

Genotyping of *Chlamydophila pneumoniae* isolate in Moroccan patients with cardiovascular diseases

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Chlamydophila pneumoniae (*C. pneumoniae*) is an obligate intracellular bacterial pathogen characterized by a wide range of vertebrate host, which cause respiratory diseases and strongly involved in cardiovascular diseases. Both whole-genome sequencing and specific gene typing suggest that there is relatively little genetic variation in human isolates of *C. pneumoniae* worldwide.

The main objective of our study is to identify and characterize *C. pneumoniae* detected strains in peripheral blood mononuclear cells (PBMCs) and atheroma plaques tissue in Moroccan patients with cardiovascular diseases.

The DNA of 55 and 28 *C. pneumoniae* strains detected respectively in PBMCs and atheroma plaques tissue of patients with cardiovascular diseases were amplified by nested PCR using cpn5P/Cpn3P and Cpn5N/Cpn3N primers targeting 366 bp fragment of the outer-membrane protein-A (ompA) variable domain 4 (VD4) gene. The PCR products were sequenced in both directions using BigDye Terminator Chemistry in an automatic capillary DNA sequencer. The chromatograms were analyzed with BioEdit. Sequences were compared with entries retrieved from GenBank. The phylogenetic tree was constructed by using the MEGA6 software.

The sequences analysis and comparison with human *C. pneumoniae* reference strains isolated in different countries (J138, AR39, CWL029, IOL207, TOR1, AO3, LKK1) showed more than 98% homology. However many SNPs were revealed at different positions. The phylogenetic comparison between our strains and the previous human cited strains and animal once (African frog, koala, horse and Western barred bandicoot) showed an identity between our strains and other *C. pneumoniae* retrieved from GenBank. Furthermore, animal strains were shown basal with some of our strains on the phylogeny tree, suggesting a zoonotic transmission. Our results show that *C. pneumoniae* Moroccan detected strains are identical to the circulating once worldwide, and allow suggesting an inter-human or a zoonotic transmission.

Key words: *Chlamydophila pneumoniae*, Molecular characterization.