS patients.

Quality assessment / Risk of bias analysis The tool developed by Joanna Briggs Institute (JBI) (https://jbi.global/critical-appraisal-tools) for quality assessments for case reports, case series, and cross-sectional research will be used.

Strategy of data synthesis The following data, if available, will extract from the included references: (i) Strict phenotypic criteria of SLC29A3-RS , (ii) Causative gene, (iii) Inheritance, (iv) Associated features, (v) Immunological features.

Subgroup analysis Not applicable.

Sensitivity analysis Not applicable.

Language restriction English.

Country(ies) involved Iran.

Keywords SLC29A3, SLC29A3-related syndromes, Inborn Errors of Immunity, hENT3, Exome Sequencing, RNA Sequencing, Inflammation.

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