# Article information:

Metagenomic next-generation sequencing for detection of pathogens in children with hematological diseases complicated with infection - ScienceDirect  
<https://www.sciencedirect.com/science/article/pii/S0890850822001001?via%3Dihub>

# Article summary:

1. The positive rate of mNGS is significantly higher than that of culture for detecting pathogens in children with hematological diseases.

2. mNGS can detect more cases of Pneumocystis jeroveci, Aspergillus flavus, viruses, and some rare pathogens than culture.

3. Clinical anti-infective treatment was adjusted according to the results of mNGS, and the conditions of most patients improved.

# Article rating:

May be slightly imbalanced: The article presents the information in a generally reliable way, but there are minor points of consideration that could be explored further or claims that are not fully backed by appropriate evidence. Some perspectives may also be omitted, and you are encouraged to use the research topics section to explore the topic further.

# Article analysis:

This article provides a detailed overview of the value of metagenomic next-generation sequencing (mNGS) in the detection of causative pathogens in children with hematological diseases. The study is based on a retrospective analysis of 67 pediatric patients admitted to Sun Yat-Sen University between June 2019 and September 2021, and 96 specimens were collected for culture and mNGS. The results showed that the positive rate of mNGS was significantly higher than that of culture (57.2% vs 12.5%, P < 0.01). Furthermore, mNGS detected more cases with Pneumocystis jeroveci, Aspergillus flavus, viruses, and some rare pathogens than culture. Mixed infections were also detected by mNGS in 16 cases. Clinical anti-infective treatment was adjusted according to the results of mNGS, and the conditions of most patients improved as a result.

The article is generally reliable and trustworthy due to its use of scientific methods such as retrospective analysis and collection of data from 96 specimens for both culture and mNGS testing. Furthermore, it provides clear evidence for its claims by citing previous studies on similar topics as well as providing statistical data from its own study to support its conclusions about the superiority of mNGS over traditional pathogen cultures for detecting infectious agents in children with hematological diseases. However, there are some potential biases present in this article which should be noted when considering its trustworthiness; firstly, it does not provide any information on possible risks associated with using mNGS or any counterarguments against using it instead of traditional pathogen cultures; secondly, it does not explore any other potential methods for detecting infectious agents in these patients; thirdly, it does not provide any information on how long it takes for results from either method to be obtained or how much they cost; fourthly, it does not discuss any ethical considerations related to using either method; finally, it does not provide any information on how many false positives or false negatives were obtained from either method or what implications this may have had on patient care decisions made based on their results.

In conclusion, this article is generally reliable and trustworthy due to its use of scientific methods such as retrospective analysis and collection of data from 96 specimens for both culture and MGS testing; however there are some potential biases present which should be noted when considering its trustworthiness including lack of discussion regarding possible risks associated with using MGS or counterarguments against using it instead traditional pathogen cultures as well as lack exploration into other potential methods for detecting infectious agents in these patients among others

# Topics for further research:

* Risks associated with metagenomic next-generation sequencing
* Alternatives to metagenomic next-generation sequencing
* Time and cost of metagenomic next-generation sequencing
* Ethical considerations of metagenomic next-generation sequencing
* False positives and false negatives of metagenomic next-generation sequencing
* Implications of false positives and false negatives of metagenomic next-generation sequencing on patient care decisions

# Report location:

<https://www.fullpicture.app/item/b34768a9fb852c83b9eeaeef91b1b6a2>