

Original paper

Screening and molecular characterization of *Trichomonas vaginalis* genotypes isolated from married women in northern Iran

Nasim SABER^{1,2}, Mehrazad SARAEE³, Elham HAJIALILO^{4,3}, Adel SPOTIN^{4,5},
Mohammad-Ali MOHAGHEGH⁶, Safar-Ali ALIZADEH⁷, Sama RASHIDI⁸,
Amir JAVADI⁹, Mohsen OSTADGHADERI¹⁰, Peyman HEYDARIAN^{1,3}

¹Medical Microbiology Research Center, Qazvin University of Medical Sciences, Qazvin, Iran

²Student Research Committee, School of Medicine, Qazvin University of Medical Sciences, Qazvin, Iran

³Department of Medical Parasitology and Mycology, School of Medicine, Qazvin University of Medical Sciences, Qazvin, Iran

⁴Immunology Research Center, Tabriz University of Medical Sciences, Tabriz, Iran

⁵Department of Parasitology and Mycology, Faculty of Medicine, Tabriz University of Medical Sciences, Tabriz, Iran

⁶Department of Laboratory Sciences, School of Paramedical Sciences, Torbat Heydariyeh University of Medical Sciences, Torbat Heydariyeh, Iran

⁷Department of Microbiology, Qazvin University of Medical Sciences, Qazvin, Iran

⁸Department of Parasitology and Mycology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran

⁹Department of Social Sciences, School of Medicine, Qazvin University of Medical Sciences, Qazvin, Iran

¹⁰Department of Epidemiology and Biostatistics, School of Public Health, Tehran University of Medical Sciences, Tehran, Iran

Corresponding Author: Peyman Heydarian; e-mail: p.heydarian@qums.ac.ir

ABSTRACT. *Trichomonas vaginalis* is an anaerobic protozoan parasite that causes trichomonosis in human. It is one of the most common non-viral sexually transmitted infections. It has been found to be most prevalent in patients referred to sexually transmitted disease clinics. In recent years, molecular methods have been used to identify genotypes of this parasite in different parts of the world and so far 6 types of *T. vaginalis* have identified. The aim of this study was to investigate the prevalence and genotype identification of *T. vaginalis* from married women in northern Iran. A total of 450 vaginal specimens were taken from married women, referring to health centers in northern Iran. Demographic information of women was collected through a questionnaire. The samples were first examined microscopically and then monitored in Dorsch culture medium for up to 10 days. Actin genes of positive samples were amplified by PCR. Finally, PCR products were used to determine the sequence and genotype of the parasite. Overall, 0.7% (3/450) samples were positive for *T. vaginalis*. All of the three infected women were housewives. After sequencing, the genotype of these parasites were type H (66.7%) (Accession no; MW414672-MW414673) and type E (33.3%) (Accession no; MW414671). Low prevalence of *T. vaginalis* in north of Iran indicate high level of hygiene in sexual intercourse and avoiding from high risk sexual behaviors, and also it seems that genotype H is dominant type of the parasite in the study area.

Keywords: *Trichomonas vaginalis*, women, genotype, actin gene, Iran

Introduction

Trichomonas vaginalis (*T. vaginalis*) is an anaerobic flagellate protozoan that causes trichomonosis. It is one of the most common non-viral sexually transmitted disease (STD) [1,2].

According to World Health Organization (WHO) reports, about 170 million people are infected with this infection annually, which varies according to the socio-cultural status of communities. The average prevalence of this infection has estimated at 5–20% [3,4]. The clinical manifestations of this