original article

Toxoplasma genotyping among infected human and animal hosts using PCR-Restriction Fragment Length Polymorphism: Study in Al-Madinah, Saudi Arabia

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ABSTRACT

Background and Objective

The progression and severity of *Toxoplasma* disease differ due to several variables, including host and parasite genetics. Exposing the possible correlation between the genotypes and the severity of the disease might be of value to identify the outcomes of the infection and hence, the proper management of infected cases. This study was conducted to identify the possible lineage type of *Toxoplasma* from blood samples of humans and animals for the first time in Al Madinah, Saudi Arabia.

Methods

Preliminary detection of *Toxoplasma* B1 gene was done by a nested PCR. Subsequent identification of *Toxoplasma* strain was done for 91 positive samples using PCR- Restriction fragment length polymorphism (RFLP) at the *SAG2* loci of *T. Gondii* and restriction enzymes *Hha*I and *Sau3*AI.

Results

Type II isolate was found to be the predominant one (45.1%). The other genotypes I and III were detected in 20.9% and 21.9% of cases respectively. The remaining 11 cases (12.1%) were of unknown genotypes. In general, there was no clear correlation between strain genotype and the different clinical forms. Except for genotype III which was not detected among the 7 congenitally infected cases, all the three classical types and the unknown one were detected in all clinical forms

Conclusion

It remains uncertain to what extent the genotype of the parasite directly contributes to the clinical severity of human toxoplasmosis. Further studies are recommended, using larger number of samples, especially in cases of congenital toxoplasmosis infection where treatment might be improved.

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INTRODUCTION

Toxoplasma gondii (T. gondii) is a common cause of infection in many warm-blooded animals, including humans. Between 15 and 85% of the world adult human population is chronically infected with *T. gondii* depending on geographical location.[1] Most cases of human infection are mild, but devastating disease can occur in immunocompromised individuals and congenitally infected fetuses in which the manifestations of the disease, which are mainly neurological or eye problems appear either early after labour or later on during life.[2] The progression and severity of the disease differ in patients due to several variables, including host and parasite genetics[3] and it is known that the virulence of *T. gondii* differs in animals, depending on the *T. gondii* strain.[4] There is no published data concerning genotypes of *T. gondii* in Saudi Arabia, knowing such information besides exposing the possible correlation between the severity of the disease and strain genotyping might be of value to identify the outcomes of the infection and hence proper management of infected cases.[5] Three classical genotypes named (types I, II, and III) are previously identified applying Restriction fragment length polymorphism (RFLP) which is commonly used for *T. gondii* strain identification in PCR-amplified *SAG2* loci.[2] Fuentes et al, 2001[6] had shown the possibility of performing the technique directly on clinical samples. Our aim in this study is to identify the possible lineage type of *Toxoplasma* from blood samples of humans and animals using RFLP in PCR-amplified *SAG2* loci of *Toxoplasma* products for the first time in Al Madinah, Saudi Arabia.

METHODOLOGY

Study population, sample collection and processing

Considering the ethical issues, human samples were collected from outpatient clinics of obstetrics and gynecology, neurosurgery and pediatrics in different setting (Taibah University, King Fahad hospital, Alsafa hospital, Almadinah, Saudi Arabia). Animal samples were collected from different farm animals in Almadinah. After clinical examination, 2 ml blood