To determine the genotypes of Toxoplasma gondii strains associated with human toxoplasmosis, we developed a sensitive approach for typing parasites grown from clinical samples by short-term in vitro culture. A newly described nested PCR assay was capable of amplifying genomic DNA from as few as five parasites in the presence of host tissues. Typing was based on DNA polymorphisms at the SAG2 locus, encoding tachyzoite surface antigen p22. Restriction fragment length polymorphisms in PCR-amplified SAG2 products were used to classify strains into one of the three major lineages of T. gondii. This approach was successfully used to determine the genotypes of 68 of 72 samples that had been previously isolated from patients with congenital, cerebral, and disseminated toxoplasmosis. Type II strains of T. gondii were found in a majority of the samples, accounting for 55 (81%) of the 68 toxoplasmosis cases. In contrast, type I and III strains were found in only 7 (10%) and 6 (9%) of the 68 cases, respectively. The results of this study support the previous finding that type II strains are most often associated with human toxoplasmosis. Nested PCR analysis at the SAG2 locus provides rapid assignment of T. gondii to a specific genotype that should be useful in analyzing a variety of clinical samples.

Toxoplasma gondii is a ubiquitous intracellular protozoan parasite that chronically infects approximately one-third of the adult human population in the United States and up to 85% of the adults in parts of Europe (3). Although infections with this parasite are typically non-pathogenic in healthy individuals, T. gondii causes substantial morbidity and mortality in immunocompromised patients (mainly AIDS patients and bone marrow and organ transplant recipients) (9, 10) and in congenitally infected infants (19). Substantial variation in the progression and severity of disease is observed between cases of toxoplasmosis, both congenital and immunocompromise related, and these differences are presumably due to several variables, including host (11, 17) and parasite (7, 15) genetics.

T. gondii has a highly clonal population structure (1, 6, 15), despite the opportunity for genetic recombination. Population genetic analysis based on restriction fragment length polymorphisms (RFLPs) indicates that T. gondii consists of only three clonal lineages, designated types I, II, and III, which occur in both animals and humans (6). In a previous study of 68 independent human strains, more than 70% of human disease cases of toxoplasmosis were associated with the type II strains (6). A similar pattern was also seen in a largely independent group of samples analyzed by multilocus isoenzyme electrophoresis (1). In contrast, both type II and III strains were equally prevalent in a sample of 34 naturally infected animals, suggesting a specific association of parasite genotype II with clinical disease in humans (6). However, all of these previously analyzed strains were isolated by repeated passage in mice and in vitro culture, and therefore the apparent frequencies of specific lineages may have been biased against strains that were more difficult to isolate. Consequently, it would be advantageous to develop methods to directly analyze the parasite genotype from primary clinical samples or following minimal parasite growth. Direct analysis would also provide valuable information on the genotypes of T. gondii strains in archived samples (e.g., cerebrospinal fluid [CSF], blood, culture slides, and formalin-fixed and paraffin-embedded tissues) from patients with clinical toxoplasmosis when isolation of live strains is not feasible.

In this report, we describe the development of an amplification-based assay for genetic analysis of the SAG2 locus. This assay was used to analyze 72 primary T. gondii isolates from fixed culture slides collected from toxoplasmosis patients between 1988 and 1996 at the Hôpital Saint-Louis, Paris, France.

**MATERIALS AND METHODS**

**Experimental samples.** The following representative strain types were used for standardization of PCR assays: strain RH (type I), strain Me49 or PLK (type II), and strain CEP (type III) (6). Parasites were grown in human foreskin fibroblast (HFF) cells and prepared as previously described (6). To test the sensitivity of nested SAG2 PCR, purified RH strain tachyzoites were used to spike samples of HFF cells, CSF, or normal mouse brain tissue. HFF monolayers grown on 16-mm round coverslips were fixed in cold acetone, air dried, and spiked with freshly isolated RH strain tachyzoites prior to extraction. Human CSF was obtained from a human immunodeficiency virus-positive patient with negative toxoplasma serology; PCR amplifications of the B1 locus were repeatedly negative for this sample. Mouse brain tissue was isolated from formalin-fixed, paraffin-embedded blocks by treatment with xylene followed by washing with 100% ethanol. Spiked and negative control samples were processed in parallel for nested SAG2 PCR as described above. Among each set of samples analyzed, a water blank was included in all steps of the PCR to ensure the absence of contamination of samples during analysis.

**Clinical samples.** Clinical samples were inoculated onto MRC5 monolayers grown on glass coverslips. After 4 days of incubation, the cultures were fixed with cold acetone, dried, and incubated with a rabbit anti-T. gondii primary antibody, followed by a fluorescent anti-rabbit secondary antibody (2). The coverslips were counterstained with Evans blue, mounted in phosphate-buffered saline–glycerol, and examined with a fluorescence microscope. The slides were assigned a score of 5 + 1 +, according to the number of parasites observed: 5 + corresponds to >10 parasites per microscopic field (magnification, ×200), 4 + corresponds to 1 to 10 parasites per microscopic field, 3 + corresponds to >50 parasites per coverslip, 2 + corresponds to 10 to 50 parasites per coverslip, and 1 + corresponds to <10 parasites per coverslip. Samples were stored at 4°C until analysis.

Over the course of a 10-year period, 72 toxoplasma-positive samples were obtained by this method. Forty-eight of the 72 samples were obtained from AIDS...
for amplification were shortened to encompass only the relevant polymorphisms. Primers were selected to separately amplify the 5’ and 3’ ends of the T. gondii SAG2 locus as 241-bp and 221-bp products, respectively. Digestion of the 5’ amplification products with Sau3AI distinguished allele 3 (type III strains) from alleles 1 and 2 (type I and II strains) (Fig. 1B), and digestion of the 3’ amplification products with HhaI distinguished allele 2 (type II strains) from alleles 1 and 3 (type I and III strains) (Fig. 1C).

To test the sensitivity of the nested PCR assay, normal host tissues were spiked with T. gondii parasites and used for nested PCR amplifications. SAG2 was readily amplified from samples of HFF cells that were spiked with 25 or 5 parasites, while no product was detected from control cultures to which no parasites were added (Fig. 2A). Likewise, SAG2 was successfully amplified when as few as five parasites were spiked into normal human CSF (Fig. 2B). In the absence of added parasites, this CSF sample was reproducibly negative by nested SAG2 PCR (data not shown). Amplification of SAG2 was slightly less sensitive in the presence of mouse brain tissue, and a positive signal was detected only from samples spiked with 25 parasites (Fig. 2B). Negative controls remained free of amplified products (Fig. 2 and data not shown).

A collection of fixed culture slides containing parasites from 72 unrelated toxoplasmosis patients were analyzed in this study. The number of parasites observed on most of the slides was low, with 52 (72%) of the slides scored only 1+ or 2+ (corresponding to fewer than 50 parasites in a background of approximately 10⁵ host cells). Despite the low number of parasites on many of the slides, amplification of both the 5’ and 3’ ends of the SAG2 locus from 68 of the 72 samples was successful. The four slides that were untypeable were scored 1+ or 2+ and were derived from three AIDS cases (two disseminated and one pneumonitis) and one congenital case. The failure to amplify the SAG2 locus from these samples was presumably a result of too few parasites or poor sample preservation.

No mixed infections were detected, and all 68 of the successfully amplified samples were assigned to one of three distinct lineages based on SAG2 alleles detected by RFLP analysis. Most of the strains, including 55 (81%) of the 68 samples, belonged to the type II lineage (Table 1). Type I strains were found in seven samples (10%), and type III strains were found in one sample (1%).
in six samples (9%). Of the 45 samples from AIDS patients successfully analyzed, 34 (76%) contained a type II strain of *T. gondii*. All 13 of the samples from cases of congenital toxoplasmosis contained a type II strain, while 6 of the 10 samples from non-AIDS immunosuppressed patients were found to contain type II strains. No correlations were apparent between the genotype of parasite strains and clinical presentation or the slide score based on in vitro growth (data not shown). There was also no correlation between the genotype of the parasites detected and the source of the clinical samples (i.e., bronchoalveolar lavage, biopsy, or blood leukocytes) (data not shown).

**DISCUSSION**

In the present report, we describe a rapid and efficient protocol for determining the genotype of *T. gondii* strains isolated from congenital, cerebral, and disseminated toxoplasmosis by short-term growth on MRC5 coverslip monolayers. Nested PCR amplification of the *SAG2* locus, followed by RFLP analysis, allowed assignment of all samples to one of three specific lineages of *T. gondii*. Type II strains of *T. gondii* were most often encountered in these samples, providing further evidence that strains of this genotype cause the majority of toxoplasmosis in humans.

PCR has previously been used for detection of *T. gondii* in clinical samples from patients with toxoplasmosis (18). Most investigators have used the *B1* or *SAG1* gene for detection (18); however, these loci are not sufficiently polymorphic to allow strain typing (6, 6a, 15). Consequently, we chose to develop a nested PCR assay based on the polymorphic *SAG2* locus (6). This gene is ideally suited for rapid genotyping, as it contains multiple lineage-specific polymorphisms. *SAG2* encodes two separate forms of the surface tachyzoite protein p22 that are recognized by strain-specific monoclonal antibodies: type I and III strains share the same protein allele, while type II strains have a second, distinct form (5, 12). Additional polymorphisms are present at the DNA level, allowing all three clonal genotypes to be rapidly identified by RFLP analysis at this single locus (6). Relying on a single marker for genotyping is generally not possible; however, in this case it is supported by the unusual population structure of *T. gondii*. Type II strains of *T. gondii* are most often encountered in these samples, providing further evidence that strains of this genotype cause the majority of toxoplasmosis in humans. The high prevalence of type II strains in human toxoplasmosis may simply reflect the source of strains that lead to human infection. We have previously reported that chronic infections of domestic and wild animals were equally split between type II and III strains (6). However, recent studies involving larger numbers of strains isolated from agricultural food animals indicate a high prevalence of type II strains in animals such as pigs in the United States (11a) and sheep in the United Kingdom (17a). These recent studies indicate a potentially important epidemiological link between chronic infections in some food animals that may underlie the prevalence of *T. gondii* genotypes causing human disease.

The nested *SAG2* PCR assay described here is highly sensitive, being able to detect as few as five parasites in samples that also contain mammalian genomes. Consequently, it should also be possible to use this analysis on primary clinical samples to detect toxoplasmosis. Nested *SAG2* PCR analysis has the advantage of also providing rapid, unambiguous assignment of a parasite genotype by RFLP analysis. The nested PCR assay makes possible additional retrospective studies on clinical samples that have been archived over the years in different laboratories; these studies are important, as they will provide a better understanding of the association between parasite genotypes and human toxoplasmosis.

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**TABLE 1. Prevalence of *T. gondii* strain types in clinical samples**

<table>
<thead>
<tr>
<th>Clinical condition (no. of samples)</th>
<th>Type I</th>
<th>Type II</th>
<th>Type III</th>
</tr>
</thead>
<tbody>
<tr>
<td>AIDS (45)</td>
<td></td>
<td>0</td>
<td>3</td>
</tr>
<tr>
<td>Encephalitis</td>
<td></td>
<td>2</td>
<td>4</td>
</tr>
<tr>
<td>Pneumonitis</td>
<td></td>
<td>3</td>
<td>17</td>
</tr>
<tr>
<td>Disseminated infection</td>
<td></td>
<td>1</td>
<td>10</td>
</tr>
<tr>
<td>Unclassified infection</td>
<td></td>
<td>6 (13)</td>
<td>34 (76)</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td>7 (10)</td>
<td>55 (81)</td>
</tr>
<tr>
<td>Non-AIDS immunosuppression (10)</td>
<td></td>
<td>1 (10)</td>
<td>8 (80)</td>
</tr>
<tr>
<td>Congenital infection (13)</td>
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<td>13 (100)</td>
</tr>
<tr>
<td>Total (68)</td>
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<td>7 (10)</td>
<td>55 (81)</td>
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REFERENCES


