INPLASY PROTOCOL

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None declared.

The diagnostic value of metagenomic next-generation sequencing in sepsis: A protocol for systematic review and meta-analysis

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Review question / Objective: **P:patients with sepsis; I:traditional pathogenic detection and mNGS; C:traditional pathogenic detection only; O:Survival rate of sepsis patients after anti-infective therapy according to the results of pathogenic detection; S:RCT.**

Condition being studied: **Although metagenomic next-generation sequencing(mNGS) has been used in the etiological diagnosis of various complex infections, it still has the problems of false positive, high cost and low detection rate of some pathogens. It is not clear whether the use of mNGS can improve the pathogenic detection rate and accuracy in patients with sepsis. The aim of this study is to summarize previous evidence, assessing the diagnostic value of metagenomic next-generation sequencing in sepsis.**

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 01 June 2022 and was last updated on 09 June 2022 (registration number INPLASY202260008).

INTRODUCTION

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with sepsis. The aim of this study is to summarize previous evidence, assessing the diagnostic value of metagenomic next-generation sequencing in sepsis.

METHODS

Participant or population: Studies with patient age ≥18years old, a minimum hospital stay of 24h and a diagnosis of sepsis.

Intervention: With traditional pathogen detection and mNGS.

Comparator: With traditional pathogen detection only.

Study designs to be included: RCT.

Eligibility criteria: The inclusion criteria for the study will include:1. studies with patient age ≥18years old, a minimum hospital stay of 24h and a diagnosis of sepsis;2. conference abstracts were only included when they provided adequate relevant information for assessment;3. the patients with sepsis were divided into two groups (traditional pathogenic detection and mNGS, or traditional pathogenic detection only).

Information sources: We will search the CNKI, PubMed, EMBASE, WANFANG DATA, Web of Knowledge, Cochrane Library and ClinicalTrials.gov from inception to December 30, 2022 to retrieve relevant studies using the search strategy: ("mNGS" OR "metagenomic next-generation sequencing") AND ("sepsis" OR "septic" OR "septic shock" OR "infect" OR "infection" OR "Infected"). No language restrictions will be applied. We will also search citations of relevant primary and review. Authors of abstract in the meeting will be further searched in PubMed for potential full articles. To minimize the risk of publication bias, we will conduct a comprehensive search that included strategies to find published and unpublished studies.

Main outcome(s): Survival rate of sepsis patients after anti-infective therapy according to the results of pathogenic detection.

Quality assessment / Risk of bias analysis: Risk of bias assessment will be carried out according to the Newcastle–Ottawa Scale (NOS) to rate the internal validity of the individual studies, and funnel plots will be constructed to assess the risk of publication bias.

Strategy of data synthesis: All pairwise meta-analytic calculations will be performed with Review Manager software (RevMan) version 5.3 (Cochrane Collaboration). Heterogeneity will be examined by computing the Q statistic and I2 statistic, and presence of reporting bias by visual inspection of funnel plots. Statistical significance was considered when the P value <0.05.

Subgroup analysis: 1.Sepsis patients using traditional pathogen detection and mngs to simultaneously detect pathogenic microorganisms 1.1.Sepsis patients with different basic diseases; 1.2Sepsis patients with different infection sites.

Sensitivity analysis: Heterogeneity will be examined by computing the Q statistic and I2 statistic, and presence of reporting bias by visual inspection of funnel plots. Statistical significance was considered when the P value <0.05.

Country(ies) involved: China.

Keywords: mNGS, metagenomic next-generation sequencing, sepsis, meta-analysis, systematic review.

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