INPLASY PROTOCOL

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Support: None.

Review Stage at time of this submission: Formal screening of search results against eligibility criteria.

Conflicts of interest:
None declared.

Metagenomics Next Generation Sequencing for the Diagnosis of Central Nervous System Infection: A Systematic Review and Meta-analysis

Qu, C[1]; Chen, Y[2]; Ouyang, Y[3]; Lu, R[4]; Zeng, Y[5]; Liu, Z[6].

Review question / Objective: This meta-analysis was aimed at systematically analyzing and estimate the effect of mNGS on diagnosis of CNS infections.

Condition being studied: All kinds of CNS infection are caused by various pathogens. As a vital organ for us, many conditions result in serious complications, such as paralysis, coma, even death. The traditional detection methods, such as culture, have limitations in sensitivity, specificity, timeliness, amount of information, and so on. The metagenomic sequencing method with many advantages is being gradually popularized in clinical practice.

INTRODUCTION

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detection methods, such as culture, have limitations in sensitivity, specificity, timeliness, amount of information, and so on. The metagenomic sequencing method with many advantages is being gradually popularized in clinical practice.

METHODS

Participant or population: In line with the criteria for essential central nervous system infection, the patient's sex, age, race, onset time and source of cases are not limited.

Intervention: Metagenomics next generation sequencing.

Comparator: The control group was diagnosed by conventional methods, such as culture.

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

Eligibility criteria: Randomized clinical trials will be included irrespective of blinding, publication status or language.

Information sources: We will search the databases (PubMed, Cochrane Library, EMBASE, Web of Science, ClinicalKey, Chinese Clinical Trial Registry, Clinical Trials) for the systematic review or meta-analysis.

Main outcome(s): Sensitivity and specificity.

Quality assessment / Risk of bias analysis: Two investigators will use a revised tool for the Quality Assessment of Diagnostic Accuracy Studies (QUADAS-2) to independently assess study quality. The discrepancy between reviewers was resolved via a discussion with a third investigator.

Strategy of data synthesis: Random effects models will be used. Publication bias will be assessed by a funnel plot for meta-analysis. Statistical analysis will be conducted using STATA.

Subgroup analysis: We will consider subgroups such as type of research and sample pre-treatment.

Sensitivity analysis: We will use STATA for sensitivity analysis.

Country(ies) involved: China.

Keywords: Metagenomic next-generation sequencing; Central Nervous System Infection; Diagnosis; Meta-analysis.

Contributions of each author:
Author 1 - Chunrun Qu.
Author 2 - Yu Chen.
Author 3 - Yuzhen Ouyang.
Author 4 - Ruoyu Lu.
Author 5 - Yu Zeng.
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