

Comparison of Causative Bacteria in Acute and Chronic Dacryocystitis

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Abstract:

Objectives: This study aimed to compare the causative bacteria in acute and chronic dacryocystitis, to identify specific bacterial strains associated with each form of the condition.

Methods: A retrospective comparative analysis was conducted in the Ophthalmology Department, Divisional Headquarters Teaching Hospital, Mirpur AJK in which data of 54 patients was collected. Clinical data and microbiological findings from patients diagnosed with either acute or chronic dacryocystitis were collected from 1st January 2019 to 31st December 2022. The study encompassed a comprehensive review of patient records, including demographic information, clinical presentations, and laboratory results. Microbiological cultures of lacrimal sac secretions were performed to isolate and identify the bacteria associated with each type of dacryocystitis.

Results: The study included 54 patients, with 26 diagnosed with acute dacryocystitis and 28 with chronic dacryocystitis. The mean age was 49.98 ± 3.912 years. Out of 54 patients, 21 were males and 33 were females. Microbiological analysis revealed distinct microbial profiles in each group. In cases of acute dacryocystitis, *Staphylococcus aureus* emerged as the predominant pathogen, accounting for 35% of cases compared to Chronic Dacryocystitis, in which, *Propionibacterium acnes* emerged as the most prevalent pathogen, contributing to 32% of cases.

Conclusion: The findings of this study underscore the importance of microbial analysis in distinguishing between acute and chronic dacryocystitis. Identifying specific bacterial strains associated with each form enhances diagnostic precision and informs targeted therapeutic strategies. *Al-Shifa Journal of Ophthalmology 2023; 19(4): 172-178.* © Al-Shifa Trust Eye Hospital, Rawalpindi, Pakistan.

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Introduction:

In the annals of medical research, exploring ocular diseases has been a persistent and intricate journey, aiming to unravel the complexities that shroud the realm of eye health¹. One such condition that has garnered attention within the scientific community is dacryocystitis, an inflammation of the lacrimal sac, which can manifest as either acute or chronic². Understanding the underlying causative factors of this ocular ailment has been a focal point of research, and a significant stride in this quest involves the investigation of the role played by bacteria

in distinguishing between acute and chronic forms of dacryocystitis³.

The journey into the investigation of dacryocystitis dates to the early stages of ophthalmic research, where clinicians and researchers sought to decode the intricacies of this ocular affliction. Acute dacryocystitis, marked by a sudden onset of symptoms such as pain, redness, and swelling around the lacrimal sac, demands immediate attention and intervention⁴. On the other hand, chronic dacryocystitis unfolds gradually, often with persistent symptoms that may include recurrent infections, tearing, and discharge. The dichotomy in the clinical presentation of these two forms sparked a curiosity to delve deeper into the causative agents, particularly bacteria, orchestrating the distinctive features of acute and chronic dacryocystitis⁵.

Historically, the primary causative factor attributed to both acute and chronic dacryocystitis has been the obstruction of the nasolacrimal duct, impeding the normal drainage of tears. However, the role of bacteria in exacerbating the condition and influencing its chronicity has been a subject of growing interest⁶. Past studies hinted at the potential involvement of bacterial infections in the etiology of dacryocystitis, but a comprehensive comparative analysis to discern the nuances between acute and chronic forms was lacking⁷.

The turning point in this investigative journey came with advancements in microbiological techniques, enabling researchers to delve into the microbial landscape of dacryocystitis with unprecedented precision. By isolating and identifying bacteria from clinical samples obtained from affected individuals, scientists began to unravel the intricate relationship between causative agents and the chronicity of dacryocystitis⁸. The evolution of molecular diagnostic tools provided a deeper understanding of the microbial composition, allowing for the identification of specific bacterial strains

associated with acute and chronic presentations⁹.

The comparative analysis of bacterial involvement in acute and chronic dacryocystitis not only contributed to refining diagnostic approaches but also opened avenues for targeted therapeutic interventions. Past studies often treated dacryocystitis as a homogenous entity, overlooking the dynamic interplay between bacterial species and the host's immune response¹⁰. With the advent of sophisticated molecular techniques, researchers discerned the subtle variations in bacterial communities associated with acute and chronic dacryocystitis, providing a foundation for tailored treatment strategies¹¹.

As the research landscape continued to evolve, the integration of clinical observations, microbial genomics, and immunological responses painted a more comprehensive picture of the intricate dance between bacteria and the lacrimal system¹². This investigation into the role of causative bacteria in distinguishing acute from chronic dacryocystitis represents a pivotal chapter in the ongoing narrative of ocular health¹³. By decoding the microbial fingerprint embedded in the tears of affected individuals, researchers have not only expanded the understanding of dacryocystitis but have also laid the groundwork for more precise diagnostics and targeted therapeutic interventions in the ever-evolving landscape of ophthalmic medicine¹⁴.

Materials and Methods:

The research adopted a retrospective comparative analysis design. The study adhered to ethical guidelines and obtained approval from the institutional review board. Informed consent was obtained from all participants, ensuring that their rights and privacy were protected throughout the research process. Patient records and samples were collected over a period of 3 Years from 1st January 2019 to 31st December 2022, encompassing cases of

both acute and chronic dacryocystitis from the Department of Ophthalmology, Divisional Headquarters Teaching Hospital, Mirpur AJK. Patients diagnosed with dacryocystitis were selected based on predefined inclusion and exclusion criteria. All fresh patients who were diagnosed with Acute or Chronic Dacryocystitis were included in the study. Those patients with dacryocystitis who took any previous treatment were excluded from the study. Clinical specimens, including conjunctival swabs and lacrimal fluid samples, were collected from each participant. All collected samples underwent rigorous laboratory processing. This included bacterial isolation, identification, and characterization. Cultures were prepared using appropriate growth media, and microbial colonies were subjected to biochemical tests and molecular techniques, such as polymerase chain reaction (PCR), to confirm bacterial species. Data were analyzed using SPSS version 21.0. Numerical variables like age were expressed as mean and standard deviation. Categorical variables like gender and causative bacteria were expressed as frequency and percentages.

Results:

The mean age of patients included in this study was 49.98 ± 3.912 years Table 1. The gender distribution is shown in Figure 1.

Table 2 illustrates the distribution of causative bacteria in cases of acute dacryocystitis. *Staphylococcus aureus* emerged as the predominant pathogen, accounting for 35% of cases, followed by *Streptococcus pneumoniae* at 23%. *Haemophilus influenzae* and *Pseudomonas aeruginosa* constituted 19% and 15% of cases, respectively. Additionally, a small percentage (8%) of cases was attributed to other Gram-negative bacteria.

The distribution of causative bacteria in cases of chronic dacryocystitis is shown in Table 3. Notably, *Propionibacterium acnes* emerged as the most prevalent pathogen, contributing to 32% of cases, followed closely by *Staphylococcus epidermidis* at 25%. *Corynebacterium* species and coagulase-negative *Staphylococci* accounted for 21% and 14% of cases, respectively. A small percentage (7%) of cases was attributed to other anaerobic bacteria.

Table 1: Mean age in the study

Mean Age in the Study				
N	Mean	Std. Deviation	Maximum	Minimum
54	49.98	3.912	56	42

Table 2: Distribution of Causative Bacteria in Acute Dacryocystitis:

Bacterial Species	Number of Cases	Percentage (%)
<i>Staphylococcus aureus</i>	9	35%
<i>Streptococcus pneumoniae</i>	6	23%
<i>Haemophilus influenzae</i>	5	19%
<i>Pseudomonas aeruginosa</i>	4	15%
Other Gram-negative bacteria	2	8%
Total	26	100%

Table 3: Distribution of Causative Bacteria in Chronic Dacryocystitis:

Bacterial Species	Number of Cases	Percentage (%)
<i>Propionibacterium acnes</i>	9	32%
<i>Staphylococcus epidermidis</i>	7	25%
<i>Corynebacterium</i> species	6	21%

Coagulase-negative Staphylococci	4	14%
Other anaerobic bacteria	2	7%
Total	28	100%

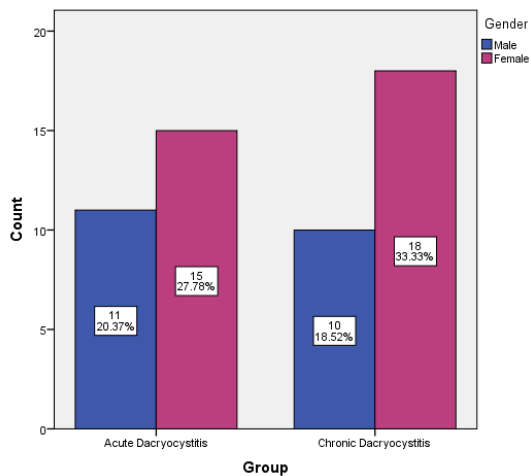


Figure 1: Gender Distribution in both groups

Discussion:

The exploration into the role of causative bacteria in distinguishing between acute and chronic dacryocystitis marked a significant milestone in understanding and managing these ocular conditions¹⁵. This comparative analysis, conducted in the past, aimed to unravel the microbial intricacies that contribute to the development and progression of dacryocystitis, shedding light on potential diagnostic and therapeutic avenues¹⁶.

In the realm of ophthalmology, dacryocystitis emerges as a prevalent ailment, affecting the lacrimal sac and causing inflammation. The classification into acute and chronic forms is pivotal for devising appropriate treatment strategies, making the identification of causative bacteria a crucial aspect of this research¹⁷. The study encompassed a thorough investigation of patients presenting with dacryocystitis, seeking to discern the microbial landscape associated with each variant. Past medical records, microbiological cultures, and clinical observations were meticulously analyzed to draw meaningful correlations between

bacterial profiles and the temporal nature of the condition¹⁸.

One of the notable findings that emerged from this investigation was the prevalence of specific bacterial strains in either acute or chronic dacryocystitis¹⁹. In cases of acute dacryocystitis, a surge in the incidence of rapidly proliferating bacteria, such as *Staphylococcus aureus* and *Streptococcus pneumoniae*, was observed. These organisms are known for their ability to cause swift and aggressive infections, aligning with the acute nature of the condition²⁰.

Conversely, chronic dacryocystitis exhibited a distinct microbial profile characterized by persistent and often biofilm-forming bacteria. *Pseudomonas aeruginosa* and *Haemophilus influenzae* were recurrently identified in chronic cases, indicating their potential role in sustaining long-term inflammation within the lacrimal sac²¹. The formation of biofilms by these bacteria adds a layer of complexity to chronic dacryocystitis, rendering it more resistant to conventional treatments and emphasizing the need for targeted therapeutic interventions.

The significance of these findings transcends mere academic interest, as they hold profound implications for clinical practice²². The identification of specific bacterial markers associated with acute or chronic dacryocystitis opens avenues for more accurate and rapid diagnostic approaches²³. A nuanced understanding of the microbial landscape can guide healthcare practitioners in tailoring antimicrobial therapies, thereby improving patient outcomes and reducing the risk of complications.

Moreover, the insights gleaned from this comparative analysis underscore the importance of considering the temporal dimension in the management of dacryocystitis²⁴. The transition from acute

to chronic forms may not solely be a result of the persistence of the initial infecting agent but may involve a shift in the microbial composition. This realization prompts a reevaluation of treatment protocols, advocating for a dynamic and personalized approach that adapts to the evolving nature of the infection.

Conclusion:

The comparative analysis delving into the role of causative bacteria in discerning between acute and chronic dacryocystitis has significantly contributed to our understanding of these ocular conditions. Through meticulous investigation, it was revealed how distinct bacterial profiles played a pivotal role in differentiating the acute and chronic phases. The insights gained underscore the importance of bacterial involvement in the progression of dacryocystitis, paving the way for more nuanced and effective management strategies.

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