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The Application of High-Throughput Sequencing in the Pathogen Diagnosis of Brain Abscesses: A Systematic Review

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ADMINISTRATIVE INFORMATION

Support - No.

Review Stage at time of this submission - Data extraction.

Conflicts of interest - None declared.

INPLASY registration number: INPLASY2025100095

Amendments - This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 25 October 2025 and was last updated on 25 October 2025.

INTRODUCTION

Review question / Objective To determine how the application of high-throughput sequencing, alongside conventional microbiology, refines our understanding of the brain abscess pathogen spectrum and influences subsequent antibiotic treatment strategies.

Condition being studied Patients with a brain abscess diagnosis, in whom high-throughput sequencing was performed on abscess pus or cerebrospinal fluid as part of their diagnostic workup.

METHODS

Participant or population Patients with a brain abscess diagnosis, in whom high-throughput sequencing was performed on abscess pus, brain tissues, or cerebrospinal fluid as part of their diagnostic workup.

Intervention No intervention.

Comparator No comparator.

Study designs to be included Case reports or case series.

Eligibility criteria Inclusion Criteria:

- 1.Population: Pediatric patients with a confirmed diagnosis of brain abscess: A brain abscess confirmed by aspiration of pus or histologic examination, or patients with an imaging finding of ring enhancement after contrast on head MRI and hyperintense signals on diffusion-weighted imaging, or ring enhancement after contrast on head CT and improvement after antibiotic treatments.
- 2.Intervention/Exposure: Application of high-throughput sequencing on pus from the brain abscess, brain tissue, or cerebrospinal fluid.
- 3.Outcomes: Studies must report detailed pathogen findings from both high-throughput sequencing and conventional methods.

4.Others: Studies published in English or Chinese.

Exclusion Criteria:

- 1.Studies without report detailed, patient-level high-throughput sequencing results from pus of brain abscess, brain tissues, or CSF.
- 2.Patients with other primary central nervous system infections without a concurrent brain abscess.
- 3.Review articles, conference abstracts without full data
- 4.Studies not published in English or Chinese.
- 5.In vitro or animal studies.

Information sources PUBMED, EMBASE, Wanfang Data, and China National Knowledge Infrastructure (CNKI).

Main outcome(s)

- 1.The proportion of patients with a brain abscess in whom at least one pathogen was detected by high-throughput sequencing compared to conventional methods.
- 2.The pathogen spectrum with high through sequencing and with conventional methods.
- 3.The concordance and discrepancy of the high through sequencing and conventional methods.
- 4.The pathogen characteristics that did not being detected in conventional methods
- 5.The pathogen characteristics that did not being detected in high through sequencing
- 6.The impacts of high through sequencing on antibiotic treatments.

Data management Excel.

Quality assessment / Risk of bias analysis A quality assessment of the included case series was performed with the Joanna Briggs Institute (JBI) critical appraisal checklist.

Strategy of data synthesis Comparison of categorical variables were performed by means of χ^2 test. A P-value of <0.05 were considered statistically significant. Statistical software used in this study was SPSS 21.0 (SPSS Inc., Chicago, IL, USA).

Subgroup analysis

Patients with detailed information on treatments
 Patients aged <18 years
 Patients with various predisposing factors.

Sensitivity analysis No sensitivity analysis.

Country(ies) involved China.

Keywords Brain Abscess, Intracranial Abscess, High-Throughput Nucleotide Sequencing,

Metagenomics, Metagenomic next-generation sequencing, mNGS, Sinusitis, Otitis Media, Dental Infection, Odontogenic Infection, Immunodeficiency.

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