ORIGINAL RESEARCH

Unravelling the Aetiologies of Meningoencephalitis: A Study from a Tertiary Care Centre in North India

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ABSTRACT

Introduction: Meningoencephalitis is a syndrome leading to fatality and neurological damages. It is a severe neurological condition characterized by the simultaneous inflammation of the meninges and brain parenchyma., with infection being the most common cause of meningoencephalitis. The clinical presentation often overlaps with other central nervous system disorders, making timely diagnosis and treatment critical for patient survival and outcomes. The aim of this study is to determine the etiological causes of meningoencephalitis for facilitating early diagnosis and treatment. **Materials and Methods:** It is a prospective observational study, conducted in 180 cases, in a tertiary care hospital of North India. clinical examination was done followed by CSF culture, detection by Molecular biology techniques. **Results:** out of total 180, total positive case for infectious agents were 47, out of which bacterial Culture positive were 19. PCR positive viral case were 18 and bacterial positive case were 8, Tubercular aetiology were found in 2(4.25%), age group ranged from 5 days to 90 years. Majority of patients were males 119(66%).

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INTRODUCTION

Meningitis is a serious infection of the meninges that surround the brain and spinal cord ^[1].Encephalitis is a serious form of neurological disease with inflammation of the brain parenchyma^[2] with invariable presence of a degree of leptomeningeal inflammation^[1]. Meningoencephalitis refers to the inflammation of meninges and brain and is considered as a neurological emergency. Infective meningitis is an acute purulent infection within subarachnoid space that is followed by a central nervous system inflammatory reaction that causes coma, seizure, raised intracranial pressure and stroke. The meninges, subarachnoid space and the brain parenchyma are all involved in the inflammatory reaction, hence meningoencephalitis is a more accurate descriptive term ^[4]. The infection may be caused by bacteria such as Streptococcus pneumoniae, Hemophillus influenza and Mycobacterium tuberculosis etc; viruses like *Herpes simplex*, fungi like *Cryptococcus neoformans* or parasites like plasmodium ^[3] Tubercular meningitis is a very critical disease in terms of fatal outcome and permanent sequelae, requiring rapid diagnosis and treatment. Death may occur as a result of missed diagnosis and delayed treatment.

Meningoencephalitis is a severe neurological condition that results in significant morbidity and mortality ^[5].Early diagnosis and treatment can have major impact on the ultimate outcome for a patient with meningoencephalitis ^[6]. Correct early diagnosis and administration of symptomatic and specific treatment will lead to increased influence upon survival and also decreases the extent of neurological consequences ^[7].Distinguishing the aetiologies and identification of specific agent helps in terms of both reducing antibiotic usage, prognosis, hospital bed occupancy and reassuring contacts of cases and healthcare staff ^[8]. The objective of the present study was to observe the clinical profile and aetiological causes of meningoencephalitis

MATERIALS AND METHODS

This prospective observational study was conducted at MGUMST, a tertiary care hospital in North India, involving a total of 180 patients clinically diagnosed with meningoencephalitis with symptoms such as fever, altered sensorium, seizures, neck stiffness, or other neurological deficits. Patients with known preexisting neurological disorders or those unwilling to provide consent were excluded.

All enrolled patients underwent a detailed clinical evaluation, including a thorough medical history and physical examination. Vital parameters, neurological signs, and systemic findings were recorded. Demographic data, including age, gender, and comorbidities, were also documented.

Cerebrospinal fluid (CSF) samples were collected via lumbar puncture under sterile conditions.

All cerebrospinal fluid (CSF) samples were inoculated onto culture media, including blood agar, MacConkey agar, and Chocolate agar, and incubated aerobically at 37°C to identify bacterial pathogens. Bacterial identification was performed using the VITEK2-COMPACT automated system.

Molecular assays (PCR) were employed to detect specific bacterial and viral DNA/RNA targets. These included amplification for pathogens such as *Mycobacterium tuberculosis*, *Neisseria meningitidis*, *Streptococcus pneumoniae*, and common viral agents, including herpesviruses and enteroviruses. Nucleic acid extraction was carried out using the PerkinElmer extraction system, and amplification of the extracted nucleic acids was performed on Bio-Rad and ABI 7500 Fast DX Real-Time PCR platforms.

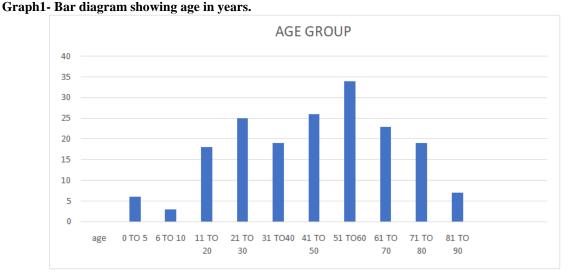
The study utilized targeted PCR tests for the detection of specific viral pathogens such as HSV-1, HSV-2, EBV, CMV, VZV, enteroviruses (EV), Dengue virus, and Chikungunya virus. Additionally, tests for *Mycobacterium tuberculosis* (TB PCR) and a bacterial meningitis panel targeting *Streptococcus pneumoniae*, *Haemophilus influenzae*, *Listeria monocytogenes*, and *Neisseria meningitidis* were performed. The amplification kits used included the TRUPCR kit from 3B Black Biotech.

This methodology ensured comprehensive identification of the causative pathogens of meningoencephalitis, utilizing both culture-based and molecular diagnostic approaches for enhanced sensitivity and specificity.

The data collected were compiled and statistically analysed.

RESULTS

The present study included 180 patients with clinically suspected meningoencephalitis. The age of the patients ranged from 5 days to 90 years. The majority of the patients were male (n=119; 66.11%), while females accounted for 61 cases (33.89%). The most affected age group was 51–60 years, comprising 34 patients (18.89%), followed by the 41–50 years age group with 26 cases (14.44%). A significant number of cases were also observed in the 61–70 years age group, which accounted for 25 patients (13.33%).



From 180 cerebrospinal fluid (CSF) samples from patients diagnosed with meningoencephalitis 47 samples (26.11%) tested positive through bacterial culture and molecular methods. Bacterial growth was seen in 19 cases (40.42%). Bacterial DNA was detected by PCR in 8 cases (17.02%) and Viral pathogens were identified by PCR in 18 cases (38.28%). Mycobacterium tuberculosis was identified in 2 cases (4.25%) through specific molecular diagnostic methods (PCR).

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S no	Organism	Number of Cases	Percentage		
1	Escherichia coli (E. coli)	5	10.6		
2	Staphylococcus spp.	7	14.89		
3	Acinetobacter spp.	6	12.76		
4	Klebsiella spp.	1	2.12		

Among bacterial culture-positive cases, the most frequently identified organism was *Staphylococcus* spp followed by *Acinetobacter* spp. and *E. coli*.

runogens Detected sy morecular methods					
S no	Target Virus	Number of Cases	Percentage		
1	Herpes Simplex Virus 1 (HSV-1)	6	12.76		
2	Herpes Simplex Virus 2 (HSV-2)	0	00		
3	Epstein-Barr Virus (EBV)	5	10.63		
4	Cytomegalovirus (CMV)	3	6.38		
5	Varicella Zoster Virus (VZV)	4	8.51		
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Table 2: Viral Pathogens Detected by Molecular Methods

Viral pathogens were identified in 18 cases, with HSV-1 being the most common, followed by EBV.

S no	Targeted Bacteria	Number of Cases	Percentage
1	Streptococcus pneumoniae	4	8.51
2	Haemophilus influenzae	2	4.25
3	Listeria monocytogenes	0	00
4	Neisseria meningitidis	2	4.25

Targeted PCR confirmed bacterial infections in 8 cases, with *Streptococcus pneumoniae* accounting for the majority.

DISCUSSION

The study revealed a predominance of middle-aged patients (41–60 years). These findings align with patterns observed in other regional and global studies, The age distribution showed a peak in the middle-aged population, similar to findings by Amruth et al. ⁽¹²⁾, where the 31–50 years age group accounted for 46.2% of cases. Other studies, such as those by Sarvepalli and Dharana ⁽¹³⁾, and Dey et al. ⁽²²⁾, also reported that meningoencephalitis was most common in middle-aged groups, further supporting our observations.

Our study shows higher incidence among males (66% males vs. 33.89% females). This also aligns with studies by Amruth et al. ⁽¹²⁾ and Naeima Hussein et al. ⁽⁵⁾, where males comprised the majority of cases, accounting for 61.4% and 66.7%, respectively.

The present study highlights the etiological distribution of meningoencephalitis in a tertiary care hospital in North India, and demonstrates the value of combining traditional culture techniques with advanced molecular diagnostics for accurate pathogen identification. Of the 180 patients studied, bacterial infections accounted for the majority of confirmed cases, with culture positivity in 40.42%, followed by viral aetiologies at 38.28%, and bacterial DNA detection via PCR in 17.02%. Tubercular aetiologies, although less common, were still clinically significant (4.25%).

Here we compare our findings with several similar studies to highlight trends in the distribution of etiological agents across populations and settings. In a study by Tan et al. ⁽⁶⁾ involving 116 patients, bacterial, viral, and tubercular aetiologies were reported as 31.0%, 53.4%, and 3.4%, respectively, which are comparable to the findings of the present study. Similarly, Modi and Anand ⁽⁹⁾ observed bacterial causes in 36.7%, viral in 28.3%, and tubercular in 4.2% of 120 patients, closely aligning with our results. Yerramilli et al. ⁽¹¹⁾ observed bacterial and viral aetiologies in 28.1% and 39% of cases, respectively, which also closely correlate with our findings. On the

other hand, Pandey and Mahale⁽¹⁰⁾ identified a higher prevalence of tubercular aetiology (54%) in their study population. In another study by Amruth et al. ⁽¹²⁾ on 184 patients, bacterial, viral, and tubercular aetiologies were identified in 21.19%, 25%, and 51.6% of cases, respectively. These findings differed slightly from our study, likely due to differences in patient recruitment, diagnostic methods, and emphasizing the geographical and demographic variations in the distribution of causative pathogens Globally, the aetiology of meningoencephalitis varies widely specially for tubercular meningitis, depending on geographic location, age distribution, and diagnostic methodologies.

In broader prospect, the present study aligns with global patterns, showing bacterial and viral pathogens as the predominant causes, with a smaller contribution from tubercular pathogens, emphasizing that bacterial and viral pathogens remain the leading causes of meningoencephalitis in both developing and developed settings.

Strengths and Limitations

The present study underscores the critical importance of integrating molecular diagnostic methods with traditional culture techniques for the effective diagnosis of meningoencephalitis. While bacterial culture remains a cornerstone for identifying pathogens, molecular methods, such as PCR, have proven invaluable in enhancing diagnostic sensitivity and providing rapid results. In this study, molecular techniques identified 17.02% additional bacterial cases that were culture-negative, highlighting their potential to detect fastidious or low-burden pathogens that conventional routine methods might miss.

The incorporation of molecular diagnostics also significantly reduces the time required for pathogen identification. Traditional culture methods often take 48–72 hours or longer, while PCR can provide results within a few hours, enabling earlier initiation of targeted therapy. This reduction in diagnostic time is especially crucial in meningoencephalitis, where

delays in treatment can lead to severe morbidity and mortality.

The widespread adoption of molecular techniques, accelerated by advancements during the COVID-19 pandemic, has made these tools more accessible and affordable. This represents a transformative step in clinical microbiology, allowing for a more comprehensive and rapid approach to diagnosing infectious diseases like meningoencephalitis.

However, variations in findings across studies highlight the need for standardization of diagnostic methods and larger multicentre studies to better understand the geographical and demographic factors influencing aetiology.

In conclusion, the combination of traditional and molecular methods not only improves diagnostic accuracy but also ensures timely interventions, ultimately enhancing patient outcomes. The findings of this study highlight the need to incorporate molecular diagnostics as a routine practice in healthcare facilities, to address the diagnostic challenges of complex infections effectively.

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