INPLASY

Application of Metagenomic Next-Generation Sequencing in the Diagnosis of Central Nervous System Infections after Craniotomy: A Systematic Review and Meta-Analysis

INPLASY202380100

doi: 10.37766/inplasy2023.8.0100

Received: 22 August 2023

Published: 22 August 2023

Jiang, BJ[1]; Li, YP[2]; Wu, HY[3]; Mao, DD[4].

Corresponding author:
Jiang Bingjie

jiangbingjie2013@126.com

Author Affiliation:
The Quzhou Affiliated Hospital of Wenzhou Medical University, Quzhou People's Hospital.

ADMINISTRATIVE INFORMATION

Support - Zhejiang Medical Association Clinical Research Fund Project.

Review Stage at time of this submission - The review has not yet started.

Conflicts of interest - None declared.

INPLASY registration number: INPLASY202380100

Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 22 August 2023 and was last updated on 22 August 2023.

INTRODUCTION

Review question / Objective To systematically analyze and estimate the value of metagenomic next-generation sequencing (mNGS) in diagnosing central nervous system infections in patients after neurosurgery.

Condition being studied Central nervous system (CNS) infections following neurosurgical procedures, such as craniotomy, can lead to significant complications and worsen patient prognosis if not diagnosed and treated promptly. Traditional methods for diagnosing CNS infections typically rely on pathogenic microbial culture, which has limitations in terms of sensitivity, specificity, and timeliness. On the other hand, metagenomic next-generation sequencing (mNGS) offers a powerful alternative diagnostic approach. This technique involves reading the DNA and RNA molecular sequences of pathogenic microorganisms present in a patient's biological sample, allowing for a comprehensive and unbiased analysis of the pathogens causing the infection. In terms of speed, metagenomic next-generation sequencing can provide rapid results compared to traditional culture-based methods. The sequencing process can be completed within a matter of hours to a few days, depending on the specific workflow and technology used. This rapid turnaround time enables clinicians to initiate timely and individualized treatment based on the identified pathogens, which is crucial in managing CNS infections and improving patient outcomes.

METHODS

Participant or population Patients who have undergone craniotomy and develop intracranial infections can come from diverse backgrounds and are not limited by factors such as gender, age, ethnicity, or the source of cases.

Intervention Metagenomic next-generation sequencing.

Comparator The control group was diagnosed by traditional methods, such as pathogenic microbial culture.

Study designs to be included Literature search, literature screening, data extraction, software analysis, and conclusion.

Eligibility criteria We will include randomized clinical trials without considering the factors of blinding, publication status, or language.

Information sources For the systematic review or meta-analysis, we will conduct searches in the following databases: PubMed, Cochrane Library, EMBASE, Web of Science, Clinical Key, Chinese Clinical Trial Registry, and Clinical Trials.

Main outcome(s) The main outcomes of interest for the study will be sensitivity and specificity.

Quality assessment / Risk of bias analysis In this study, two investigators will employ a revised tool called QUADAS-2 (Quality Assessment of Diagnostic Accuracy Studies) to independently assess the quality of included studies. In case of any discrepancies between the two reviewers' assessments, a discussion will be held with a third investigator to resolve the discrepancies and reach a consensus.

Strategy of data synthesis We will employ random effects models for the synthesis of data and assess publication bias through the use of a funnel plot during the process of meta-analysis. Furthermore, statistical analysis will be performed using STATA software.

Subgroup analysis Subgroup analysis will be conducted, considering factors such as the type of research and sample pre-treatment.

Sensitivity analysis Using STATA for statistical analysis, we aim to comprehensively address heterogeneity, evaluate bias, and make robust statistical inferences in the meta-analysis.

Country(ies) involved China.

Keywords Metagenomic next-generation sequencing; Neurosurgery; Craniotomy; Central nervous system; Meta-analysis.

Contributions of each author

Author 1 - Jiang Bingjie - Drafted the manuscript.
Email: jiangbingjie2013@126.com
Author 2 - Li Yunping - The author contributed statistical expertise to the study.
Email: ypl019@163.com
Author 3 - Wu Huayong - The author played a role in developing the selection criteria and the strategy for assessing the risk of bias.
Email: huayongwoo@163.com
Author 4 - Mao Dandan - The author read, provided feedback and approved the final manuscript.
Email: frank4232201@163.com