Prevalence of *Chlamydia trachomatis* and Mutation of *L4,L22* and *23SrRNA* Genes in Patients with Ovarian Cancer Refered to Imam Hossein Hospital of Tehran in 2014

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Abstract

Background and aim: Ovarian cancer (Ovarian cancer) or a silent killer is the fifth common cancer and the second common cancer in women reproductive system and it is more than other types of cancer in these organs causes the deaths.No firm conclusions about the cause of ovarian cancer has been found,However, 10-15 percent of ovarian cancer cases can be attributed to genetic predisposition.In the majority of patients with ovarian cancer the disease diagnosed when their cancer is at an advanced stage.The aim of this study was to determine the prevalence of *Chlamydia trachomatis* and mutation of *L4,L22,23SrRNA* genes in patients with ovarian cancer who refered to Imam Hossein hospital of Tehran.

Materials and Methods: This study was conducted on 124 paraffinized ovarian tissue which obtained from 62 patients with ovarian cancer (case group) and 62 patients with benign ovarian hyperplasia (control group).All samples were analyzed with using Nested PCR method for the presence of *Chlamydia trachomatis*. Designed specific primers and using standard PCR method to determine the presence of *L4,L22,23SrRNA* genes after isolation of *Chlamydia trachomatis*.

Results: Nested PCR results showed that *Chlamydia trachomatis* was present in 22.5% of patients with ovarian cancer and in 0% of the control group. There was no positive identification of *Chlamydia trachomatis* in 62 ovarian tissue samples in control group. There was no mutation in *L4,L22,23SrRNA* genes.

Conclusions: Our results confirm the important role of *Chlamydia trachomatis* as a risk factor to develop ovarian cancer. Further studies are needed to determine the role of infectious agents in ovarian cancer,and to develop of new therapies and finally prevention of ovarian cancer.

Keywords: *Chlamydia trachomatis*,Ovarian Cancer,PCR