

Chlamydia Trachomatis Infection and Distribution of Serovars in the Eastern Highlands Province, Papua New Guinea

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Abstract

We have used nested polymerase chain reaction (PCR) and the PCR-based endonuclease digestion method to genotype *Chlamydia trachomatis* serovars in 460 infected individuals from the Eastern Highlands Province of Papua New Guinea. Our study groups comprised women who presented in labour to the Goroka Base Hospital, their newborn infants, symptomatic children who presented to the hospital's Outpatients Department and men and women from 15 randomly selected villages in the Asaro Valley. In this analysis, the major outer membrane protein (MOMP) gene, *omp1*, of *C. trachomatis* was amplified using DNA obtained from the endocervix of women, urine from men, and both the eye and nasopharynx of children. Amplified DNAs were digested concurrently using *AluI* and a combination of *EcoRI*, *HinI* and *HpaII* restriction enzymes. The mixtures were separated on electrophoretic gels and the respective serovars designated on the basis of resolved digested DNA patterns. Our results, which were confirmed also by *omp1* sequence data, show serovars D, E, F, G, H and L3 to be present in the studied communities. The overall relative frequencies of these serovars were 30%, 21%, 25%, 1%, 20% and 2% respectively, with serovars D, E, F and H accounting for 97% of these infections. Double infections among these principal serovars were also detected in all our study groups but at a low overall frequency of 3%. Serovar D was the major agent involved in the aetiology of chlamydial infection in both children and adults though serovar F was the most frequent in newborn infants. Serovar H was relatively less frequent in symptomatic children. No trachoma-related serovars were detected, confirming the rarity of this disease in Papua New Guinea. In contrast, although clinical cases of lymphogranuloma venereum have not been described in the country, the detection of serovar L3 in this study suggests that it may occur. However, the association of L3 also with childhood infection indicates that it may be causing the same pathology as the serovars D-K that are associated with non-ulcerative sexually transmitted infections.