Abstract: Background and Objectives: Phospholipase of Mycobacterium tuberculosis plays an important role in pathogenesis through breaking up phospholipids and production of diacylglycerol. Phospholipase C genes include A, B, C and D segments. Three of these genes, plcA, plcB and plcC, are organized in tandem (locus plcABC). The fourth gene, plcD, is located in a different region. Tuberculosis remains a global threat to public health. The problem is further complicated by the emergence of multidrug-resistant tuberculosis as a consequence of the widespread use and incorrect administration of antibiotics. In these conditions, the Beijing MTB strain has attracted special attention because of its global emergence and resistance to multiple drugs. In this study, we examined the Beijing strains of Mycobacterium tuberculosis isolated from Iranian patients for the genes encoding this enzyme.

Materials and Methods: DNA extraction was performed using CTAB (cetyltrimethylammonium bromide) from positive culture specimens in tuberculosis patients. PCR was then used to amplify the plcA, plcB, plcC genes of Beijing strain, and non-Beijing strains were identified by spoligotyping.

Results: Of 200 specimens, 19 (9.5%) were Beijing strain and 181 (90.5%) were non-Beijing strains. The results of PCR for Beijing strains were as follows: 16 strains (84.2%) were positive for plcA, 17 (89.4%) were positive for plcB and 17 (89.4%) were positive for plcC genes. The standard strain (H37RV) was used as control.

Conclusion: The majority of Beijing strains have phospholipase C genes which can contribute to their pathogenesis but we need complementary studies to confirm the role of phospholipase C in pathogenicity of Mycobacterium tuberculosis.

Keywords: Mycobacterium tuberculosis, Beijing strains, phospholipase C.