

Research article

Molecular Characterization and Serotype Distribution of *Chlamydia trachomatis* Infections in HIV Patients in Owerri, Nigeria

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Abstract**Background:** *Chlamydia trachomatis* is a prevalent bacterial sexually transmitted infection globally, often causing severe reproductive health complications due to its frequently asymptomatic nature. Understanding the molecular characteristics and serotype distribution of *C. trachomatis* is crucial for effective public health interventions.**Objective:** This cross-sectional study investigated the molecular and sero-epidemiological prevalence of *C. trachomatis* in Owerri, Imo State, Nigeria.**Methodology:** A total of 40 symptomatic and asymptomatic patients from the Federal Medical Center, Owerri, were enrolled. Molecular characterization was performed using Polymerase Chain Reaction (PCR), targeting the ompA gene for serotyping.**Results:** The PCR successfully amplified the ompA gene in 26 (65%) of the 40 analyzed samples. Molecular analysis revealed that *C. trachomatis* serotypes E, G, and D were the endemic serovars in Owerri, with serovar G identified as the most common. A comparison between symptomatic and asymptomatic subjects showed no statistically significant difference ($p > 0.05$) in the magnitude of infection.**Conclusion:** These findings show the silent spread of *C. trachomatis* in the region and the importance of molecular surveillance to identify circulating serotypes. The high prevalence although not significant in asymptomatic individuals and the identification of potentially more virulent serotypes like G emphasize the need for comprehensive screening programs and targeted public health education campaigns to mitigate the long-term health consequences of *C. trachomatis* in Owerri.

1. Introduction

Chlamydia trachomatis, an obligate intracellular bacterium, is the most common cause of bacterial sexually transmitted infections (STIs) globally and a major public health concern, particularly in sub-Saharan Africa [1, 2]. It is estimated that 92.6 million new cases of curable STIs, including *C. trachomatis*, occur annually in Africa. The infection is often asymptomatic, especially in women, which leads to a large reservoir of infected individuals who can transmit the disease without knowing [1]. This "silent" nature of the infection makes early detection difficult and is a major contributing factor to its high prevalence and severe sequelae, such as pelvic inflammatory disease (PID), tubal infertility, and ectopic pregnancy [2].

C. trachomatis is classified into 18 serovars based on the major outer membrane protein (MOMP), which is encoded by the omp1 gene. Serovars D through K are primarily responsible for sexually transmitted infections in adults. The distribution of these serotypes varies by geographic location and is important for epidemiological studies and the development of vaccines.

In Nigeria, the prevalence of *C. trachomatis* infection has been reported to vary widely, ranging from as low as 13.3% in Benin City to as high as 56.1% in Jos [1, 3]. Other studies have reported prevalence rates of 29.4% in Enugu [4] and 51% in Lagos among pregnant and non-pregnant women [1]. This variation in prevalence highlights the need for localized studies to understand the true burden of the disease. Despite these studies, there remains a paucity of data on the molecular characteristics and serotype distribution of *C. trachomatis* in Owerri, Imo State, which is located in southeastern Nigeria. This study aims to address this knowledge gap by investigating the molecular and sero-epidemiological prevalence of *C. trachomatis* infections among patients in Owerri.

2. Methodology

2.1. Study Design and Area

This research was designed as a cross-sectional study to determine the molecular and sero-epidemiological prevalence of *Chlamydia trachomatis* infection. The study was carried out in Owerri, Imo State, Nigeria, at the Federal Medical Center, where subjects were recruited from various clinics.

2.2. Ethical Considerations

The study was conducted in accordance with ethical guidelines for human subjects. Informed consent was obtained from all participants.

2.3. Study Population and Sample Collection

The study enrolled a total of 40 HIV patients, comprising 20 symptomatic and 20 asymptomatic individuals. The subjects were conveniently recruited from the outpatient clinics at the Federal Medical Center. Clinical samples were collected from the genital sites of the participants.

2.4. Molecular Characterization and Serotyping

The diagnosis and molecular characterization of *C. trachomatis* were performed using the Polymerase Chain Reaction (PCR) method, which was utilized as the gold standard for its high sensitivity and specificity. The PCR targeted the Major Outer Membrane Protein (MOMP) gene, the endogenous plasmid, and the 16S and 23S rRNA gene. The MOMP gene was specifically targeted for genotyping and determination of the prevailing serotypes.

2.5. Statistical Analysis

Statistical analyses were performed to determine the prevalence of infection, and to assess the relationship between socio-demographic factors and infection rates. Data analysis also included the distribution of the identified *C. trachomatis* serotypes within the study population.

3. Results

3.1. Molecular Characterization and Serotype Distribution

The Polymerase Chain Reaction (PCR) method was used for the molecular characterization of the infection. Of the 40 samples analyzed by PCR, the *ompA* gene was successfully amplified in 26 (65%) samples as seen in Figure 1 below. The molecular analysis revealed that *Chlamydia trachomatis* serotypes E, G, and D were the endemic serovars in Owerri, with serovar G being the most common Figure 2. The *Omp1A* gene of isolates P10, P27, P19, and P2 showed 100% similarity to other species, and the evolutionary distances computed were consistent with the phylogenetic placement of the *OmpA* of the isolates within the *Chlamydia* species Figure 3.

PCR Amplification Success Rate for *Chlamydia trachomatis* (Total Samples: 40)

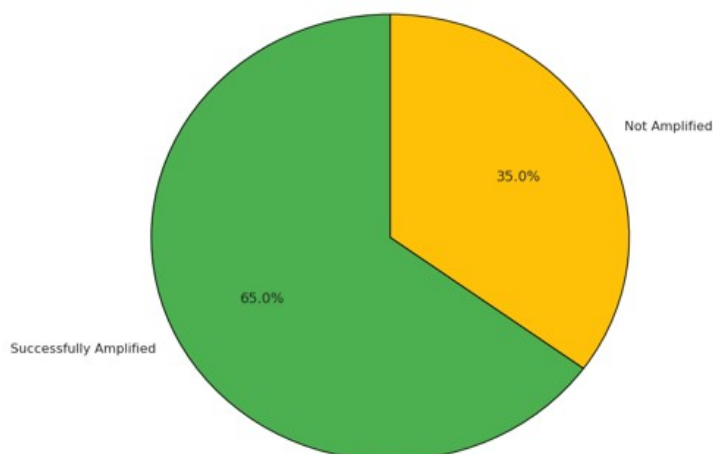


Figure 1: PCR Amplification Success Rate for *Chlamydia trachomatis*

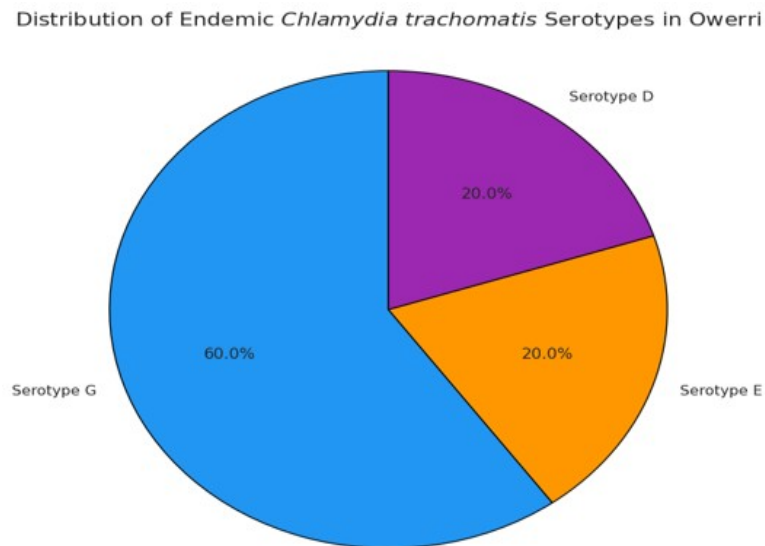


Figure 2: Distribution of Endemic *Chlamydia trachomatis* Serotypes in Owerri

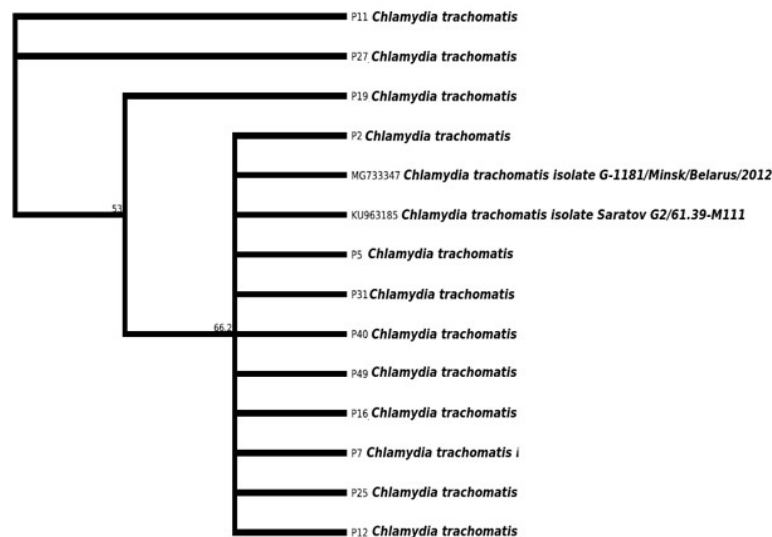


Figure 3: Phylogenetic Tree Based on the Nucleotide Sequence of the omp1 Gene Variable Domain Strains

The result presented in Figure 4 above showed no statistically significant difference ($p > 0.05$) in the magnitude of infection between symptomatic and asymptomatic subjects. This finding suggests a high prevalence of genital chlamydial infection among asymptomatic subjects in the population.

4. Discussion

This study aimed to investigate the molecular and sero-epidemiological prevalence of *Chlamydia trachomatis* infection in Owerri, Imo State, Nigeria, with a particular focus on the prevailing serotypes. Understanding the local epidemiology and serotype distribution is crucial for effective control strategies and public health interventions, especially given the largely asymptomatic nature of *C. trachomatis* infections and their severe reproductive health complications [1, 5].

The molecular characterization aspect of this study, utilizing Polymerase Chain Reaction (PCR), successfully amplified the ompA gene in 26 (65%) out of 40 samples, as depicted in Figure 1: PCR Amplification Success Rate for *Chlamydia trachomatis*. This molecular analysis further revealed that *Chlamydia trachomatis* serotypes E, G, and D were the prevailing endemic serovars in Owerri, with serovar G being the most common, as shown in Figure 2: Distribution of Endemic *Chlamydia trachomatis* Serotypes in Owerri. The Omp1A gene of isolates P10, P27, P19, and P2 showed 100% similarity to other species, and the computed evolutionary distances were consistent with the phylogenetic placement of the OmpA of these isolates within the *Chlamydia* species, as illustrated in Figure 3: Phylogenetic Tree Based on the Nucleotide Sequence of the omp1 Gene Variable Domain Strains. This finding is consistent with reports from other regions, such as the Slavic population [6], suggesting some commonality in circulating strains. The identification of specific serotypes is vital for understanding clonal diversification, transmission patterns, and the potential role of co-infection with multiple variants [6]. The predominance of serovar G is particularly noteworthy, as studies have linked it to an increased risk of cervical cancer [4], which has

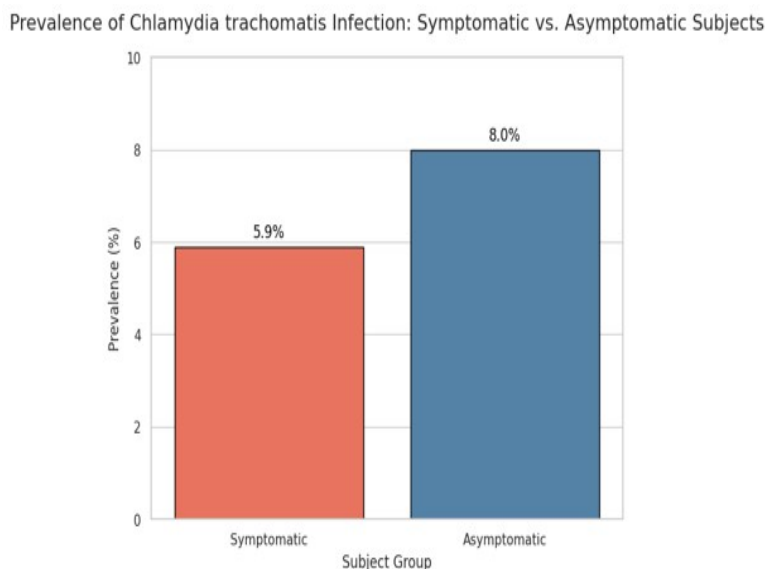


Figure 4: Comparison of *Chlamydia trachomatis* Infection between Symptomatic and Asymptomatic Subjects

significant public health implications for the region. The use of PCR, targeting the *ompA* gene, proved effective in identifying these active infections and their serotypes, highlighting its importance as a diagnostic gold standard [5].

The comparison of *Chlamydia trachomatis* infection between symptomatic and asymptomatic subjects, presented in Figure 4, showed no statistically significant difference ($p > 0.05$) in the magnitude of infection between these two groups. This finding reinforces the well-documented asymptomatic nature of *C. trachomatis* infection [5, 7]. The high prevalence among asymptomatic individuals highlights a significant public health challenge, as these individuals can unknowingly transmit the infection, contributing to its widespread dissemination and the development of severe long-term sequelae without overt symptoms. This implies that syndromic management alone may be insufficient for effective control in settings like Owerri, necessitating broader screening initiatives.

5. Conclusion

The high prevalence among asymptomatic individuals and the identification of potentially more virulent serotypes like G show a persistent public health challenge. The findings emphasize the need for comprehensive screening programs and targeted public health education campaigns to address the silent spread of *C. trachomatis* and mitigate its long-term health consequences in the region.

Article Information

Disclaimer (Artificial Intelligence): The author(s) hereby declare that NO generative AI technologies such as Large Language Models (ChatGPT, COPILOT, etc.), and text-to-image generators have been used during writing or editing of manuscripts.

Competing Interests: Authors have declared that no competing interests exist.

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