

OMP1 GENOTYPING OF *CHLAMYDIA TRACHOMATIS* FROM
BRAZILIAN PATIENTS

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Introduction: *Chlamydia trachomatis* is responsible for a wide range of inflammations in the urogenital tract of men and women, especially in the young population. Recent data alert to the high number of asymptomatic infections which are around 50% in the male population, reaching 75% in the female. **Objective:** To characterize the genotypes of *C. trachomatis* detected in women assisted at a STD Public Clinic. Endocervical samples were tested for chlamydial infection with PCR directed to the bacteria cryptic plasmid. Genotyping of positive samples were done after *omp1* amplification and sequencing. **Results:** The overall prevalence of *C. trachomatis* infection was 19%. We found 10 genetic variants out of a total of 12 *omp1* gene sequences and four genotypes were characterized: D, E, F and K. Minor sequence variations in genotype F were found and genotype E showed the highest mutation rate. We also found a co-infection of genotypes D and E in one woman. **Conclusions:** *C. trachomatis* genotyping is important for epidemiological studies. It also allows the characterization of mixed infections, which is important to investigate the efficacy of treatment and detection of *C. trachomatis* drug resistance.

Key words: *Chlamydia trachomatis*, *Chlamydia* genital infections,

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