INPLASY

Identifying and validating biomarkers associated with peroxisome in sepsis: Integrating transcriptome, single-cell RNA sequencing, mendelian randomization and meta-analysis

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ADMINISTRATIVE INFORMATION

Support - Yunnan Fundamental Research Projects.

Review Stage at time of this submission - Preliminary searches.

Conflicts of interest - None declared.

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Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 1 June 2025 and was last updated on 1 June 2025.

INTRODUCTION

Review question / Objective The aim of this study was to elucidate the correlation analysis between the expression of FLOT1, NMI, and LY9 and the risk of developing sepsis.

Condition being studied Sepsis is a potentially fatal condition characterized by acute organ failure resulting from a dysfunctional immune response to infection, posing significant risks to global health and survival. Approximately 20% to 30% of patients admitted to an intensive care unit (ICU) have sepsis, but the pathogenesis of sepsis and its diagnostic and therapeutic strategies have not yet been fully elucidated.

METHODS

Participant or population Septic patients.

Intervention FLOT1, NMI, and LY9 Highly Expressed Populations.

Comparator FLOT1, NMI, and LY9 low expression populations.

Study designs to be included Meta-Analysis.

Eligibility criteria Concurrent fulfillment of confirmed or suspected infection and ≥2 point increase in SOFA score from baseline.

Information sources China Knowledge Network, Wanfang, CBM, Pubmed.

Main outcome(s) Correlation analysis between the expression of FLOT1, NMI, and LY9 and the risk of developing sepsis.

Quality assessment / Risk of bias analysis Newcastle-Ottawa Scale.

Strategy of data synthesis The data from each study were extracted and pooled using either random-effect models depending on the degree of heterogeneity determined by I-squared (I^2) statistics.

Subgroup analysis None.

Sensitivity analysis Sensitivity analyses were performed by STATA software, which responded to the sensitivity of changing articles by the change in effect size after deleting one of them.

Country(ies) involved China.

Keywords Sepsis, Peroxisome, Biomarker, Single cell analysis, meta-analysis.

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