INPLASY PROTOCOL

To cite: Guo et al. Metagenomic Next Generation Sequencing for the Diagnosis pathogeny of Respiratory Infection : A Systematic Review and Meta-analysis. Inplasy protocol 202180036. doi: 10.37766/inplasy2021.8.0036

Received: 10 August 2021

Published: 10 August 2021

Corresponding author:
Shihai Zhang

zhangshihai888@126.com

Author Affiliation:
Department of clinical laboratory, Anhui Provincial Children's Hospital, 230032, Hefei, China.

Support: **None.**

Review Stage at time of this submission: **Preliminary searches.**

Conflicts of interest:
None declared.

Metagenomic Next Generation Sequencing for the Diagnosis pathogeny of Respiratory Infection: A Systematic Review and Meta-analysis

Guo, Q[1]; Ye, X[2]; Ge, X[3]; Su, X[4]; Zhang, S[5].

Review question / Objective: **This meta-analysis was aimed at systematically analyzing and estimate the sensitivity and specificity of mNGS on the diagnosis of respiratory infections.**
Condition being studied: **Respiratory infections are caused by bacteria, viruses, mycoplasma, fungi, parasites and other microorganisms. They are common and frequently occurring diseases in clinical practice. With the gradual increase of drug-resistant bacteria, the aging of the population and the increase of the number of people with immunodeficiency disorders, the number of patients with infectious diseases is increasing. Due to delayed or unconfirmed etiological diagnosis, it is sometimes difficult to achieve accurate clinical treatment, affecting the efficacy and prognosis of patients, or even leading to the spread of unknown pathogens among susceptible people. With the development of molecular biology, the value of whole genome-based next-generation sequencing (NGS) has gradually been recognized, especially for the detection of rare, atypical, or slow-growing microbes.**

INPLASY registration number: This protocol was registered with the International Platform of Registered Systematic Review and Meta-Analysis Protocols (INPLASY) on 10 August 2021 and was last updated on 10 August 2021 (registration number INPLASY202180036).

INTRODUCTION

Review question / Objective: **This meta-analysis was aimed at systematically analyzing and estimate the sensitivity and specificity of mNGS on the diagnosis of respiratory infections.**

Condition being studied: **Respiratory infections are caused by bacteria, viruses, mycoplasma, fungi, parasites and other microorganisms. They are common and frequently occurring diseases in clinical practice. With the gradual increase of drug-resistant bacteria, the aging of the population and the increase of the number**

of people with immunodeficiency disorders, the number of patients with infectious diseases is increasing. Due to delayed or unconfirmed etiological diagnosis, it is sometimes difficult to achieve accurate clinical treatment, affecting the efficacy and prognosis of patients, or even leading to the spread of unknown pathogens among susceptible people. With the development of molecular biology, the value of whole genome-based next-generation sequencing (NGS) has gradually been recognized, especially for the detection of rare, atypical, or slow-growing microbes.

METHODS

Participant or population: Studies with patients diagnosed with respiratory infections via mNGS were included, and there were no restrictions on gender, age, and nations.patients with respiratory 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 PCR, culture.

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

Eligibility criteria: We included different types of studies, such as case-control, retrospective, and prospective studies. Full text original studies that assessed the efficacy of mNGS for the diagnosis of respiratory infections were included. The true-positive (TP), false-positive (FP), false-negative (FN), and true-negative (TN) values for the assay can be extracted or calculated directly from the studies. However, case reports, articles written in languages other than Chinese and English, studies with < 10 specimens, conference reports, and abstracts without full articles were excluded.We included different types of studies, such as case-control, retrospective, and prospective studies. Full text original studies that assessed the efficacy of mNGS for the diagnosis of TBM were included. The true-positive (TP), false-positive (FP), false-negative (FN), and true-negative (TN) values for the assay can be extracted or calculated directly from the studies. However, case reports, articles written in languages other than Chinese and English, studies with < 10 specimens, conference reports, and abstracts without full articles were excluded.

Information sources: We will search the databases (PubMed, Cochrane Library, EMBASE, Web of Science, ClinicalKey, China National Knowledge Infrastructure, Wanfang Database)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: If the necessary data are available, subgroup analysis will be done to evaluate the specificity of diagnose the pneumonia between mNGS and PCR.

Sensitivity analysis: We will use STATA for sensitivity analysis.

Language: No restriction.

Country(ies) involved: China.

Keywords: Metagenomic next-generation sequencing; respiratory infections; Diagnosis; Meta-analysis.

Contributions of each author:
Author 1 - Qiang Guo.
Email: zhongxia10086@163.com
Author 2 - Xiulin Ye.
Email: yexiulin0801@163.com
Author 3 - Xiaoxing Ge.
Email: xx521gk@163.com
Author 4 - Xiaoji Su.
Email: suxiaoji@126.com
Author 5 - Shihai Zhang.
Email: zhangshihai888@126.com